

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2005, 15:26:51 ; Search time 274 Seconds
(without alignments)
4042.634 Million cell updates/sec

Title: US-10-009-002-2

Perfect score: 13376
Sequence: 1 MPVISTGTPVPAPTRKNK.....KYLAVIVFALGLIAVLAI 2864

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15376	100.0	2864	4 AAB59171	Aab59171 Protein e
2	15366	99.9	2864	6 ADA77730	Ada77730 Genomic h
3	15317	99.6	2864	2 AAR82072	Aar82072 Hepatitis
4	15317	99.6	2864	3 AAB09268	Aab09268 Hepatitis
5	7380	48.0	1422	2 AAB09038	Aab09038 Hepatitis
6	7375	48.0	1422	2 AAR82068	Aar82068 Hepatitis
7	3277.5	21.3	3033	4 AAB31168	Aab31168 Amino aci
8	3277.5	21.3	3033	4 AAB59172	Aab59172 Protein e
9	3277.5	21.3	3033	4 AAB30729	Aab30729 Amino aci
10	3268.5	21.3	3033	2 AAR33539	Aar33539 NANBH vir
11	3265.5	21.2	3033	5 ABG33688	Abg33688 Human HCV
12	3263	21.2	3010	5 ABG32457	Abg32457 Hepatitis
13	3262	21.2	3010	5 ABG32451	Abg32451 Hepatitis
14	3262	21.2	3010	5 ABG32460	Abg32460 Hepatitis
15	3262	21.2	3010	5 ABG32453	Abg32453 Hepatitis
16	3262	21.2	3010	5 ABG32461	Abg32461 Hepatitis
17	3260	21.2	3010	5 ABG32458	Abg32458 Hepatitis
18	3260	21.2	3010	5 ABG32459	Abg32459 Hepatitis
19	3260	21.2	3033	2 AAR33538	Aar33538 NANBH vir
20	3258	21.2	3010	5 ABG32454	Abg32454 Hepatitis
21	3256	21.2	3010	5 ABG32455	Abg32455 Hepatitis
22	3256	21.2	3010	5 ABG32452	Abg32452 Hepatitis
23	3253	21.2	3010	4 AAB59174	Aab59174 Protein e
24	3252.5	21.2	3011	5 ABG32456	Abg32456 Hepatitis
25	3247	21.1	3010	2 AAW98022	Aaw98022 Infectiou

26	3247	21.1	3010	4 AAB31170	Aab31170 Amino aci
27	3247	21.1	3010	8 ADO36227	Ado36227 Hepatitis
28	3247	21.1	3010	8 ADO79401	Ado79401 Hepatitis
29	3234.5	21.0	3011	5 AAU84597	Aau84597 HCV poly
30	3232	21.0	3010	5 AAE20477	Aae20477 HCV-S1 fu
31	3228	21.0	2984	4 AAE00447	Aae00447 Hepatitis
32	3226	21.0	2984	4 AAE00442	Aae00442 Hepatitis
33	3223	21.0	3010	2 AAY06423	Aay06423 Non-A, no
34	3223	21.0	3010	7 ADF88597	Adf88597 Hepatitis
35	3222.5	21.0	3011	2 AAR66995	Aar66995 Hepatitis
36	3220	20.9	2984	4 AAE00449	Aae00449 Hepatitis
37	3218	20.9	3010	2 AAR20111	Aar20111 Non-A, no
38	3218	20.9	3010	2 AAR20091	Aar20091 Non-A, no
39	3217	20.9	3010	2 AAR68864	Aar68864 Hepatitis
40	3216	20.9	3010	2 AAR68622	Aar68622 HCV prote
41	3216	20.9	3010	2 AAR82694	Aar82694 Partial H
42	3214.5	20.9	3011	4 AAB59173	Aab59173 Protein e
43	3214.5	20.9	3011	4 AAB31169	Aab31169 Amino aci
44	3214.5	20.9	3011	5 AAU79221	Aau79221 Hepatitis
45	3214.5	20.9	3011	8 ADJ56744	Adj56744 Hepatitis

ALIGNMENTS

RESULT 1
AAB59171
ID AAB59171 standard; protein; 2864 AA.
XX
AC AAB59171;
XX
DT 11-SEP-2003 (revised)
DT 21-MAR-2001 (first entry)
XX
DE Protein encoded by infectious GB virus B genome.
XX
KW GBV-B; hepatitis C virus; HCV; vaccine.
XX
OS Hepatitis GB virus B.
XX
PN WO200075337-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015293.
XX
PR 04-JUN-1999; 99US-0137694P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Bukh J, Yanagi M, Emerson SU, Purcell RH;
XX
DR WPI; 2001-091214/10.
XX
PT New infectious nucleic acids of the GB virus-B clone, useful for indirectly studying the molecular properties of hepatitis C virus (HCV) and in developing vaccines and therapeutics for HCV.
XX
PS Disclosure; Page 64-75; 96pp; English.
XX
CC The present invention relates to GB virus-B. The nucleic acid molecules of the invention are useful for indirectly studying the molecular properties of hepatitis C virus (HCV). The infectious nucleic acid sequence of the GB virus-B clone and the HCV/GBV-B chimera may be used in the development of vaccines and therapeutics for HCV. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 2864 AA;

Query Match 100.0%; Score 15376; DB 4; Length 2864;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 2864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPVISTQSPVAPRTRKNKQTOQASYPVSIKTSVERGORAKRKVQORDAPRPNYKIAGIHD 60
DB 1 MPVISTQSPVAPRTRKNKQTOQASYPVSIKTSVERGORAKRKVQORDAPRPNYKIAGIHD 60
QY 61 GLQTLAQAALPAHNGRQDPRHKSRLNLGILDYPLGWI G DVVTHTPPLVPLVAGAVRPV 120
DB 61 GLQTLAQAALPAHNGRQDPRHKSRLNLGILDYPLGWI G DVVTHTPPLVPLVAGAVRPV 120
QY 121 COI VRLLEDGWNWATGWFVGHLPVVCCLASLAPCSCGARVTDPTNTTILTNCCQBNQVIY 180
DB 121 COI VRLLEDGWNWATGWFVGHLPVVCCLASLAPCSCGARVTDPTNTTILTNCCQBNQVIY 180
QY 181 CSPSTCLHEPGCVICADCECWPNANPYISHPSNWTGDSFLADHIDFVMGALVTCDALDIG 240
DB 181 CSPSTCLHEPGCVICADCECWPNANPYISHPSNWTGDSFLADHIDFVMGALVTCDALDIG 240
QY 241 ELCGACVLVGWLVNRHLIHIIDLNETGTCYLEVPTGIDPGFLGFTGMWAGKVEAVIFLTK 300
DB 241 ELCGACVLVGWLVNRHLIHIIDLNETGTCYLEVPTGIDPGFLGFTGMWAGKVEAVIFLTK 300
QY 301 LASQVPYAIATMFSSVHYLAVGALIIYASRGKWQLLALMLYI EATSGNPIRVP TGCSI 360
DB 301 LASQVPYAIATMFSSVHYLAVGALIIYASRGKWQLLALMLYI EATSGNPIRVP TGCSI 360
QY 361 AEFCSPLMIPCCHSYLSENSEVICYSPKWTRPITILEYNNISISWYPYTI PGARGCMVKF 420
DB 361 AEFCSPLMIPCCHSYLSENSEVICYSPKWTRPITILEYNNISISWYPYTI PGARGCMVKF 420
QY 421 KNTWGCCRIRNVPSCYTMGTDAVNDTRNTYEACGVTPWLTTAWHNGSALKJAILQYPG 480
DB 421 KNTWGCCRIRNVPSCYTMGTDAVNDTRNTYEACGVTPWLTTAWHNGSALKJAILQYPG 480
QY 481 SKEMFKPHNWSGHLVFGSDTPIVYFDPVNSTLLPPERWARLPCTPPVVRGSLQVPQ 540
DB 481 SKEMFKPHNWSGHLVFGSDTPIVYFDPVNSTLLPPERWARLPCTPPVVRGSLQVPQ 540
QY 541 GFYSDVKDLATGLITKDAWKNYQVLYSATGALSITGVTTKAVVLILGLGCKSKYLILAY 600
DB 541 GFYSDVKDLATGLITKDAWKNYQVLYSATGALSITGVTTKAVVLILGLGCKSKYLILAY 600
QY 601 LCYLSLFCGRASGYPLRPLVPSQSYLQAGWDVLSKAQVAPFALIPFI CCYLRCRLRYAAL 660
DB 601 LCYLSLFCGRASGYPLRPLVPSQSYLQAGWDVLSKAQVAPFALIPFI CCYLRCRLRYAAL 660
QY 661 LGFVPMAGLPLTFFVAAAQAQPDVDMVRLIVAGLWAGNRGHR TALLVGPMP LVAL 720
DB 661 LGFVPMAGLPLTFFVAAAQAQPDVDMVRLIVAGLWAGNRGHR TALLVGPMP LVAL 720
QY 721 LTLHLVTPASAFDTEIIGGLTIPPVVALVMSRFGFFAHLLPRCALVNSYLMQRWENWF 780
DB 721 LTLHLVTPASAFDTEIIGGLTIPPVVALVMSRFGFFAHLLPRCALVNSYLMQRWENWF 780
QY 781 WNVTLRPERFPLVLCVFPGATVDALVTPCVCHVALLCLITSSAASFFGTDSRVRAHRMLVR 840
DB 781 WNVTLRPERFPLVLCVFPGATVDALVTPCVCHVALLCLITSSAASFFGTDSRVRAHRMLVR 840
QY 841 LGKCHAWTSHVYLFKFFLAVFGENGVFFYKHLHGDVLPNDPASKLPQBPFPFPEGKARVY 900
DB 841 LGKCHAWTSHVYLFKFFLAVFGENGVFFYKHLHGDVLPNDPASKLPQBPFPFPEGKARVY 900
QY 901 RNEGRRLACGDTVDGLPVVARGDLVFAGLAMPDPGMAITAPFTIQCCLSERGTLSAMAVV 960
DB 901 RNEGRRLACGDTVDGLPVVARGDLVFAGLAMPDPGMAITAPFTIQCCLSERGTLSAMAVV 960
QY 961 MTGIDPRTWTGTIFRLGSLATSYMGFVCDNVLYTAHHGSKGRLAHP TGSIHPI TVDAAN 1020
DB 961 MTGIDPRTWTGTIFRLGSLATSYMGFVCDNVLYTAHHGSKGRLAHP TGSIHPI TVDAAN 1020
QY 1021 DODIYQPPCGAGSLTRCSCGETKGVLVTRGLSLVEVNSKDDPYWCVC GALPMNAVAKGSSG 1080
DB 1021 DODIYQPPCGAGSLTRCSCGETKGVLVTRGLSLVEVNSKDDPYWCVC GALPMNAVAKGSSG 1080
QY 1081 APILCSSGHVIGMFTAARNSGGSVSIQIRVRPLVCAGYHPQVTAHATLDTKTPTVPNEYSVQ 1140

DB 1081 APILCSSGHVIGMFTAARNSGGSVSIQIRVRPLVCAGYHPQVTAHATLDTKTPTVPNEYSVQ 1140
QY 1141 ILIIAPTSGSKSTKLPLSYMQBKEIVLVLPNSVATTASMPKYMHAATYGVNPNCYFNGKCTN 1200
DB 1141 ILIIAPTSGSKSTKLPLSYMQBKEIVLVLPNSVATTASMPKYMHAATYGVNPNCYFNGKCTN 1200
QY 1201 TGA SLTSTYTGMYLTGACSRNYDVIICDECHATDATTVLGIGKVLTEAPSKNRLVLV LAT 1260
DB 1201 TGA SLTSTYTGMYLTGACSRNYDVIICDECHATDATTVLGIGKVLTEAPSKNRLVLV LAT 1260
QY 1261 ATPFGVIPTPHANITEIQLTDEGTIPPHGKKIKEENLKKGRHLIFEATKKHCD ELANELA 1320
DB 1261 ATPFGVIPTPHANITEIQLTDEGTIPPHGKKIKEENLKKGRHLIFEATKKHCD ELANELA 1320
QY 1321 RKGITAVSYRGCDISKIPEGDCV VVATDALCTGTGDFSDVDCSLMVEGTCHVDL DPT 1380
DB 1321 RKGITAVSYRGCDISKIPEGDCV VVATDALCTGTGDFSDVDCSLMVEGTCHVDL DPT 1380
QY 1381 FTMGVRVCGVS AIVKGORRGRTGRAGIYVYVDGSC TTPSGMVPECNIVEAFDAAKAWYG 1440
DB 1381 FTMGVRVCGVS AIVKGORRGRTGRAGIYVYVDGSC TTPSGMVPECNIVEAFDAAKAWYG 1440
QY 1441 LSSTEAQTIILDTYRTQPLPAIGANLDEWADLF SMVNPPEPSFVN TAKRTADNYLLTAAQ 1500
DB 1441 LSSTEAQTIILDTYRTQPLPAIGANLDEWADLF SMVNPPEPSFVN TAKRTADNYLLTAAQ 1500
QY 1501 LQLCHQVGYAAPNDAPRWQARGKPCGVLRJLDGADACPGPEPSEVTRYQMC FTEVNT 1560
DB 1501 LQLCHQVGYAAPNDAPRWQARGKPCGVLRJLDGADACPGPEPSEVTRYQMC FTEVNT 1560
QY 1561 SGTAAALAVGCVNAVAYLAIDTFGATCVRRCWSITSVPTGATVAPV DDEEIVEECASFI P 1620
DB 1561 SGTAAALAVGCVNAVAYLAIDTFGATCVRRCWSITSVPTGATVAPV DDEEIVEECASFI P 1620
QY 1621 LEAMVAAIDKLKSTITTTSPFTLEALEKNTFLGPHAAATILAIIEYCCGLVTLTPDN PFA 1680
DB 1621 LEAMVAAIDKLKSTITTTSPFTLEALEKNTFLGPHAAATILAIIEYCCGLVTLTPDN PFA 1680
QY 1681 SCVFAFAGITTPPHKIKMPLSLFGGAIASKLTDARGALAFMMAGAGTAGLTWTSVGF 1740
DB 1681 SCVFAFAGITTPPHKIKMPLSLFGGAIASKLTDARGALAFMMAGAGTAGLTWTSVGF 1740
QY 1741 VFDMLGGYAAASSTACLT EFKLGMGEWPTMDQAGLVTSAFNPAAGVGVLSACAMFALT T 1800
DB 1741 VFDMLGGYAAASSTACLT EFKLGMGEWPTMDQAGLVTSAFNPAAGVGVLSACAMFALT T 1800
QY 1801 AGPDHWPNRLLTMLARSNTVCNEYFIATRDTRRRIKILGILEASTPWSVISACIRMLHTPTE 1860
DB 1801 AGPDHWPNRLLTMLARSNTVCNEYFIATRDTRRRIKILGILEASTPWSVISACIRMLHTPTE 1860
QY 1861 DDCGLIANGLEIWOYVCNFFVVICENVLKAGVQSMVNI PGCPFYSCQKYGKPGWIGSGMLQ 1920
DB 1861 DDCGLIANGLEIWOYVCNFFVVICENVLKAGVQSMVNI PGCPFYSCQKYGKPGWIGSGMLQ 1920
QY 1921 ARCPGCGAELIFSVBNGFAKLYKGPRTC SNYWRGAVPVNARLCGSARPDPTDWTSLV VNYG 1980
DB 1921 ARCPGCGAELIFSVBNGFAKLYKGPRTC SNYWRGAVPVNARLCGSARPDPTDWTSLV VNYG 1980
QY 1981 VRDYCKYKMGDHI FVTAVSSPNVCFTQVPPTLRAAAVADGVQVQCYLGE PKTPMTWTSAC 2040
DB 1981 VRDYCKYKMGDHI FVTAVSSPNVCFTQVPPTLRAAAVADGVQVQCYLGE PKTPMTWTSAC 2040
QY 2041 CYGPDGKGKTVKLPFRVDGHTPGVRMQLNLRDAL ETNDCNSTNTNTPSD EAAVSALVFKEQ 2100
DB 2041 CYGPDGKGKTVKLPFRVDGHTPGVRMQLNLRDAL ETNDCNSTNTNTPSD EAAVSALVFKEQ 2100
QY 2101 LRRTNQLLEATSAGVDITTKLPAPSI EEVVRKROFRARTGSLTLP PPRPSVPGVSCPSL 2160
DB 2101 LRRTNQLLEATSAGVDITTKLPAPSI EEVVRKROFRARTGSLTLP PPRPSVPGVSCPSL 2160
QY 2161 QRSDFLEGSPSLPPSPVQLQAMPMP LLGAGECNPFTTAIGCAMTETGCGPD DLPSYPKK 2220


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Db 2161 QRSPLGSPNLPSPVVLQALPMPILLGAGCNPFTTAICAMTETGGPDDLPSPYPPK 2220
Qy EVSWSDESSTATTASSYVTGPPYKIRGKDSQSAKAPAKRPTKKLKGKSEFSCSMSTW 2280
Db 2221 EVSWSDESSTATTASSYVTGPPYKIRGKDSQSAKAPAKRPTKKLKGKSEFSCSMSTW 2280
Qy TDVISFKTASKVLASATRAITSGFLKQKSLVYVTEPRDAELRKQKVTINRQPLFPSPYHKQ 2340
Db 2281 TDVISFKTASKVLASATRAITSGFLKQKSLVYVTEPRDAELRKQKVTINRQPLFPSPYHKQ 2340
Qy VRLAKEKASKVGVWMDYDEVAATTPSKAKSHITGLRGTDVRSAGARKAVLDLQKVEA 2400
Db 2341 VRLAKEKASKVGVWMDYDEVAATTPSKAKSHITGLRGTDVRSAGARKAVLDLQKVEA 2400
Qy GEIPSHYRQTVIVPKEEVFKTPQKPKPRLISYPHLEMRCKEKMYYGOVAPDVVKAV 2460
Db 2401 GEIPSHYRQTVIVPKEEVFKTPQKPKPRLISYPHLEMRCKEKMYYGOVAPDVVKAV 2460
Qy MGDAYGFVDPRTVRKRLLSMMSPDVAGATCDTVCFDSTITPEDIMVETDIYSAKLSDQH 2520
Db 2461 MGDAYGFVDPRTVRKRLLSMMSPDVAGATCDTVCFDSTITPEDIMVETDIYSAKLSDQH 2520
Qy RAGIHTIARQLYAGPIIADYDREIGYRRCSSGYTTSSNSLTCWLKVNAAAEQAGMK 2580
Db 2521 RAGIHTIARQLYAGPIIADYDREIGYRRCSSGYTTSSNSLTCWLKVNAAAEQAGMK 2580
Qy NPFLICGDDCTVIWKSAGADADQAMRVFASMMKVMGAPQDCVPQPKYSLLEELTSCSN 2640
Db 2581 NPFLICGDDCTVIWKSAGADADQAMRVFASMMKVMGAPQDCVPQPKYSLLEELTSCSN 2640
Qy VTSGITKSGPYYFLTRDRIPLGRCSAEGILGYNPSAAWIGYLIHHPCLWVSRLVAHF 2700
Db 2641 VTSGITKSGPYYFLTRDRIPLGRCSAEGILGYNPSAAWIGYLIHHPCLWVSRLVAHF 2700
Qy MEQMLFEDKLPETVTFDYGKNTVVPVEDLPSIIAGVHGIEAFSVRYTNAEILRVSQSL 2760
Db 2701 MEQMLFEDKLPETVTFDYGKNTVVPVEDLPSIIAGVHGIEAFSVRYTNAEILRVSQSL 2760
Qy TDMTPPLRAWRKKARAVLASAKRGGAHAKLARFLWHATSRPLDLDKTSVARYTTFN 2820
Db 2761 TDMTPPLRAWRKKARAVLASAKRGGAHAKLARFLWHATSRPLDLDKTSVARYTTFN 2820
Qy YCDVYSPGDFVITPQRRLQKFLVKYLAVIVFALGLIAVGLAIS 2864
Db 2821 YCDVYSPGDFVITPQRRLQKFLVKYLAVIVFALGLIAVGLAIS 2864

RESULT 2
ADA77730
ID ADA77730 standard; protein; 2864 AA.
XX
AC ADA77730;
XX
DT 20-NOV-2003 (first entry)
XX
DE Genomic hepatitis B virus B (GBV-B) replicon protein sequence.
XX
KW GB virus-B; GBV-B; replicon; autonomous replication; NS3-NS5B; HCV;
KW hepatitis C virus; antiviral; anti-HCV; neomycin phosphotransferase gene;
KW neo.
XX
OS Hepatitis B virus B.
XX
FH Key Location/Qualifiers
FT Protein 2275..2864
FT /note= "Non structural protein 5B, RNA dependent RNA
FT polymerase"
XX
PN WO2003059944-A2.
XX
PD 24-JUL-2003.
XX
PF 13-JAN-2003; 2003WO-EP000281.
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XX
PR 15-JAN-2002; 2002US-0348573P.
XX 06-JUN-2002; 2002US-0386655P.
XX (RICE-) 1ST RICERCHE BIOL MOLECOLARE ANGELETTI.
XX De Tomassi A, Graziani R, Paonessa G, Traboni C;
XX WPI; 2003-598503/56.
XX N-PSDB; ADA7752.
XX
XX New GB virus B (GBV-B) replicon for identifying compounds that inhibit
XX GBV-B or hepatitis C virus, comprises a GBV-B 5' UTR, a selection or
XX reporter sequence, an internal ribosome entry site, an NS3-NS5B sequence,
XX and a GBV-B 3' UTR.
XX Disclosure; Fig 3; 81pp; English.
XX
XX This invention relates to a novel GB virus-B (GBV-B) replicon and
XX replicon enhanced cells. A GBV-B replicon is an RNA molecule able to
XX autonomously replicate in a cultured cell to produce detectable levels of
XX one or more GBV-B proteins. Specifically, it may comprise the GBV-B 5'
XX UTR, GBV-B structural region, selection or reporter sequence, internal
XX ribosome entry site, NS3-NS5B sequence, and GBV-B 3' UTR. Accordingly,
XX they are useful in providing tools for studying GBV-B replication,
XX polypeptide production and processing, identifying compounds that inhibit
XX GBV-B, providing a surrogate model for identifying compounds that inhibit
XX HCV, and providing a scaffold for producing GBV-B/HCV chimeric replicons.
XX Due to the similarity between GBV-B and the hepatitis C virus (HCV),
XX compounds that inhibit GBV-B may be useful antiviral agents, specifically
XX anti-HCV agents. The GBV-B subgenomic replicon constructs termed GBV-B-
XX neo-RepA (neo-RepA), neo-RepB, neo-RepC and neo-RepD were produced by
XX replacing the regions coding for structural proteins and the NS2 protein
XX with the sequences of neomycin phosphotransferase gene (neo) and
XX encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) in
XX the plasmid FL3/pAC7C177. This polypeptide sequence is the GBV-B replicon
XX protein sequence of the invention.
XX
XX Sequence 2864 AA;
XX
XX Query Match 99.9%; Score 15366; DB 6; Length 2864;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 2860; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPVISTQTSVPAPRTKRNKQTSQSPVSIKTSVERGQAKRKVQDARPRNYKIAGIHD 60
Db 1 MPVISTQTSVPAPRTKRNKQTSQSPVSIKTSVERGQAKRKVQDARPRNYKIAGIHD 60
Qy 61 GLQTLAQAALPAHGWGRQDPRHKSRLGILLDYPVGWIGDVTTHTPLVGPLVAGAVRPV 120
Db 61 GLQTLAQAALPAHGWGRQDPRHKSRLGILLDYPVGWIGDVTTHTPLVGPLVAGAVRPV 120
Qy 121 QIVRLLEDGWNWATGFWGHVLFVCLLSLACSCSGARVTDPTNTTILNCCORNOVIY 180
Db 121 QIVRLLEDGWNWATGFWGHVLFVCLLSLACSCSGARVTDPTNTTILNCCORNOVIY 180
Qy 181 CSPSTCLHEPGCVICADCECWPNAPYISHPSNWTGDSFLADHIDFVWGALVTCDAIDIG 240
Db 181 CSPSTCLHEPGCVICADCECWPNAPYISHPSNWTGDSFLADHIDFVWGALVTCDAIDIG 240
Qy 241 ELCGACVLVDLVRHRLIHDNETGTCYLEVPTGIDPGFLGFGIMWAGKVEAIFLTK 300
Db 241 ELCGACVLVDLVRHRLIHDNETGTCYLEVPTGIDPGFLGFGIMWAGKVEAIFLTK 300
Qy 301 LASQVPIATMFSSVHYLAVGALIIYASRGKYLQALLMLLYEATSGNPIRPTGCSI 360
Db 301 LASQVPIATMFSSVHYLAVGALIIYASRGKYLQALLMLLYEATSGNPIRPTGCSI 360
Qy 361 AEFCSPLMI PCCHSYLSENVSEVICSPKWTPTITLEYNNISWYPTIIPGARGCWVKF 420
Db 361 AEFCSPLMI PCCHSYLSENVSEVICSPKWTPTITLEYNNISWYPTIIPGARGCWVKF 420
Qy 421 KNNTWGCCIRIRNVP SYCTMGTDVAVNDTRNTYEAGVTPLMTTAWHNGSALKLAILQYPG 480
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||||| 421 KNNTWGCCIRNVPSTGMDTAVWMDTRNTYEACGVTPWLTATWHNGSALKLAILQYFG 480
QY SKEMFKPHNMWSGHLYFGSDTPIVYFVDPVNSTLLPPERWARLPGTTPVVRGSMLOVQ 540
Db SKEMFKPHNMWSGHLYFGSDTPIVYFVDPVNSTLLPPERWARLPGTTPVVRGSMLOVQ 540
QY GFYSDVKDLATGLITKDKAWKNYQVLYSATGALSITGVTTKAVVLILGLGSGSKYLILAY 600
Db GFYSDVKDLATGLITKDKAWKNYQVLYSATGALSITGVTTKAVVLILGLGSGSKYLILAY 600
QY LCYLSLFCGRASGYPLRPVLPSQSYLOQAGWDVLSKAQVAPFALIPFI CCYLRCRLRYAAL 660
Db LCYLSLFCGRASGYPLRPVLPSQSYLOQAGWDVLSKAQVAPFALIPFI CCYLRCRLRYAAL 660
QY LGFVPMAGLPLTFEPVAAAQPDYDWMVRLLVAGLVWAGNRGHR TALLVGPWPLVAL 720
Db LGFVPMAGLPLTFEPVAAAQPDYDWMVRLLVAGLVWAGNRGHR TALLVGPWPLVAL 720
QY LTLLHLVTPASAFDTEIIGGLTIPPVVALVMSRFGFFAHLLPRCALVNSYLMQRWENWF 780
Db LTLLHLVTPASAFDTEIIGGLTIPPVVALVMSRFGFFAHLLPRCALVNSYLMQRWENWF 780
QY WNVTLRPRRFLVLVCFPGATYDALVTPFCVCHVALLCLTSSAASFFGTDSRVRAHRMLVR 840
Db WNVTLRPRRFLVLVCFPGATYDALVTPFCVCHVALLCLTSSAASFFGTDSRVRAHRMLVR 840
QY LGKCHAWYSHVYLFKFLVFGENGFFYFKHLHGDVLPNDFASKLPLQEPFFPFEGKARVY 900
Db LGKCHAWYSHVYLFKFLVFGENGFFYFKHLHGDVLPNDFASKLPLQEPFFPFEGKARVY 900
QY RNEGRRLACGTVDCGLPVVARGLDLVFAGLAMPDPGMAITAPFTLQCLSERGTLISAMAVV 960
Db RNEGRRLACGTVDCGLPVVARGLDLVFAGLAMPDPGMAITAPFTLQCLSERGTLISAMAVV 960
QY MTGIDPRTWTGTIFRLGSLATSYMGFVCDNVLYTAAHSGSKRRLAHTPGTSHIPTVDAAN 1020
Db MTGIDPRTWTGTIFRLGSLATSYMGFVCDNVLYTAAHSGSKRRLAHTPGTSHIPTVDAAN 1020
QY DODIYQPPCGAGSLTRCSETGKGLVTRLGLSLVEVNSKDDPYWCAGALPMAVAKGSG 1080
Db DODIYQPPCGAGSLTRCSETGKGLVTRLGLSLVEVNSKDDPYWCAGALPMAVAKGSG 1080
QY APILCSSHVIGMFTAARNSGGSVSQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYSVQ 1140
Db APILCSSHVIGMFTAARNSGGSVSQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYSVQ 1140
QY ILIAPTSGKSTKPLPLSYMOEKYEVVLNPSVATTASMPKYMHAITYGVNPNICYFNGKCTN 1200
Db ILIAPTSGKSTKPLPLSYMOEKYEVVLNPSVATTASMPKYMHAITYGVNPNICYFNGKCTN 1200
QY TGA SLTYSTYGMWLTGACSRNYDVII CDECHATDATTVLGKVLTEAPSKNVRVLVLAT 1260
Db TGA SLTYSTYGMWLTGACSRNYDVII CDECHATDATTVLGKVLTEAPSKNVRVLVLAT 1260
QY ATPPGVITPPHANITFIQLTDBEGTIPFHGKKI KEENLKKGRHLIFEATKKHCELANELA 1320
Db ATPPGVITPPHANITFIQLTDBEGTIPFHGKKI KEENLKKGRHLIFEATKKHCELANELA 1320
QY RKGITAVSYRGCDISKIPEGDCVVVATDALCTGYTGDFDSYVDCSLAVEGTCHVDLDPT 1380
Db RKGITAVSYRGCDISKIPEGDCVVVATDALCTGYTGDFDSYVDCSLAVEGTCHVDLDPT 1380
QY FTMGVRVCGVSAIVKQRRGRTGRAGIYYVYDGSCTPSCGMVPCNIVEAPDAAKAWYG 1440
Db FTMGVRVCGVSAIVKQRRGRTGRAGIYYVYDGSCTPSCGMVPCNIVEAPDAAKAWYG 1440
QY LSSTEAQITLDTYRTPQGLPAIGANLDEWADLFSMVNPEPSFVNTAKRTADNYLLTAAQ 1500
Db LSSTEAQITLDTYRTPQGLPAIGANLDEWADLFSMVNPEPSFVNTAKRTADNYLLTAAQ 1500
QY LQCHQYGYAAPNDAPRWQGARLGKPCGVLRWLDGADACPGPEPSEVTRYQMCFTEVNT 1560

Db 1501 LQCHQYGYAAPNDAPRWQGARLGKPCGVLRWLDGADACPGPEPSEVTRYQMCFTEVNT 1560
QY SGTAAALAVGVVAMAYLAIDTFGATCVRRCWSITSVPTGATVAPVWDEEIEVEECASIP 1620
Db SGTAAALAVGVVAMAYLAIDTFGATCVRRCWSITSVPTGATVAPVWDEEIEVEECASIP 1620
QY LEAMVAAIDKLKSTITTTTSPFTLEALEKNTFLGPHAAATILAIIEYCCGLGVLTPDPNPPA 1680
Db LEAMVAAIDKLKSTITTTTSPFTLEALEKNTFLGPHAAATILAIIEYCCGLGVLTPDPNPPA 1680
QY SCVFAFAGITTPPHKIKMFLSLPGGAIASKLTDARGALAPMAGAAGTAGTALGTWTSVGF 1740
Db SCVFAFAGITTPPHKIKMFLSLPGGAIASKLTDARGALAPMAGAAGTAGTALGTWTSVGF 1740
QY VEDMLGGVAAAASSTACLTFCCLMGEMPTMDQAGLVYSAFNPAAGVGVLSACAMFALT 1800
Db VEDMLGGVAAAASSTACLTFCCLMGEMPTMDQAGLVYSAFNPAAGVGVLSACAMFALT 1800
QY AGPDHWPNRLLTMLARSNTVCNEYFIATRDIRRRKILGLEASTPWSVISACIRMLHTPTE 1860
Db AGPDHWPNRLLTMLARSNTVCNEYFIATRDIRRRKILGLEASTPWSVISACIRMLHTPTE 1860
QY DDCLLIANGLEBIWQVNCFFVI CFNVLKAGVQSMWNIPGCCPFYSCQYKGPWIGSGMLQ 1920
Db DDCLLIANGLEBIWQVNCFFVI CFNVLKAGVQSMWNIPGCCPFYSCQYKGPWIGSGMLQ 1920
QY ARCPGCAELIIPSVBNGFAKLYKGPRTCNRYWRGAPVFNARLCCGSARPDPTDWTSLVNVYG 1980
Db ARCPGCAELIIPSVBNGFAKLYKGPRTCNRYWRGAPVFNARLCCGSARPDPTDWTSLVNVYG 1980
QY VRDYCKYEKMGDHI FVTAVSSPNVCFVTQVPTLRAAAVAADVGVQCYLGEPEKTPMTTSAC 2040
Db VRDYCKYEKMGDHI FVTAVSSPNVCFVTQVPTLRAAAVAADVGVQCYLGEPEKTPMTTSAC 2040
QY CYGPDGKGKTVKLPFRVDGHTPGVRMQLNLRDALLETDCNSTNTNTPDSEAAVSALVFQOE 2100
Db CYGPDGKGKTVKLPFRVDGHTPGVRMQLNLRDALLETDCNSTNTNTPDSEAAVSALVFQOE 2100
QY LRRTNQLLEASAGVDITTKLPAPSI EEEVVVRKROFRARTGSLTLPPPPRSVPGVSCPSL 2160
Db LRRTNQLLEASAGVDITTKLPAPSI EEEVVVRKROFRARTGSLTLPPPPRSVPGVSCPSL 2160
QY QRSDPLEGPSNLPPSPVQLAMPPLLIGAGECNPFTAIGCAMTETGGGDDPLPSYPKK 2220
Db QRSDPLEGPSNLPPSPVQLAMPPLLIGAGECNPFTAIGCAMTETGGGDDPLPSYPKK 2220
QY EVSWSDESWSSTATASVYTGPPYPKIRGKDSQSPAPKPTKKLKGSEFSCMSYTW 2280
Db EVSWSDESWSSTATASVYTGPPYPKIRGKDSQSPAPKPTKKLKGSEFSCMSYTW 2280
QY TDVLSFKTASKVL SATRAITSGFLKQBSLVVYVTEPRDAELRKQKVTINRQPLFPSPYHKQ 2340
Db TDVLSFKTASKVL SATRAITSGFLKQBSLVVYVTEPRDAELRKQKVTINRQPLFPSPYHKQ 2340
QY VRLAKEKASKVGVWMDYDEVAHAHTPSKASHITGLRGTDVRSGAARKAVLDLQKCEA 2400
Db VRLAKEKASKVGVWMDYDEVAHAHTPSKASHITGLRGTDVRSGAARKAVLDLQKCEA 2400
QY GEIPSHYRQTVI VPKEEVFKTPQKPTKPPRLISYPHLEMRCEVMKYGVQVADPVKAV 2460
Db GEIPSHYRQTVI VPKEEVFKTPQKPTKPPRLISYPHLEMRCEVMKYGVQVADPVKAV 2460
QY MGDAYGFDVDPTRVKRLLSMWSPDAVGATCTVCFDSTITPEDIMVETDIYSAAKLSDOH 2520
Db MGDAYGFDVDPTRVKRLLSMWSPDAVGATCTVCFDSTITPEDIMVETDIYSAAKLSDOH 2520
QY RAGIHTTARQLYAGGPMIAYDGRIGYRRCRSSGVYTTSSNSLTCMLKVNAAAEQAGWK 2580
Db RAGIHTTARQLYAGGPMIAYDGRIGYRRCRSSGVYTTSSNSLTCMLKVNAAAEQAGWK 2580
QY NPFILICGDDCTVIWKSGADADKOAMRVFASWKMVGAPQDCVPQPKYSLEELTSCSSN 2640
Db NPFILICGDDCTVIWKSGADADKOAMRVFASWKMVGAPQDCVPQPKYSLEELTSCSSN 2640

Qy 2641 VTSGITKSGKPYFLTRDPRIPRLGRCSAEGIGYNPSAAWIGYLIHHYPCLWVSRVLAVHF 2700
Db 2641 VTSGITKSGKPYFLTRDPRIPRLGRCSAEGIGYNPSAAWIGYLIHHYPCLWVSRVLAVHF 2700
Qy 2701 MEQMLFEDKLPETVTFDYGKNTVPVEDLPSIIAGVHGIEAFSVVYTNAEILRVQSOL 2760
Db 2701 MEQMLFEDKLPETVTFDYGKNTVPVEDLPSIIAGVHGIEAFSVVYTNAEILRVQSOL 2760
Qy 2761 TDMTPPLRAWRKARAVLASAKRGGAHAKLARFLWLHATSRPLDLDKTSVARYTTFN 2820
Db 2761 TDMTPPLRAWRKARAVLASAKRGGAHAKLARFLWLHATSRPLDLDKTSVARYTTFN 2820
Qy 2821 YCDVYSPGDDVFITPQRLQKFLVKYLAVIYFALGLIAVGLAIS 2864
Db 2821 YCDVYSPGDDVFITPQRLQKFLVKYLAVIYFALGLIAVGLAIS 2864
RESULT 3
AAR82072
ID AAR82072 standard; protein; 2864 AA.
XX
AC AAR82072;
XX
DT 27-AUG-2003 (revised)
DT 02-JUL-1996 (first entry)
XX
DE Hepatitis GB virus (HGBV) clone GB contig B protein prod.
XX
KW Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine; reagents; non-A;
KW non-B; non-C; non-D; non-E; clone; GB contig B; tamarin; infected plasma;
KW lambda phage; cDNA library.
XX
OS Hepatitis G virus.
XX
EN WO9521922-A2.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-US002118.
XX
PR 14-FEB-1994; 94US-00196030.
PR 13-MAY-1994; 94US-00242654.
PR 29-JUL-1994; 94US-00283314.
PR 23-NOV-1994; 94US-00344185.
PR 23-NOV-1994; 94US-00344190.
PR 27-JAN-1995; 95US-00344557.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Simons JN, Pilot-Matias TJ, Dawson GJ, Schlauder GG, Desai SM;
PI Leary TP, Muerhoff AS, Erker JC, Buijk SL, Mushahwar IK;
XX
DR WPI; 1995-293123/38.
DR N-ESDB; AAT00130.
XX
PT Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful for
PT diagnosis and therapy of hepatitis GB virus.
XX
PS Example 9; Page 434-447; 661pp; English.
XX
CC Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV infected
CC tamarin plasma, using standard procedures, was used to prepare a lambda
CC phage HGBV cDNA library. Clones were rescued from the lambda phage,
CC searched against a sequence database and found to be unique HGBV
CC sequences. The clones were then used to assemble the sequences
CC AAT00129/30 (GB contig A and B) which encode the proteins AAR94345-47
CC (the 3 possible coding strand reading frames) and AAR82072, respectively.
CC Reagents which comprise the HGBV DNA, or its protein prods. can be used
CC for the diagnosis, therapy or in a vaccine to prevent HGBV infection.
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 2864 AA;

Query Match 99.6%; Score 15317; DB 2; Length 2864;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2852; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MPVISTQTSVPAPRTRKNKQTOASYPVSIKTSVERGORAKRVQORDARNYKIAGIHD 60
Db 1 MPVISTQTSVPAPRTRKNKQTOASYPVSIKTSVERGORAKRVQORDARNYKIAGIHD 60
Qy 61 GLQTLAAQALPAHGWGRQDPRHKSRLGILLDPLGWIIGDVTTHTPLVGLVAGAVRPV 120
Db 61 GLQTLAAQALPAHGWGRQDPRHKSRLGILLDPLGWIIGDVTTHTPLVGLVAGAVRPV 120
Qy 121 CQIVRLLEDGVNWTATGFWGVLHVFWCLLSLACPCSGARVTDPTNTTILNCCORNOVIY 180
Db 121 CQIVRLLEDGVNWTATGFWGVLHVFWCLLSLACPCSGARVTDPTNTTILNCCORNOVIY 180
Qy 181 CSPSTCLHERGCVCICADECWVPANPYISHPSNNWTGDSFLADHIDFVNGALVTCDAJDIG 240
Db 181 CSPSTCLHERGCVCICADECWVPANPYISHPSNNWTGDSFLADHIDFVNGALVTCDAJDIG 240
Qy 241 ELCGACVLVGDWLVRHWHLIHIDLNETGTCYLEVPTGIDPGFLGFIGHMAGKVEAVIFLTK 300
Db 241 ELCGACVLVGDWLVRHWHLIHIDLNETGTCYLEVPTGIDPGFLGFIGHMAGKVEAVIFLTK 300
Qy 301 LASQVPYAIATMFSSVHYLAVGALIYYASRGKYLALLMLYIEATSGNPVRVPTGCSI 360
Db 301 LASQVPYAIATMFSSVHYLAVGALIYYASRGKYLALLMLYIEATSGNPVRVPTGCSI 360
Qy 361 AEFCSPLMIPCCHSYLSENVSEVICSPKWTPTITLYNNSISWYPTTIPGARGCMVKF 420
Db 361 AEFCSPLMIPCCHSYLSENVSEVICSPKWTPTITLYNNSISWYPTTIPGARGCMVKF 420
Qy 421 KNTWGCCRI RNVPSTCTMGTDVWMDTRNTYBACGVTPLMTTAWHNGSALKLAILOYPG 480
Db 421 KNTWGCCRI RNVPSTCTMGTDVWMDTRNTYBACGVTPLMTTAWHNGSALKLAILOYPG 480
Qy 481 SKEMFKPHNMWSGHLYPEGSDTPIVVPYDPVNSTLLPPERWARLPPTPVVRSWMLQVPQ 540
Db 481 SKEMFKPHNMWSGHLYPEGSDTPIVVPYDPVNSTLLPPERWARLPPTPVVRSWMLQVPQ 540
Qy 541 GYSDVKDLATGLITKDKAWNTQVLYSATGALS LGTGTTKAVVLLILLGCGSKYLILAY 600
Db 541 GYSDVKDLATGLITKDKAWNTQVLYSATGALS LGTGTTKAVVLLILLGCGSKYLILAY 600
Qy 601 LCYLSLCFGRASGVPLRPVLPQSQYLQAGWDVLSKAQVAPFALIFCICYLRCLRVAAL 660
Db 601 LCYLSLCFGRASGVPLRPVLPQSQYLQAGWDVLSKAQVAPFALIFCICYLRCLRVAAL 660
Qy 661 LGFVPMAGLPLTFFVAAAAAQPDYDMWVRLLVAGLVLMAGRNRGHRHRIALLVGPWPLVAL 720
Db 661 LGFVPMAGLPLTFFVAAAAAQPDYDMWVRLLVAGLVLMAGRNRGHRHRIALLVGPWPLVAL 720
Qy 721 LTLHLVTPASAFDTEIIIGLTIPTPVVALVYNSRFGFFAHLPRCALVNSYLWQWENWF 780
Db 721 LTLHLVTPASAFDTEIIIGLTIPTPVVALVYNSRFGFFAHLPRCALVNSYLWQWENWF 780
Qy 781 WNVTLRPERFLVLCVCPGATYDALVTFVCVCHVALLCLTSSAASFFCTDSRVRAHRLMVR 840
Db 781 WNVTLRPERFLVLCVCPGATYDALVTFVCVCHVALLCLTSSAASFFCTDSRVRAHRLMVR 840
Qy 841 LGKCHAWSHYVLKFFLLVFGENGVPFFYKHLHGDVLPNDPASKLPLOEFFFFPPEGKARVY 900
Db 841 LGKCHAWSHYVLKFFLLVFGENGVPFFYKHLHGDVLPNDPASKLPLOEFFFFPPEGKARVY 900
Qy 901 RNEGRRLACGDTVDGLPVVARLGDVLPAGLAMPDGDGWAITAPFTLQCLSERGTLSAMAVV 960
Db 901 RNEGRRLACGDTVDGLPVVARLGDVLPAGLAMPDGDGWAITAPFTLQCLSERGTLSAMAVV 960
Qy 961 MTGIDPRTWTGTIFRLGSLATSVMGVCNDNVLYTAHHGSKRRRLAHPGTGSHIPTVDAAN 1020
Db 961 MTGIDPRTWTGTIFRLGSLATSVMGVCNDNVLYTAHHGSKRRRLAHPGTGSHIPTVDAAN 1020

QY 1021 DDIYQPCGAGSLTRCSCGETKGYLVTRLGSLVEVKNKSDDPYWCVCALPMAVAKGSSG 1080
DB 1021 DDIYQPCGAGSLTRCSCGETKGYLVTRLGSLVEVKNKSDDPYWCVCALPMAVAKGSSG 1080
QY 1081 APILCSSGHVIGMFTTAARNSSGVSQIRVRPLVLCAGYHPQYTAHATLDTKPTVPNEYSVQ 1140
DB 1081 APILCSSGHVIGMFTTAARNSSGVSQIRVRPLVLCAGYHPQYTAHATLDTKPTVPNEYSVQ 1140
QY 1141 ILIAPTSGSGSKTKPLSLSYMOKYEVVLNPSVATTASMPKYMHAATGYVNPNCYFNKGCTN 1200
DB 1141 ILIAPTSGSGSKTKPLSLSYMOKYEVVLNPSVATTASMPKYMHAATGYVNPNCYFNKGCTN 1200
QY 1201 TGAISLYTYGMYLTCAGSRNDYIICDECHADATTVLIGKVLTEAPSKNVRVLVLAT 1260
DB 1201 TGAISLYTYGMYLTCAGSRNDYIICDECHADATTVLIGKVLTEAPSKNVRVLVLAT 1260
QY 1261 ATPPGVITPTPHANITEIQLTDBGTTIPFGKKI KEENLKKGRHLI IFEATKKGHDELANELA 1320
DB 1261 ATPPGVITPTPHANITEIQLTDBGTTIPFGKKI KEENLKKGRHLI IFEATKKGHDELANELA 1320
QY 1321 RKGITAVSYRGCDLSKIPEGDCVVVATDALCTGYTGFDSVYDCSLMVEGTCCHVDLDPT 1380
DB 1321 RKGITAVSYRGCDLSKIPEGDCVVVATDALCTGYTGFDSVYDCSLMVEGTCCHVDLDPT 1380
QY 1381 FTMGVRVCGVSAIVKQRRGRTGRAGIYYVVDGSCCTPSGMVPECNIVEAFDAAKAWYG 1440
DB 1381 FTMGVRVCGVSAIVKQRRGRTGRAGIYYVVDGSCCTPSGMVPECNIVEAFDAAKAWYG 1440
QY 1441 LSSTBAQIILDTYRQPLPAIGANLDEWADLFSMNWPEPSVNTAKRTADNYVLLTAAQ 1500
DB 1441 LSSTBAQIILDTYRQPLPAIGANLDEWADLFSMNWPEPSVNTAKRTADNYVLLTAAQ 1500
QY 1501 LQLCHOYGVAAPNDAPRWQARGLKPCGVLRWLDGADACPGPESEVTRYOMCFTEVNT 1560
DB 1501 LQLCHOYGVAAPNDAPRWQARGLKPCGVLRWLDGADACPGPESEVTRYOMCFTEVNT 1560
QY 1561 SGTAAALAVGVGVAMAYLAIDTEGATCVRRCWSITSVPTGATVAPVVDDEEIVEECASFIP 1620
DB 1561 SGTAAALAVGVGVAMAYLAIDTEGATCVRRCWSITSVPTGATVAPVVDDEEIVEECASFIP 1620
QY 1621 LEAMVAAIDKLKSTITTTSPFLETALCKNTFLGPHAAATILAIIEYCCGLVTLDPNPPA 1680
DB 1621 LEAMVAAIDKLKSTITTTSPFLETALCKNTFLGPHAAATILAIIEYCCGLVTLDPNPPA 1680
QY 1681 SCVFAPAGITTPPLPHKIMFLSLFGGATASKLTDAARGALAPMAGAGTALGTWTSVGF 1740
DB 1681 SCVFAPAGITTPPLPHKIMFLSLFGGATASKLTDAARGALAPMAGAGTALGTWTSVGF 1740
QY 1741 VFDMLGGVAAAASSTACLTFFKCLMGSEWPTMDQLAGLVYSAFNPAGVGVLSACAMFALT 1800
DB 1741 VFDMLGGVAAAASSTACLTFFKCLMGSEWPTMDQLAGLVYSAFNPAGVGVLSACAMFALT 1800
QY 1801 AGPDHWPRLLTMLARSNTVCNEYFIATRDIRKILGLEASTPWSVISACTIRWLHTPTE 1860
DB 1801 AGPDHWPRLLTMLARSNTVCNEYFIATRDIRKILGLEASTPWSVISACTIRWLHTPTE 1860
QY 1861 DDCGLIANGLETWQVVCNFFVLCENVLKAGVOSMWNIPCCPFYSCQKGYKGPWIGSGMLQ 1920
DB 1861 DDCGLIANGLETWQVVCNFFVLCENVLKAGVOSMWNIPCCPFYSCQKGYKGPWIGSGMLQ 1920
QY 1921 ARCPGCAELIFSVEGFAKLYKGPRTCSNYMRGAVPVNARLCSARPDPDWTSLVNVYG 1980
DB 1921 ARCPGCAELIFSVEGFAKLYKGPRTCSNYMRGAVPVNARLCSARPDPDWTSLVNVYG 1980
QY 1981 VRDYCKYERMGDHIIFVTAVSSNVCFQVPPPLRAAAVADGVQVQCYLGEPTKPTWTTGAC 2040
DB 1981 VRDYCKYERMGDHIIFVTAVSSNVCFQVPPPLRAAAVADGVQVQCYLGEPTKPTWTTGAC 2040
QY 2041 CYGPPGKGTVKLPRVDGHTPGVMQLNLDALETNDNCNTNTPSPDEAAVSALVFKQE 2100
DB 2041 CYGPPGKGTVKLPRVDGHTPGVMQLNLDALETNDNCNTNTPSPDEAAVSALVFKQE 2100
QY 2101 LRRTNQLLEAISAGVDTTTKLPAPSIIEVVVRKQFRARTGSLTLPPLPPRSVPGVSCPESL 2160

DB 2101 LRRTNQLLEAISAGVDTTTKLPAPSIIEVVVRKQFRARTGSLTLPPLPPRSVPGVSCPESL 2160
QY 2161 QRSPLBEGPSNLPSPVQLAMPWPLLGAGECNPFTTAIGCAMTETGGGDDLPSPPKK 2220
DB 2161 QRSPLBEGPSNLPSPVQLAMPWPLLGAGECNPFTTAIGCAMTETGGGDDLPSPPKK 2220
QY 2221 EVSEWSDESWSSTATTASSYVTGPPYKIRGKDSQTSAPAKRPTKKKLGKSFSCSMSYTW 2280
DB 2221 EVSEWSDESWSSTATTASSYVTGPPYKIRGKDSQTSAPAKRPTKKKLGKSFSCSMSYTW 2280
QY 2281 TDVTSFKTASKVLSATRAITSGFLKQKRSLLVVTSPRDAELRKQKVTINRQPLFPSPSYHKQ 2340
DB 2281 TDVTSFKTASKVLSATRAITSGFLKQKRSLLVVTSPRDAELRKQKVTINRQPLFPSPSYHKQ 2340
QY 2341 VRLAKEKASKVGVWMDYDEVAHTPSKSAKSHITGLRGTDVRSGAARKAVLDLQKVEA 2400
DB 2341 VRLAKEKASKVGVWMDYDEVAHTPSKSAKSHITGLRGTDVRSGAARKAVLDLQKVEA 2400
QY 2401 GEIPSHYRQTVIVPKKEEVFKTPQKPTKPPRLISYPHLEMRCEVKMYYGQVAPDVVKAV 2460
DB 2401 GEIPSHYRQTVIVPKKEEVFKTPQKPTKPPRLISYPHLEMRCEVKMYYGQVAPDVVKAV 2460
QY 2461 MGDAYGFVDPRTVRKRLLSMMSPDAGATCTVCFDSTITPEDIMVETDIYSAAKLSQKH 2520
DB 2461 MGDAYGFVDPRTVRKRLLSMMSPDAGATCTVCFDSTITPEDIMVETDIYSAAKLSQKH 2520
QY 2521 RAGIHTTARQLYAGGPMIAYDGREIGYRRCRSSGYTTSNLSLTCWLKVNAAAEOAGMK 2580
DB 2521 RAGIHTTARQLYAGGPMIAYDGREIGYRRCRSSGYTTSNLSLTCWLKVNAAAEOAGMK 2580
QY 2581 NPFLLICGDDCTVIWKSAGADADQAMRVFASWKMVMGAPQDCVPQKYSLEELTSCSN 2640
DB 2581 NPFLLICGDDCTVIWKSAGADADQAMRVFASWKMVMGAPQDCVPQKYSLEELTSCSN 2640
QY 2641 VTSGITKSGKPYFLTRDPRIPLCRCSAEGLYGNPSAAWIGYLIIHHPCLWVSRVLAHVF 2700
DB 2641 VTSGITKSGKPYFLTRDPRIPLCRCSAEGLYGNPSAAWIGYLIIHHPCLWVSRVLAHVF 2700
QY 2701 MEQMLFEDKLPTETVTFDYGKNTYVPVEDLPSIIAGVHGIEAFSVRYTNAEILRVSOGL 2760
DB 2701 MEQMLFEDKLPTETVTFDYGKNTYVPVEDLPSIIAGVHGIEAFSVRYTNAEILRVSOGL 2760
QY 2761 TDMTMPPLRARWKKARAVLASAKERGGHAHAKLARFLWHATSRLPDLDKTTSVARYTTFN 2820
DB 2761 TDMTMPPLRARWKKARAVLASAKERGGHAHAKLARFLWHATSRLPDLDKTTSVARYTTFN 2820
QY 2821 YCDVYSPBGDVFTTPQRRLOKFLVKYLAVIVFALGLIAVGLAIS 2864
DB 2821 YCDVYSPBGDVFTTPQRRLOKFLVKYLAVIVFALGLIAVGLAIS 2864

RESULT 4

AAB09268

ID AAB09268 standard; protein; 2864 AA.

XX AAB09268;

XX 06-AUG-2003 (revised)

DT 30-AUG-2000 (first entry)

XX Hepatitis GB virus protein sequence SEQ ID NO:394.

XX Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
detection; characterisation; hepatitis.

XX Hepatitis GB virus.

XX US6051374-A.

XX 18-APR-2000.

XX 07-JUN-1995; 95US-00488445.

XX 14-FEB-1994; 94US-00196030.
PR 13-MAY-1994; 94US-00242654.
PR 23-JUL-1994; 94US-00283314.
PR 23-NOV-1994; 94US-00344185.
PR 23-NOV-1994; 94US-00344190.
PR 30-JAN-1995; 95US-00377557.
XX
PA (ABBO) ABBOTT LAB.
XX
XX Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Ruijk SL;
PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
XX
DR WPI; 2000-338307/29.
XX
PT Detecting target hepatitis GB virus nucleic acid in a test sample
PT suspected of containing HGBV comprises reacting the test sample the HGBV
PT polynucleotide probe and detecting the complex that contains target HGBV.
XX
PS Claim 1; Col 437-452; 369pp; English.
XX
XX The present invention describe a method for detecting target hepatitis GB
CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of
CC containing HGBV. The method involves reacting (T) with a HGBV
CC polynucleotide probe (1) containing 15 contiguous nucleotides, and which
CC selectively hybridises to the HGBV genome or its full complement, and
CC detecting the complex that contains THN, indicating the presence of
CC target HGBV. The method is used for detecting target HGBV nucleic acid in
CC the test sample suspected of containing HGBV and for characterisation of
CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
CC -E hepatitis causing agents collectively termed as hepatitis GB virus.
CC AA55270 to AA55489 and AAB0985 to AAB09480 represent nucleotide and
CC protein sequences used in the exemplification of the present invention.
CC (Updated on 06-AUG-2003 to correct OS field.)
XX
XX Sequence 2864 AA;

Query Match 99.6%; Score 15317; DB 3; Length 2864;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2852; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MPVISTQSPVAPRTRKXKQOTASYPVSIKTSVERGQAKRKVQDARPNRYKIAGIHD 60
DB 1 MPVISTQSPVAPRTRKXKQOTASYPVSIKTSVERGQAKRKVQDARPNRYKIAGIHD 60
QY 61 GLQTLAQAALPAHGWGRQDPRHKRNIGILLDYPPLGWIGDVTHTPLVGLVAGAVVRPV 120
DB 61 GLQTLAQAALPAHGWGRQDPRHKRNIGILLDYPPLGWIGDVTHTPLVGLVAGAVVRPV 120
QY 121 CQIVRLLEDGVNWTATGFWGHLFVVCLLSLACPCSGARVTDPTNTTILTNCCQORNOVIY 180
DB 121 CQIVRLLEDGVNWTATGFWGHLFVVCLLSLACPCSGARVTDPTNTTILTNCCQORNOVIY 180
QY 181 CSPSTCLHEPCCVTCADECWVPANPYISHPSNWTGDSFLADHDIFVNGALVTCDAIDIG 240
DB 181 CSPSTCLHEPCCVTCADECWVPANPYISHPSNWTGDSFLADHDIFVNGALVTCDAIDIG 240
QY 241 ELGCACVLVGDWLVHRVHLIHDINETGTCYLEVPTGIDPGFLGFIGMAGKVEAVIFLTK 300
DB 241 ELGCACVLVGDWLVHRVHLIHDINETGTCYLEVPTGIDPGFLGFIGMAGKVEAVIFLTK 300
QY 301 LASQVPAIATMFSVSHYLVAGALIYYASRGKWYQLLALMLYTEATSGNPIRVPTGCSI 360
DB 301 LASQVPAIATMFSVSHYLVAGALIYYASRGKWYQLLALMLYTEATSGNPIRVPTGCSI 360
QY 361 AEFCSPLMPCPCHSYLSENSEVIVCSYKTRITILEYNNISISWYPYTIPIGARGCMVKF 420
DB 361 AEFCSPLMPCPCHSYLSENSEVIVCSYKTRITILEYNNISISWYPYTIPIGARGCMVKF 420
QY 421 KNTWGCCIRIRNVSYSCTMGTDVAVNDTRNTYEACGVTPWLTAAHNGSALKLAILQVPG 480
DB 421 KNTWGCCIRIRNVSYSCTMGTDVAVNDTRNTYEACGVTPWLTAAHNGSALKLAILQVPG 480

QY 481 SKEMFKPHNMWSGHLYPEGSDTPIVYDPVNSTLLPPERWALPGTPPVVVRGSLQVQP 540
DB 481 SKEMFKPHNMWSGHLYPEGSDTPIVYDPVNSTLLPPERWALPGTPPVVVRGSLQVQP 540
QY 541 GFYSDDKDLATGLITKDKAWKNQVLSATGALSJTGVTTKAVVLIILGLCGSKYLILAY 600
DB 541 GFYSDDKDLATGLITKDKAWKNQVLSATGALSJTGVTTKAVVLIILGLCGSKYLILAY 600
QY 601 LCYLSLCFCGRASGYPLRPLVPSQSYLQAGMDVLSKAQVAPFALIFFICCYLRCRLRYAAL 660
DB 601 LCYLSLCFCGRASGYPLRPLVPSQSYLQAGMDVLSKAQVAPFALIFFICCYLRCRLRYAAL 660
QY 661 LGFVPMAGLPLTFPVAQAAAAQPDYDWWVRLVAGLVLWAGRNCHRIALLVGPWPLVAL 720
DB 661 LGFVPMAGLPLTFPVAQAAAAQPDYDWWVRLVAGLVLWAGRNCHRIALLVGPWPLVAL 720
QY 721 LTLHLVTPASAFDETEIIGLTIIPVVALVMSRFGFFAHLPRCALVNSYLWQWENWF 780
DB 721 LTLHLVTPASAFDETEIIGLTIIPVVALVMSRFGFFAHLPRCALVNSYLWQWENWF 780
QY 781 WNTVLRPERFELVLCFPGATYDALVTFVCYCHVALLCLTSSAASFFGTDSSRVRAHRMLVR 840
DB 781 WNTVLRPERFELVLCFPGATYDALVTFVCYCHVALLCLTSSAASFFGTDSSRVRAHRMLVR 840
QY 841 LGKCHAWSHYVVKFLLVFGENGVPFYKHLHGDVLPNDPASKLPLQBPFPFPGKARVY 900
DB 841 LGKCHAWSHYVVKFLLVFGENGVPFYKHLHGDVLPNDPASKLPLQBPFPFPGKARVY 900
QY 901 RNEGRRLLACGDTVLDGLPVVARLGDVLPAGLAMPDGDWAIITAPFTLQCLSERGTLSAMAVV 960
DB 901 RNEGRRLLACGDTVLDGLPVVARLGDVLPAGLAMPDGDWAIITAPFTLQCLSERGTLSAMAVV 960
QY 961 MTGIDPRTGTGTIFRLGLSLATSYMGFVCDNVLYTAHHGSKGRRLAHPTGSIHPITVDAAN 1020
DB 961 MTGIDPRTGTGTIFRLGLSLATSYMGFVCDNVLYTAHHGSKGRRLAHPTGSIHPITVDAAN 1020
QY 1021 DQDIYQPPCAGSLTRCSCGETKGYLVTRLGLSLVEVNKSDDPYVCVCGALPMAVAKSSG 1080
DB 1021 DQDIYQPPCAGSLTRCSCGETKGYLVTRLGLSLVEVNKSDDPYVCVCGALPMAVAKSSG 1080
QY 1081 APILCSSHGHVIGMPTAARNSSGVSQIRVRPLVCAGYHPQYTAHATLDTKPTVNEYSVQ 1140
DB 1081 APILCSSHGHVIGMPTAARNSSGVSQIRVRPLVCAGYHPQYTAHATLDTKPTVNEYSVQ 1140
QY 1141 ILIAPTSGSKSTKLPLSYMOKTEVLVLPNSVATTASMPKYMHTATYGVNPNCEYNGKCTN 1200
DB 1141 ILIAPTSGSKSTKLPLSYMOKTEVLVLPNSVATTASMPKYMHTATYGVNPNCEYNGKCTN 1200
QY 1201 TGASLTSTYTGMYLTGACSRNYDVIICDECHATDATTVLGIGKVLTEAPSKNVLVLVAT 1260
DB 1201 TGASLTSTYTGMYLTGACSRNYDVIICDECHATDATTVLGIGKVLTEAPSKNVLVLVAT 1260
QY 1261 ATPGVLTPTPHANITEIQLTDEGTIPPHGKKIKEENLKKGRHLIFEATKKHCDLANELA 1320
DB 1261 ATPGVLTPTPHANITEIQLTDEGTIPPHGKKIKEENLKKGRHLIFEATKKHCDLANELA 1320
QY 1321 RKGITAVSYRGCDSIKIPGDCVWVATDALCTGYTGDPSVDSCSLMVEGTCHVDLPT 1380
DB 1321 RKGITAVSYRGCDSIKIPGDCVWVATDALCTGYTGDPSVDSCSLMVEGTCHVDLPT 1380
QY 1381 FTMGVRCVGSIAIVKGQRRGRTGRAGIYYYVDGSCCTPSGMVPECNIVEAFDAAKAWYG 1440
DB 1381 FTMGVRCVGSIAIVKGQRRGRTGRAGIYYYVDGSCCTPSGMVPECNIVEAFDAAKAWYG 1440
QY 1441 LSSTEAQTIIDTTRTOPGLPAIGANLDEWADLFSMVNPEPSFVNTAKRTADNYVLLTAAQ 1500
DB 1441 LSSTEAQTIIDTTRTOPGLPAIGANLDEWADLFSMVNPEPSFVNTAKRTADNYVLLTAAQ 1500
QY 1501 LQLCHOYGYAAPNDAPRWQGARLGKPCGVLRWLDGADACGPGPEPSEVTRYQMCFTVNT 1560
DB 1501 LQLCHOYGYAAPNDAPRWQGARLGKPCGVLRWLDGADACGPGPEPSEVTRYQMCFTVNT 1560
QY 1561 SGTAAALAVGVGAWAYLAIDTFGATCVRRCWSITSVPTGTATVAPVDEEBEIVBECASPIP 1620

Db 1561 SGTALAVGVGVAMAYLAIDTFGATCVRRCSITSVPTGATVAPVVDDEEIEECASFP 1620
Qy 1621 LEAMVAAIDKLSKSTTTTSPFTLEALEKANTFLGPHAATILAIIEYCCGLVTLPDNPPA 1680
Db 1621 LEAMVAAIDKLSKSTTTTSPFTLEALEKANTFLGPHAATILAIIEYCCGLVTLPDNPPA 1680
Qy 1681 SCVFAPFAGITPTPLPHKIMFSLFSGGAIASKLTADGALAFPMAGAGTAGTALGTWTSVGF 1740
Db 1681 SCVFAPFAGITPTPLPHKIMFSLFSGGAIASKLTADGALAFPMAGAGTAGTALGTWTSVGF 1740
Qy 1741 VFDMLGGVAAASSTACLFKCLMGSWPTWDLAGLVISAFNPAAGVGVLSACAMFALT 1800
Db 1741 VFDMLGGVAAASSTACLFKCLMGSWPTWDLAGLVISAFNPAAGVGVLSACAMFALT 1800
Qy 1801 AGPDHWPRLITMLARSNVCNEYFIATRDTRRKILGLEASTPWSVISACIRWLHTPTE 1860
Db 1801 AGPDHWPRLITMLARSNVCNEYFIATRDTRRKILGLEASTPWSVISACIRWLHTPTE 1860
Qy 1861 DDCGLIANGLEIWOVVCNFFVICFNVLKAGVQSMVNI PGCPFYSCQKGYKGPWISGMLQ 1920
Db 1861 DDCGLIANGLEIWOVVCNFFVICFNVLKAGVQSMVNI PGCPFYSCQKGYKGPWISGMLQ 1920
Qy 1921 ARCPGABELIFSVENGFAKLYKGPRTCSNYWRGAVPVNARLCSARPDPDWTSLVNVYG 1980
Db 1921 ARCPGABELIFSVENGFAKLYKGPRTCSNYWRGAVPVNARLCSARPDPDWTSLVNVYG 1980
Qy 1981 VRDYCKYKMGDHIIFVTAVSSSNVCFTQVPPTLRAAVADGVOCYLGEPKTPWTTISAC 2040
Db 1981 VRDYCKYKMGDHIIFVTAVSSSNVCFTQVPPTLRAAVADGVOCYLGEPKTPWTTISAC 2040
Qy 2041 CYGPDGKGTVKLPFRVDGHTPGVMQNLNRLDALETNDCNSNTNTPSDEAAVSALVFQKE 2100
Db 2041 CYGPDGKGTVKLPFRVDGHTPGVMQNLNRLDALETNDCNSNTNTPSDEAAVSALVFQKE 2100
Qy 2101 LRRTNQLLEAISAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLP PPPRSPGVGSCPSL 2160
Db 2101 LRRTNQLLEAISAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLP PPPRSPGVGSCPSL 2160
Qy 2161 QRSDDPLEGSPNLPPSPVLOLAMPPLIAGACENPFTALGCAMTETGGGDDLPSPYPKK 2220
Db 2161 QRSDDPLEGSPNLPPSPVLOLAMPPLIAGACENPFTALGCAMTETGGGDDLPSPYPKK 2220
Qy 2221 EVSEMSDESWTATTASSVTPGPYKIRGKDSQSAKAPRTKKLKGKSFSCSMTW 2280
Db 2221 EVSEMSDESWTATTASSVTPGPYKIRGKDSQSAKAPRTKKLKGKSFSCSMTW 2280
Qy 2281 TDVISFKTASKVLSTRAITSGFLKORSILVYVTEPRDAELRKQKVTINRQPLFPSPYHKQ 2340
Db 2281 TDVISFKTASKVLSTRAITSGFLKORSILVYVTEPRDAELRKQKVTINRQPLFPSPYHKQ 2340
Qy 2341 VRLAKEKASKVGVNMWDYDEVAANTPSAKSHITGLRGTDVRSAAKAVLDLQKVEA 2400
Db 2341 VRLAKEKASKVGVNMWDYDEVAANTPSAKSHITGLRGTDVRSAAKAVLDLQKVEA 2400
Qy 2401 GEIPSHYRQTIVPKEEVFKTPQKPTKKPRLIISYPHLEMRCEVMKYGVAPDVXAV 2460
Db 2401 GEIPSHYRQTIVPKEEVFKTPQKPTKKPRLIISYPHLEMRCEVMKYGVAPDVXAV 2460
Qy 2461 MGDAGFVDPRTRVRLLSMSPDVAAGTCDTVCFDSTITPBDIMVETDIYSAAKLSQKH 2520
Db 2461 MGDAGFVDPRTRVRLLSMSPDVAAGTCDTVCFDSTITPBDIMVETDIYSAAKLSQKH 2520
Qy 2521 RAGIHTIAROLYAGGPMIAYDGREIGYRCRSGGVYTTSSNSLTCMLKVNAAAQAGMK 2580
Db 2521 RAGIHTIAROLYAGGPMIAYDGREIGYRCRSGGVYTTSSNSLTCMLKVNAAAQAGMK 2580
Qy 2581 NPFILICGDDCTVIWKSAGADADKQAMRVFASWKMVGAPQDCVPQPKYSLEELTSCSN 2640
Db 2581 NPFILICGDDCTVIWKSAGADADKQAMRVFASWKMVGAPQDCVPQPKYSLEELTSCSN 2640
Qy 2641 VTSGITKSGKPYFFLTRDRIPLGRCSAEGLYGNPSAAWIGYLIIHHYPCLVSRVLAVHF 2700

Db 2641 VTSGITKSGKPYFFLTRDRIPLGRCSAEGLYGNPSAAWIGYLIIHHYPCLVSRVLAVHF 2700
Qy 2701 MEQMLFEDKLPETVTFDYGKNTVPVEDLPSIIAGVHGIEAFSVRYTNAEILRVQSLS 2760
Db 2701 MEQMLFEDKLPETVTFDYGKNTVPVEDLPSIIAGVHGIEAFSVRYTNAEILRVQSLS 2760
Qy 2761 TDMTMPPLRAWRKKARAVLASAKRRGGGAHAKLARFLLWHATSRPLDLDKTSVARYTTFN 2820
Db 2761 TDMTMPPLRAWRKKARAVLASAKRRGGGAHAKLARFLLWHATSRPLDLDKTSVARYTTFN 2820
Qy 2821 YCDVYSPGDDVPITPQRRLOKFLVKYLAIVIFALGLTAVGLAIS 2864
Db 2821 YCDVYSPGDDVPITPQRRLOKFLVKYLAIVIFALGLTAVGLAIS 2864
RESULT 5
ID AAB09038 standard; protein; 1422 AA.
XX AAB09038;
XX 06-AUG-2003 (revised)
DT 30-AUG-2000 (first entry)
XX
XX Hepatitis GB virus protein sequence SEQ ID NO:83.
XX Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
XX detection; characterisation; hepatitis.
XX Hepatitis GB virus.
XX US6051374-A.
XX 18-APR-2000.
XX
XX 07-JUN-1995; 95US-00488445.
XX 14-FEB-1994; 94US-00196030.
PR 13-MAY-1994; 94US-00242654.
PR 29-JUL-1994; 94US-00283314.
PR 23-NOV-1994; 94US-00344185.
PR 23-NOV-1994; 94US-00344190.
PR 30-JAN-1995; 95US-00377557.
XX (ABBO) ABBOTT LAB.
XX
XX Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
WPI; 2000-338307/29.
XX
XX Detecting target hepatitis GB virus nucleic acid in a test sample
suspected of containing HGBV comprises reacting the test sample the HGBV
polynucleotide probe and detecting the complex that contains target HGBV.
XX
XX Example 5; Col 223-230; 369pp; English.
XX
XX The present invention describe a method for detecting target hepatitis GB
virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of
containing HGBV. The method involves reacting (T) with a HGBV
polynucleotide probe (T) containing 15 contiguous nucleotides, and which
selectively hybridises to the HGBV genome or its full complement, and
detecting the complex that contains THN, indicating the presence of
target HGBV. The method is used for detecting target HGBV nucleic acid in
the test sample suspected of containing HGBV and for characterisation of
newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
-E hepatitis causing agents collectively termed as hepatitis GB virus.
XX AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and
protein sequences used in the exemplification of the present invention.
XX (Updated on 06-AUG-2003 to correct OS field.)
XX
XX Sequence 1422 AA;

Query Match		48.0%; Score 7380; DB 3; Length 1422;
Best Local Similarity		97.3%; Pred. No. 0;
Matches 1392; Conservative		2; Mismatches 27; Indels 10; Gaps 2;
Qy	1005	AHPTGSHPIITVDANODDIYQPCGAGSLTRCSCGETKGYLVTRLSLVEVNSDDPYW 1064
Db	1	AHPTGSHPIITVDANODDIYQPCGAGSLTRCSCGETKGYLVTRLSLVEVNSDDPYW 60
Qy	1065	CVCALPMAVAKSGSAPILCSSGHVIGMFTAAARNSGSGVSIQIRVRPLVCAGYHPQYTAH 1124
Db	61	CVCALPMAVAKSGSAPILCSSGHVIGMFTAAARNSGSGVSIQIRVRPLVCAGYHPQYTAH 120
Qy	1125	ATLDTKTPVNEYSVOILIAPTGSGKSTKLPLSMQEKYEVVLNPSVATTASHPKTMHA 1184
Db	121	ATLDTKTPVNEYSVOILIAPTGSGKSTKLPLSMQEKYEVVLNPSVATTASHPKTMHA 180
Qy	1185	TYGVNPNCFYNGKCTNTGASLTYTYGYMLTGACSRNYDVIIICDECHATTATVLGIGKV 1244
Db	181	TYGVNPNCFYNGKCTNTGASLTYTYGYMLTGACSRNYDVIIICDECHATTATVLGIGKV 240
Qy	1245	LTEAPSKNRLVVLATATPPGVIPTPHANITEIQLTDEGTTIPFHGKKIKENLKKGRHLI 1304
Db	241	LTEAPSKNRLVVLATATPPGVIPTPHANITEIQLTDEGTTIPFHGKKIKENLKKGRHLI 300
Qy	1305	FEATKXGCHDELANELARKITAVSYRGCDISKIPEGDCVVVATDALCTGTGDFDSYVD 1364
Db	301	FEATKXGCHDELANELARKITAVSYRGCDISKIPEGDCVVVATDALCTGTGDFDSYVD 360
Qy	1365	CSLMVEGTCHVDLPTFTMGVRVCGVSAIVKQGRGRTGRGAGIYVYVDSCTPSGMWP 1424
Db	361	CSLMVEGTCHVDLPTFTMGVRVCGVSAIVKQGRGRTGRGAGIYVYVDSCTPSGMWP 420
Qy	1425	ECNIVEAFDAKAWYGLSSTEAQITLDTYRTQGLPAIGANLDEWADLFMSVNPPEPSFVN 1484
Db	421	ECNIVEAFDAKAWYGLSSTEAQITLDTYRTQGLPAIGANLDEWADLFMSVNPPEPSFVN 480
Qy	1485	TAKTADNYVLLTAAQLCHQYGAAPNDAPRWQGARLKKPCGVILWRLDGADACGPE 1544
Db	481	TAKTADNYVLLTAAQLCHQYGAAPNDAPRWQGARLKKPCGVILWRLDGADACGPE 540
Qy	1545	PSEVTRQMCFTVENTSTALAVGVGVAMAYLAIDTFPGATCVRCSWITSVPTGATVAP 1604
Db	541	PSEVTRQMCFTVENTSTALAVGVGVAMAYLAIDTFPGATCVRCSWITSVPTGATVAP 600
Qy	1605	VVDEEEIVEECASPIEAMVAADKLKSTITTTSPFTLETALEKLNFTFLGPHAATILAI 1664
Db	601	VVDEEEIVEECASPIEAMVAADKLKSTITTTSPFTLETALEKLNFTFLGPHAATILAI 660
Qy	1665	IEXCCGLVTLDPNPFASCVAFIAGITTPLPKHIMFLSLFGGAIASKLTDARGALAFMM 1724
Db	661	IEXCCGLVTLDPNPFASCVAFIAGITTPLPKHIMFLSLFGGAIASKLTDARGALAFMM 720
Qy	1725	AGAGTALGTWTSVGVFDMGGAASASTACLTFFKCLMGEMPTMDQLAGLVSAFNPAA 1784
Db	721	AGAGTALGTWTSVGVFDMGGAASASTACLTFFKCLMGEMPTMDQLAGLVSAFNPAA 780
Qy	1785	GVGVLSACAMFALTAGDPHWPNRLLTMLARSNTVCNEYFIATDRIRKLLGLEASTP 1844
Db	781	GVGVLSACAMFALTAGDPHWPNRLLTMLARSNTVCNEYFIATDRIRKLLGLEASTP 840
Qy	1845	WSVTSACIRWLHTPTDDCGLIANGLEITWQVVCNFFVICFNLKAGVQSMWNIPEGCFYS 1904
Db	841	WSVTSACIRWLHTPTDDCGLIANGLEITWQVVCNFFVICFNLKAGVQSMWNIPEGCFYS 900
Qy	1905	COXKYGPIWISGMLQARCPGABELISFVENGFALKYGPRTCSNYRGAVPVNRALCGS 1964
Db	901	COXKYGPIWISGMLQARCPGABELISFVENGFALKYGPRTCSNYRGAVPVNRALCGS 960
Qy	1965	ARPDPTDWTSLVNVGVRDYCKYKMGDHI FVTAVSSPNVCFTQVPTLRAAVADVQVQ 2024
Db	961	ARPDPTDWTSLVNVGVRDYCKYKMGDHI FVTAVSSPNVCFTQVPTLRAAVADVQVQ 1020
Qy	2025	QCYLGEPKTPWTSACCYGPDKGKTVKLPFRVDGHTPGVRMQLNLRDALETNDCSTNN 2084

Db	1021	OXYLGEPKTPWTSACCYGPDKGKTVKLPFRVDGHTPGVRMQLNLRDALETNDCSINN 1080
Qy	2085	TPSDEAAVSALVFQKQLRRNTQQLLEAISAGVDTTKLPAAPS-IBEVVVVRKQFRARTGSLT 2143
Db	1081	TPSDEAAVSALVFQKQLRRNTQQLLEAISAGVDTTKLPAAPSQIBEVVVVRKQFRARTGSLT 1140
Qy	2144	LPPPPSVPVGVSPESLQSRDPLLEGPSNLPPSPVVLQAMPMLLGLAGECNPFTAIGCAM 2203
Db	1141	LPPPPSVPVGVSPESLQSRDPLLEGPSXLPPSPVVLQAMPMLLGLAGECNPFTAIGCAM 1200
Qy	2204	TETGGGDDLPSPYPPKKEVSEWSEDSMTATTASSYVTGPPYKIRKGDSTQSAPAKRPT 2263
Db	1201	TETGXGXXLPSPYPPKKEVSEWSEDSMTATTASSYVTGPPYKIRKGDSTQSATAKRPT 1260
Qy	2264	KKKLGKSEFSCMSYTWTDVISFKTASKVLSTRAITSGFLKQSRSLVYVTEPRDAELRKQ 2323
Db	1261	KKKLGKSEFSCMSYTWTDVISFKTASKVLSTRAITSGFLKQSRSLVYVTEPRDAELRKQ 1320
Qy	2324	KVITINRQPLPPSPYVHKQVRLAKEKASKVGVGMMDYDEVAHAHTPSKSAKSHITGLRGTDVR 2383
Db	1321	KVITINRQPLPPSPYVHKQVRLAKEKASKVGVGMMDYDEVAHAHTPSKSAKSHITGLRGTD-- 1378
Qy	2384	SGAARKAVLDLOKCVAGEIIPSHYRQTVIIVPKBEVFVKTPQKPKKPPRLI 2434
Db	1379	-----VLDLQKCVAGEIIPSHYRQTVIIVPKBEVFVKTPQKPKKPPRLI 1422
RESULT 6		
AAR82068		
ID	AAR82068	standard; protein; 1422 AA.
XX	AAR82068;	
XX	AC	AC
XX	27-AUG-2003	(revised)
DT	02-JUL-1996	(first entry)
XX	Hepatitis GB virus (HGBV) clone protein prod.	
DE	Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine; reagents; non-A;	
KW	non-B; non-C; non-D; non-E; clone; tamarin; infected plasma;	
KW	lambda phage; cDNA library.	
XX	Hepatitis G virus.	
OS	Hepatitis G virus.	
Key	Location/Qualifiers	
FT	Misc-difference 1..1422	
FT	/notes "others correspond to degenerate or STOP codons in AAT00052"	
XX	W09521922-A2.	
XX	17-AUG-1995.	
XX	14-FEB-1995;	95WO-US002118.
XX	14-FEB-1994;	94US-00196030.
PR	13-MAY-1994;	94US-00242654.
PR	29-JUL-1994;	94US-00283314.
PR	23-NOV-1994;	94US-00344185.
PR	23-NOV-1994;	94US-00344190.
PR	27-JAN-1995;	95US-00344557.
XX	(ABBO) ABBOTT LAB.	
XX	Simons JN, Pilot-Mattias TJ, Dawson GJ, Schlauder GG, Desai SM;	
FI	Leary TP, Muerhoff AS, Erker JC, Buifk SL, Mushahwar IK;	
XX	WPI; 1995-293123/38.	
DR	N-PSDB; AAT00052.	
XX	Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful for	
FT	diagnosis and therapy of hepatitis GB virus.	

XX	Example 5; Page 245-249; 661pp; English.	
PS	Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV infected	
CC	tamarin plasma, using standard procedures, was used to prepare a lambda	
CC	phage HGBV cDNA library. The cDNA clone AAT00052, which encodes the	
CC	proteins AAR82066-71 (the 6 possible reading frames), was rescued from	
CC	the lambda phage, searched against a sequence database and found to be an	
CC	unique HGBV sequence. Reagents which comprise the HGBV DNA, or its	
CC	protein prods. can be used for the diagnosis, therapy or in a vaccine to	
CC	prevent HGBV infection. (Updated on 27-AUG-2003 to correct OS field.)	
XX	Sequence 1422 AA;	
SQ	Query Match 48.0%; Score 7375; DB 2; Length 1422;	
	Best Local Similarity 97.2%; Pred. No. 0;	
	Matches 1191; Conservative 2; Mismatches 28; Indels 10; Gaps 2;	
QY	1005 AHPTGSIHPIITVDAANDQDIYQPPCGAGSLTRCSGGETKGYLVTRLGLSLVEVNSDDPYW 1064	
DB	1 AHPTGSIHPIITVDAANDQDIYQPPCGAGSLTRCSGGETKGYLVTRLGLSLVEVNSDDPYW 60	
QY	1065 CVCAGALPMAVAKGSGAIPILCSSGHVIGFTTAARNSGGVSQIRVRPLVCAGYHPQYTAH 1124	
DB	61 CVCAGALPMAVAKGSGAIPILCSSGHVIGFTTAARNSGGVSQIRVRPLVCAGYHPQYTAH 120	
QY	1125 ATLDTPKTPVNEYSVQIILIAPTGSGKSTKPLPSYMOEYEVVLNPSVATTASMPKYMHA 1184	
DB	121 ATLDTPKTPVNEYSVQIILIAPTGSGKSTKPLPSYMOEYEVVLNPSVATTASMPKYMHA 180	
QY	1185 TYGVNPNCFYNGKCTNTGASLTSTYGYMLTGACSRNYDVIICDECHATTATTVLIGIKV 1244	
DB	181 TYGVNPNCFYNGKCTNTGASLTSTYGYMLTGACSRNYDVIICDECHATTATTVLIGIKV 240	
QY	1245 LTEAPSKVRLVVLATATPPGVIPPHANITBIQLTDEGTIPFHGKKIKEENLKGRHLI 1304	
DB	241 LTEAPSKVRLVVLATATPPGVIPPHANITBIQLTDEGTIPFHGKKIKEENLKGRHLI 300	
QY	1305 FEATKKHCDLANELARKGITAVSYRGCDSIKIPEGDCVVATDALCTGYTGDFDSYVD 1364	
DB	301 FEATKKHCDLANELARKGITAVSYRGCDSIKIPEGDCVVATDALCTGYTGDFDSYVD 360	
QY	1365 CSLMVEGTCHVDLDTFTMGVRVCGVSAIVKQRRGRTGRGRAGIYYVYDGSCTPSGMVP 1424	
DB	361 CSLMVEGTCHVDLDTFTMGVRVCGVSAIVKQRRGRTGRGRAGIYYVYDGSCTPSGMVP 420	
QY	1425 ECNIIVEADAAKAWYGLSSTEATQITLDYRTOPGLPAIGANLDEWADLFSWYNPPSFVN 1484	
DB	421 ECNIIVEADAAKAWYGLSSTEATQITLDYRTOPGLPAIGANLDEWADLFSWYNPPSFVN 480	
QY	1485 TAKRTADNVLLTAALQOLCHQYGYAAPPNDAPRWQARLKKPCGVLWRLDGDACAPGE 1544	
DB	481 TAKRTADNVLLTAALQOLCHQYGYAAPPNDAPRWQARLKKPCGVLWRLDGDACAPGE 540	
QY	1545 PSEVTRYQMCFTVNTSGTAAALAVGVGAMAYLAIDTFGATCVRRCWSITSVPTGATVAP 1604	
DB	541 PSEVTRYQMCFTVNTSGTAAALAVGVGAMAYLAIDTFGATCVRRCWSITSVPTGATVAP 600	
QY	1605 VVDEEIVEECASFPLEAMVAAIDKLSTITTTSPFLEALEKLNFTFLGPHAATILAI 1664	
DB	601 VVDEEIVEECASFPLEAMVAAIDKLSTITTTSPFLEALEKLNFTFLGPHAATILAI 660	
QY	1665 IEYCCGLVTLDPNPASCVFAFIAGITTPPHKIKWFLSFGATASKLTDARGALAFNM 1724	
DB	661 IEYCCGLVTLDPNPASCVFAFIAGITTPPHKIKWFLSFGATASKLTDARGALAFNM 720	
QY	1725 AGAAGTALGTWTSVGVFDMGLGYAASSTACITFKCLMGWEPTMDQLAGLVYSAFNPA 1784	
DB	721 AGAAGTALGTWTSVGVFDMGLGYAASSTACITFKCLMGWEPTMDQLAGLVYSAFNPA 780	
QY	1785 GVGVLSACAMPALTATAGDHPNRLLTMLARNTVCNEYFYATRDIRKILGILEASTP 1844	
DB	781 GVGVLSACAMPALTATAGDHPNRLLTMLARNTVCNEYFYATRDIRKILGILEASTP 840	

QY	1845 WSVISACIRWLHTPTEDDCGLIAMGLEIWOVCNFFVICFNVLKAGVQSMWNIPGCPFYS 1904	
DB	841 WSVISACIRWLHTPTEDDCGLIAMGLEIWOVCNFFVICFNVLKAGVQSMWNIPGCPFYS 900	
QY	1905 CQGYKGPWIGSMGLQARCPGABLIIFSVENGFAKLYKGPRTCSNYWRGAVPVNARLCS 1964	
DB	901 CQGYKGPWIGSMGLQARCPGABLIIFSVENGFAKLYKGPRTCSNYWRGAVPVNARLCS 960	
QY	1965 ARPDPDTWTSLVVNYGVDRDYCKYEKMGDHIETVTAIVSSPNVCFTQVPPTLRAAVADVQV 2024	
DB	961 ARPDPDTWTSLVVNYGVDRDYCKYEKMGDHIETVTAIVSSPNVCFTQVPPTLRAAVADVQV 1020	
QY	2025 QCYLGEPTKPTWTTTACCYGPDPGKGTWKLPFRVDGHTGEGVMQLNRLDALETDCNNTN 2084	
DB	1021 QCYLGEPTKPTWTTTACCYGPDPGKGTWKLPFRVDGHTGEGVMQLNRLDALETDCNNTN 1080	
QY	2085 TPSDEAAVSAVLFQELRRTNQLLEAISAGVDTTKLPAPS-IEEVVVKRQFRARTGSLT 2143	
DB	1081 TPSDEAAVSAVLFQELRRTNQLLEAISAGVDTTKLPAPS-IEEVVVKRQFRARTGSLT 1140	
QY	2144 LPPPRSVPVGVSCPSLQSRDPLSGPSNLPPSPVQLQAMPPLLGGAGECHNPFTAIGCAM 2203	
DB	1141 LPPPRSVPVGVSCPSLQSRDPLSGPSNLPPSPVQLQAMPPLLGGAGECHNPFTAIGCAM 1200	
QY	2204 TETGGGPDLLPSYPPKKEVSEWSDESSTATTASSYVTGPPYKIRGKDSQSAPAKRPT 2263	
DB	1201 TETGXPKXLPSPYPPKKEVSEWSDESSTATTASSYVTGPPYKIRGKDSQSAPAKRPT 1260	
QY	2264 KKLKGSFSCSMSTWTDVTSFPTASKVLSATRAITSGLFKQKSLVVTSPRDAELRKQ 2323	
DB	1261 KKLKGSFSCSMSTWTDVTSFPTASKVLSATRAITSGLFKQKSLVVTSPRDAELRKQ 1320	
QY	2324 KVTINRQPLFPSPVHKQVRLAKEKASKVGVWMDYDEVAHTPSKSAKSHITGLRGTDVR 2383	
DB	1321 KVTINRQPLFPSPVHKQVRLAKEKASKVGVWMDYDEVAHTPSKSAKSHITGLRGTD-- 1378	
QY	2384 SGAARKAVLDLQKCEAGEIPSHYRQTVIVPKEEVFKTPQKTKKPPRLI 2434	
DB	1379 -----VLDLQKCEAGEIPSHYRQTVIVPKEEVFKTPQKTKKPPRLI 1422	
RESULT 7		
AAB59172		
ID	AAB59172 standard; protein; 3033 AA.	
XX		
AC	AAB59172;	
XX		
DT	21-MAR-2001 (first entry)	
XX		
DE	Protein encoded by infectious Hepatitis C virus 2a genotype.	
XX		
KW	GBV-B; hepatitis C virus; HCV; vaccine.	
XX		
OS	Hepatitis C virus.	
XX		
PN	WO200075337-A1.	
XX		
PD	14-DEC-2000.	
XX		
PF	02-JUN-2000; 2000WO-US015293.	
XX		
PR	04-JUN-1999; 99US-0137694P.	
XX		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX		
PI	Bukh J, Yanagi M, Emerson SU, Purcell RH;	
XX		
DR	WPI; 2001-091214/10.	
XX		
PT	New infectious nucleic acids of the GB virus-B clone, useful for	
PT	indirectly studying the molecular properties of hepatitis C virus (HCV)	
PT	and in developing vaccines and therapeutics for HCV.	

[illegible]

Db	763	AASNGFLYF-----VIFVAA-----WYIKGRVPLATYS-----LTLGWS	799
Qy	717	LVALLTLHLVTPASAFDTEIIIGLTIPPVVALVMSRFGFFFAHLPRCALVNSYLQWR	776
Db	800	F--SLLLALPQQAAYADASVHGIGGAALLVMITLFTLTGYNKLLSR-----FLW--W	849
Qy	777	-----ENWFNVTLRPER---PFLVLVCPGATYDALVTFVCVHALLCLTSS	821
Db	850	LCYLLTLGEAMVQEWAPPQVQGRGDIIWAWAIFYPGVVFDITKW-----LLAVLGP	902
Qy	822	AASFFGTDSR-----VRAHRMLVRLGKC---HAWYSHYVLKPFLLVFG-NGVFFYKHL-	871
Db	903	AYLLKGNALTRVPFVRAHAL---LRMCTMARHLAGGYV-QMALLALGRWGTGIYDHLT	958
Qy	872	HGDVLNDPASKLPLOEP--FPFEGKARVYRNEGRRLACGDTVDGLPVVARGLDLVFA	928
Db	959	PMSDMAASGLRDLAVALVEPIIFSPMEKKVIMGAE--TAACGDILHGLPVSARLGREVLL	1016
Qy	929	GLAMPPD-----GWAITAPPTLOCLSERGTLSAMAVVMTCIDPRTWTGTTFRLGSLATS	983
Db	1017	G---PADGYTSKMSLLAPITAYAAQOTRGLLGTIVVSMTRGDKRTEQAGEIQVLSLTVTQSF	1073
Qy	984	MGFVCONVLTAAHSGKRRLEAHPGTSIIHPTIDAANDQDIYQPPCGAGSLTRCSCCETK	1043
Db	1074	LGTSISGLVMTVTHGAGNKTLAGSRGPVTQMYSSASGDLVGVSPPGTKLEPCTCGA	1133
Qy	1044	GYLVTRLGSILVEYNKSDDPYWCVPALPMAVARKSSGAPILCSSGHVIGMFTAARNSGG-	1102
Db	1134	LXLVTRNADVI ParrRGDKRGALLS PRPLSTLKGSGGPVLC PRGHAVGVFRAAVCSRGV	1193
Qy	1103	--SVSQRVRLPVCAGVHPQYTAHATLDTKPTVPNEYSVQILLAPTGSKGSTKLP	1160
Db	1194	AKSIDIFPVBETLIVTRSPTFSDNS---TPPAVPQTVQVGYLHAPTGSKGSTKVPVAYAA	1250
Qy	1161	EKYEVLVLPNSVATTASMPKYMHAATGVNPNPCYFNKGCTNKTGASLTYSTYKMWLT-GACS	1219
Db	1251	QGTVLVLPNSVAATLGFGLAYLSKAGININITGRTVTGTGAPITYSTYTKGLADGGCA	1310
Qy	1220	RN-YDVIICDECHATDATTVLGIKGKVLTEAPSKNVRVLVLATATPPGVIPTPHANITEIQ	1278
Db	1311	GGAYDIIICDEHAVDSTIIIGITVLDQAEAGVRLTVLATATPPGSVTTPHPNIEVA	1370
Qy	1279	LTDEGTIPFHGKKIKENLKKGRHLIFEATKHKHDELANELARKGITAVSYRGCDISKI	1338
Db	1371	LGOEGEIPFYGRAIPLSYIKGGGRHLIFCHSKKCDLAAALRMGLNSVAYYRGLDVSVI	1430
Qy	1339	P-BGDCVVAATDALCTGYCDFDSVDCSLMWEGTCHVDLDPTFTMGVRVCGVSAIVKGO	1397
Db	1431	PTQGDVVVAATDALMTGYTGDFDSVIDCNVAVTQVVDVFLDPTFTITQIQPDQAVSRSQ	1490
Qy	1398	RRGRTGRGAGIYVYDGSCTPSGWPPECNIVBFAAATAWYGLSSTEAQOTILDTRTOP	1457
Db	1491	RRGRTGRGLGIYRYSTGERASGMFDSVVLRCYDAGAAWYELTSETTVRLRAYENTP	1550
Qy	1458	GLPAIGANLDEWADLFS--WYNPEPSFVNTAKRTADNYVLLTAAQLQCHQYGYAAPNDAP	1516
Db	1551	GLPVCQDHLBFEAVFTGLTHIDAHFLSQTKSGENFAVLTAYQATVCAR----AKAPP	1606
Qy	1517	RWQARGLKXPCGVWLRLDQADAC-----PGPEP-----SEVTRY--	1551
Db	1607	SWD-----VMWK-----CLTRLKFTLVGPTPLLYRLGSLVNTNEVTLTHPVKYIA	1650
Qy	1552	--QWCFTEVNTSGTAALAVGVGVAMAYLAIDTFGATCVRRCWSTITSVPTCATVAPVVD	1609
Db	1651	TCWQADLEWMTS--TWLWAGVLAAYAYCLAT--GCVCIIORLHQ---RAVAP--DKE	1703
Qy	1610	EI-----VEBCASFIPL--BAMVAADIKLKSTI-----TTTSPFTLEALEKLN	1651
Db	1704	VLVEAPDEMEECASRAALIEEGORIAEMLKSKIQGLLQQAQKQADIQP-TVQAQSPKVE	1762
Qy	1652	TFGLGPHAANTLAIIEYCCGLVTLPDNPFASCVAFATGIITPLPHKIKMFLSFGGAIAS	1711
Db	1763	QWAKHMMNFIISGQYLAGLSTLFGNPAVAMMAFSAALTSPLSTSTTIIILILGWLAS	1822

Qy	1882	ICFNVLKAGVQSMVNI	PGCFYQCKGKGPWIGSGMLQARCPGABELI	PSVENGFAKLY	1941
Db	1994	DFKNMLTS--	KLFPKMBGLFVFCQKYGKGMAGTIGIMTRCPCGANISGNVLGSMRI-	2050	
Qy	1942	KGPRTCNSYWRGAVPVNARICGSARPDPT-	DWTSLVVNYGVDRYCKEKGMDHIFVTAVS	2000	
Db	2051	TGPKTCNNIWO	GTFPINCYTEGOCVPKPAFNFKVAIWRVAASAEYVTOHGSYHYITGLT	2110	
Qy	2001	SPNVCFQVBP--	PTLRAAVAVDGVQVQCYLGBPKTPWITS-ACCYGPDCGKTKVLPFR	2056	
Db	2111	TDNL--	KVFCQLPSPBFFSWDGVQIHRAPTPKPFPRDEVFCVGLNSFVVGSQLP	2167	
Qy	2057	VDGHTEGVRMQLNRD----	ALETNDCSNTNPTSPDEAAVSA-LVFKQELURRT	2104	
Db	2168	PEPDT-DVLMSM-LTDP	SHITAETARRLARGLARGSPPSSEASSASQLSAPSRATCTTHGKA	2225	
Qy	2105	--NQLEEA-ISAGV	DTTKLPA-----PSI-EVVVVRKQRPART	2139	
Db	2226	YDVMNDANLPMGDG	VTRIESGSKVVVLDLPMVEERSOLEPSIIPSEYMLPKKRF----	2281	
Qy	2140	GSULTPP--	PPRSYPGVSCP--ESLQSD-----PLEGSPNLPSPSP-----	2177	
Db	2282	-----PPALPAWARP	DYNPLVESWKRPDYQATVACALPPRPKTPTPPPRRRTVGLS	2336	
Qy	2178	-----VLQAM-----	PMPLGAGCNPFTAIGC-----AMTETGG-----	2208	
Db	2337	EDSIGDALQOLA	IKSFCQPPP--SGDSGLSTAGAADSGSQTPDPDELALSETSGISSMP	2393	
Qy	2209	-----CPDDL-----	PSYPPKKEV--SEMSDE-SWSTATASSYVTPGPPYKIRGKDS	2254	
Db	2394	PLEGELGDPDL	PEPQVPEPQPGVAAPOGSDSGSWSTCEEDSVV-----	2440	
Qy	2255	QSAKAPERTKK	KLKGSFSCSMSTYTTWD-VISFKTASKVLASATRAITSGFLKORSLYVT	2313	
Db	2441	-----CCSMSYSMTG	ALIITPCSPEEKLPIPLNSLLRYHNKYCT	2482	
Qy	2314	EPDABELRKQV	TINRQPLPPSPYHKQVRLAKEKASKVGVGMWDYDEVAHTSPSKASKH	2373	
Db	2483	TTKSASLR	AKKVTDRMQLVDSYDVLKDIKLAASKVTARLLTMEACQLTPHARSK	2542	
Qy	2374	ITGLRGTDVR--	SGAARKAVLDLQK-CVEAGEI PSHVRQTVIYPKEBVFVKTPOKTPKP	2430	
Db	2543	Y-GFGAKEV	RLSGRANHIKSVWKOLLESETPI-----PTTIWAKNEVFCVDTKGGKKA	2598	
Qy	2431	PRLISYPHLE	KVRCVKMYGQVAPDVVKAVMGDAYF-VDPRTVRVKLLSMWS--PDAVG	2487	
Db	2599	ARLIVYPDL	GVRCCKMALYDITQKLPQAVMGASYGFOYSPAQRVEFLLKAWAEKKDPMG	2658	
Qy	2488	ATCDTVC	FDSTITIPEDIMVETDIYSAKLSDOHRPAGIHTTARQLYAGGPMIAYDGREIGY	2547	
Db	2659	FSYDTRCFD	STVTERDITREESIRACSLPEEAHTA IHSUTERYLVGGPMFNSKGQTCGY	2718	
Qy	2548	RRCRSSG	VYTTSSNSLTCMLKVNAAEQAGMKMPRELI CGDDCTVIWKSGADADAKQAM	2607	
Db	2719	RRCBAS	GLTTSMTNTITCYVKALAAKKAAGI IAPTMLVCGDDLVLVISESQTEEDENL	2778	
Qy	2608	RVFASMKV	MGAPQDCVPQPKYSLEBITSCSSNVTSGITSGKPYXFLTRDPRILGRCS	2667	
Db	2779	RAFTEANTRY	SAPPGDPRPEYDLELITSCSSNNVSVALGPOGRRRYLLTRDPTTPIARAA	2838	
Qy	2668	AEGLGYNPS	AAWIGYLIHHYPCLVWVSVLAVHFEQMLPEDKLPTETVTDWYKGNVTPV	2727	
Db	2839	WETVRHSP	VNSWLGNIIOYAPTI IWARVLMTHFFSIIQAQDLDQNLNFEMYGAVYSVP	2898	
Qy	2728	EDLP	SIAGVHGIEAFSVVRYTNAEILRVOSLDTMTMPLLRWKRKARVASAKERGG	2787	
Db	2899	LDLPA	ILERLGLDAFSLHTYTPHELTFVASALRKLGNAPLRAWSRARAVRASLISERG	2958	
Qy	2788	AHAKLAR	PILL-WHATSR-----PLPDOKTSVARVYTTNYCDVYSPGSDVFTIPORLQKF	2842	
Db	2959	RAAVCG	RYLFNWA VKTLKLTLPPEARLLDLSWFT-----VGAGGDDIYHSVGRAPRL	3013	

Qy	2843	LVKYLAVIVFALGHLIAVGLAI	2863
		:	:
Db	3014	L-----LFGLLLLFVGVL	3027
RESULT 9			
AB30729			
ID	AA30729	standard; protein; 3033 AA.	
XX	AC	AA30729;	
XX	XX	02-APR-2001 (first entry)	
XX	XX	Amino acid sequence of infectious Hepatitis C virus strain HC-J6CH.	
DE	XX	HCV; HCV strain HC-J6CH; HCV genotype 2a; antiviral; vaccine.	
XX	XX	Hepatitis C virus.	
OS	XX	WO200075338-A2.	
XX	XX	14-DEC-2000.	
XX	XX	02-JUN-2000; 2000WO-US015446.	
PF	XX	04-JUN-1999; 99US-0137693P.	
XX	XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
FA	XX	Yanagi M, Bukh J, Emerson SU, Purcell RH;	
PI	XX	WPI; 2001-061728/07.	
XX	XX	N-PSDB; AAC86644.	
DR	XX	Nucleic acid molecule encoding human hepatitis C virus of genotype 2a for	
PT	XX	developing vaccines, for diagnosis of hepatitis C virus and in screening	
PT	XX	assays for identification of antiviral agents.	
PS	XX	Disclosure; Page 88-99; 167pp; English.	
XX	XX	The present sequence represents an amino acid sequence of infectious	
CC	XX	Hepatitis C virus (HCV) strain HC-J6CH genotype 2a. The HCV	
CC	XX	polynucleotide sequence is capable of expressing the virus when	
CC	XX	transfected into cells. The HCV protein is useful for assaying candidate	
CC	XX	antiviral agents for activity against HCV. Antibodies specific for HCV	
CC	XX	polypeptide are useful in prevention and treatment of diseases caused by	
CC	XX	HCV in animals, in particular humans. The HCV polypeptides serve as	
CC	XX	immunogens in the development of vaccines for preventing HCV in mammals	
CC	XX	or as antigens in diagnostic assays for detecting the presence of HCV in	
CC	XX	biological samples. The HCV polynucleotide is also useful for identifying	
CC	XX	cell lines capable of supporting the replication of HCV in vitro and to	
XX	XX	produce attenuated viral strains via passage in vitro or in vivo	
SQ	XX	Sequence 3033 AA;	
Query Match			
Best Local Similarity 21.3%; Score 3277.5; DB 4; Length 3033;			
Matches 987; Conservative 436; Mismatches 1197; Indels 641; Gaps 117			
Qy	8	TSPVPAPTRKNKQTQASYPVSIK-----TSVERGQRAKRVQORDAPR	51
		:	:
Db	3	TNPXPQRTKNTNR---PQDVKPPGGQIVGGVLLPRRGPRLGVRAKTRKTSRSQPR	59
		:	:
Qy	52	NYKTAGIHGGLTQAALPAH-----GWGRQDPRHKSRL	87
		:	:
Db	60	GRROPPIPKDRRSTGSKWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDRPHRSRNV	119
		:	:
Qy	88	GILLDYPGLGWIGDVTHTPLVG-PLVAGAVRVPVQIVRLLDGDVNWATG---WFGVHLF	143
		:	:
Db	120	GKVIDTLTCGFADLNGYIPVVGAPL--GGVARALAHGVRLDGDVNFATGNLPGCSFSIF	177
		:	:
Qy	144	VVCLLS-LACPCSGARVTDPTNTTILTNCCORNQVIYCSPTCLHPCVCIVC-----AD	197
		:	:


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QY 2105 --NQLEA-1SAGVDTTKLPA-----PSI-EEVVRKQFRART 2139
D 2236 YDVMVDANLFWGDDVTRIESGSKVVVLDSDPMVEERSDLEPSIPSEVMLPKKF----- 2281
QY 2140 GSLTLP--PPRSVGVSCP--ESLQSD-----PLEGPSNLPPSP-- 2177
D 2282 -----PPALPAWAPDYNPPLVESWKRDPYQATVAGCALPPRKTPTPPRRRTTVGLS 2336
QY 2178 -----VLQJAM-----PMLLGAECNPFTAGC-----AMTETGG----- 2208
D 2337 EDSIGDALQQLAIFSGQPPP-----SGDSGLSTGAGAAGSGSTPPDEALSETGISMP 2393
QY 2209 -----GPDLL-----PSYPPKKGV-SWSTATTASSYVTGPPYKIRGKDS 2254
D 2394 PLEGELGPDLEPEQVEQPPQGGVAAPGSDSGSMSTSEEDDSVV----- 2440
QY 2255 QSAPAKRPTKKLKGSEFSCSMSYTWTD-VISFKTASKVLNATRAITSGFLKQRLSVYVT 2313
D 2441 -----CCSMYSYWTGALITPCSPBEKPLPINPLNSLLRYHNKVYCT 2482
QY 2314 EPRDAELRKQVTINRQPLPPSYHKQVRLAKEKAKVGVVMDYDEVAHAHTPSKSAKSH 2373
D 2483 TTKSASLRAKVKTFORMQVLDSDYDSVLKDILKAAKVTARLLTMEEAACQLTPPHSARSK 2542
QY 2374 ITGLRGTDVR--SGAARKAVLDLQK-CVEAGEIPSHYRQTIVTPKKEVFVKTPQKTKKP 2430
D 2543 Y-GFCAKEVRSLSGRAVNHKSVWKDLLEDSETPI---PTTIAMKNEVFCVDPDTKGKKA 2598
QY 2431 PRLISYPHLEMRCEVMYGVQVAPDVKAVMGDAYGF-VDPRTVRKRLLSMWS---PDVAVG 2487
D 2599 ARLLIYPLDGLVRVCEKMALEDITQKLPQAVMGASYGFQYSPAQVFEFLKAWAEKKDPMG 2658
QY 2488 ATCDTVCDFDSTTPEDIMVETDIYSAKLSDQHRAGIHTIARQLYAGGPMIAYDCRETY 2547
D 2659 FSYDTRCFDSTVEDIRTEESYRACSLPEEAHTAIHSLTERLYVGGPMFNSKQTCGY 2718
QY 2548 RRCRSSGYVTSSSSNLTCWLKVNAAAEOAGMKNPRFLICGDDCTVIWKSAGADADKQAM 2607
D 2719 RRCRASGLVITSMGNTIITCYKALAAKAAAGIIAPTMLVCGDDLAVISESQTEEDERNL 2778
QY 2608 RVFASWKMVGAPQDCVPQPKYSLELTSCSNVTSGITKSKPYFYLTRDRIPLRGCS 2667
D 2779 RAFTAMTRYSAAPPDPRPEYDLELITSCSNVSVALGPGQRRRYLYLTRDPTPIARAA 2838
QY 2668 AEGLYGNPSAAMIGYLIIHHYPCLVWSRVLAHFMEQMLFEDKLPETVTFDMYKNTYVPV 2727
D 2839 WETVRHSPNSVNLGNIITQAPTIWARMVLMTHFFSILMAQDLDQNLNFMETGAVYVSP 2898
QY 2728 EDLPSIIAGVHGIEAFSVVRYTNABILRVSQLTDMTPPLPRAWKRCARAVLASAKRRGG 2787
D 2899 LDLPALIERLHGLDAFSLHTYTPHELTTRVASALRKLGAAPLRAWKSARAVRASLISRG 2958
QY 2788 AHAKLARFLL-WHATSR-----PLDLDKTSVARYTTFNVCDVYSPGEGVFITPQRRLKF 2842
D 2959 RAAVCGRYLFNVAWVKLKLTPLEARLIDLSSWFT-----VGAGGGDIYHSVSRARPL 3013
QY 2843 LVKYLAVIYFALGLIYAVGLAI 2863
D 3014 L-----LFGLLLLLVGVGL 3027

RESULT 10
ID AAR33539
XX AAR33539 standard; protein; 3033 AA.
AC AAR33539;
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-JUL-1993 (first entry)
XX NANBH virus strain HC-J8 protein.
DE
XX
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KW Non A non B hepatitis virus; plasma; degenerate.
XX Non-A.
OS non-B hepatitis virus.
XX EP532167-A2.
XX 17-MAR-1993.
XX 30-JUL-1992; 92EP-00306952.
XX 09-AUG-1991; 91JP-00287402.
PR 05-DEC-1991; 91JP-00360441.
XX (IMMO ) IMMUNO JAPAN INC.
XX Okamoto H, Nakamura T;
XX WPI; 1993-087166/11.
DR P-PSDB; AAQ38221.
XX Polynucleotide(s), polypeptide(s) and antibodies of NANBH virus - useful
PT for detecting NANBH, as a vaccine and for screening blood samples.
XX Claim 8; Page 65-79; 93pp; English.
XX RNA was isolated from the plasma of human patients positive for NANBH
CC virus (strain HC-J8) and was subjected to reverse transcription to
CC produce cDNA. The resulting cDNA was amplified by PCR, and nucleic acid
CC sequences determined by analysis of clones obtd. by PCR amplification (42
CC clones in total). The NANBH HC-J8 genome was found to contain a
CC degenerate open reading frame encoding polypeptide precursors of 3033
CC amino acid residues. See also AAR33538 and AAR33214. (Updated on 25-MAR-
CC 2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 3033 AA;

Query Match 21.3%; Score 3268.5; DB 2; Length 3033;
Best Local Similarity 30.0%; Pred. No. 9.1e-244;
Matches 983; Conservative 433; Mismatches 1185; Indels 679; Gaps 106;

QY 8 TSPVAPRTRKNKQTSYPSVIK-----TSVERGQAKRKVORDAPR 51
D 3 TNPKP---QRKYKNTNRRPQDVKFPGGQIVGVYLLPRRGRPLGVRAKTRKTSERSQPR 59
QY 52 NYKTAGHDGQLTAAQALPAH-----CHGRODPBKHSNL 87
D 60 GRROPDKORRSTGKSMGKPGYPMPLYGNECGWAGMLLSPRGSRPWTGPTDPRHRSNL 119
QY 88 GILLDYPGLMGIDVTHTPLVGLVAGAVRPVQIVRLLEDGVNWTG---WFGVHLFV 144
D 120 GRVIDTTCGADLMGYIPVVGAPV-GGVARALAHGVRLVEDGINATGNLPGCSFSIFL 178
QY 145 VCLLS-LACPCSGARVTPDPTNTILNCCORNQVYCSPTCLHEPGCVTCABE----- 198
D 179 LALLSCVTPVPSAVEVRN-ISSVYATNDCNNSITWLTDAVLHLPVCVPCENDNGLH 237
QY 199 CWVPANPYISHPSNWTGDSFLADHIDFWMGALVTCDALDIGELCCACVLVGDMLV---- 254
D 238 CWIQVTNVAVKHKGALTRS-LRSHVDMIVMAATACSAIYVGDVCGAVMILSQAQFMVSPQ 296
QY 255 RHLLIHLDNETGTCYLEVPTGIDPGLFGFTGMWAGKVEAIVFLTKLASQVPIATATMFS 314
D 297 RH-----NFTQECNCSIYQGHITGHRMADMWMLSNSTLTMILAYAAARPELVLEIIF 349
QY 315 SVHYLAVGALIYYASRGKWQLLALLMLY--IEAT--SGNPRIPVPTCCSIAEFCSPMLI 369
D 350 GGHGWVFLAYFSGQAWAKAVIAILLVAGVDATTYSQG-----EAGRTVAGFAGLETT 405
QY 370 PCPCHSYLSE-----NVSEVIC-----YSPKWT-----RPI--- 395
D 406 GAKQNLVINTNGSWHINRSALNCNDSLOTGFLASLFYTHKFNSSGCCPERLSSCGLDGF 465
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Qy 396 -----TLEYNNIS-----W-YP-----VTIPGRCM----- 417
Db 466 RIGMTLEYETNVNDGDMRCPCHYPRPGGIVPARTVCVPVCFPTSPVVGTTDKQG 525
Qy 418 -----VRFKNT-----NGC-----CRIR-----NVPSC 437
Db 526 VPTVTGENETDVELLSTRPRGAWFGCTWMNGTGFTKTCGAPPCIRIKDYNSTIDLLC 585
Qy 438 TMGTDAVMNDTRNTYEACGVTPMLT-----TAMHNGSALKALIQ-----YPGSKEMF 485
Db 586 P--TDCFRKHDPATVLCGAGFPLTPRCLVDYPVRLMHPYCTVNTFIKARMYVGVGE-- 641
Qy 486 KPHNMMSGHLYF-----EGSDTPIVYFDPVNSTLLPERRWARLPCTPPVVRGS 534
Db 642 --HRFSACNFRGDRCKLEDRCGOQSPLLH-----ST-----TEWAVLPCS----- 682
Qy 535 WLQVPOGYPYSDKDLATGLITKDAWKYQVLYSATGALSITGVTTKAVVLILGLCGSK 594
Db 683 -----FSDLPALSTGLLHLHQNIVDVQVLYGLSPALTRYIVKWEVILFLLLADAR 734
Qy 595 YLILAYLCYLSLCFRASGYPLRPLVPSQSYLQAGWDVLSKAOVAPFALIFFICYLCR 654
Db 735 --ICACLWMLI-----ILGOAEALAKLII----- 757
Qy 655 LRYAALLGFVPMAGLPLTPFFVAAAQAQPDVWVRLLVAGLVWAGNRGHRITALLVGP 714
Db 758 -----LHSASAASANGPLWFIPTAA-----WYLGKRVVPVATYS-----VLGL 797
Qy 715 WPLVALLTLHLVTPASAFDEIIGGLTI PPVALVWMSRFGFPAHLLPRCALVNSYLM- 773
Db 798 WSP--LLVLALPOQVADALDAEAGELGLALVLSISITLTPAYKILLRSVWMLSYMLV 855
Qy 774 -----QRW-----ENWFW-NVTLRPERFLV---LVCPPGATYDALVTFVCVCHV 813
Db 856 LAEAIQIQWVPPLEVRGGRDGIIVAVILHPLRPFVETKMLAILGPAY----- 904
Qy 814 ALLCLTSSAASFFGTDSRVARHML--VRLGKCHAMYSHYVLYKFLVFGNGVFFYKHL 871
Db 905 -LLKASLLIRIPYF-----VRAHALLRVCTLVK-HLAGARYIQMLLITIGRWTGYIYDHL 957
Qy 872 HGDVLPNDPASKLPLO-----EP--FPPEGKARVYRREGRLACGDTVQG 915
Db 958 S-----PLSTWAAOGLRDLAIAVPPVVFSPMEKKVIVWGAE--TVACGDILHG 1003
Qy 916 LPVVARLDLVFAGLAMPDP-----GWAITAFTLQCLSERGILTSAMAVVMGTIDPRWT 970
Db 1004 LPVSARLGREVLG--PADGYTSKGWKLAPITAYTQOTRGLGAIIVLSITGRDNEQA 1060
Qy 971 GTIFRLGLSATSYMGFVCDNVLYTAHSGSKRRLAHPTGSIHPITVDAANDODIYQPPCG 1030
Db 1061 GOVQVLSVTQTFLGTSISGLVLTWYHGAGNKTLAGPKGPVTOMYTSAGDLVGPSPPG 1120
Qy 1031 AGSLTRCSGKTYGLVTRGLSLVEYNKSDPYVCVCGALPMVAKGSSGAPILCSSGHV 1090
Db 1121 TKSLDPCCTCGADVLYLVRNADVIVPRKDRRGLALSPLRLTKGSSGGPVLCSRGA 1180
Qy 1091 IGMFTA--ARNSGSVSQIRVRPLVACAGYHPQVTAHATLTKPTVNEYVQVLIAPTG 1147
Db 1181 VGLFRAAVCARGVAKSIDFIVESLDVARTPTPSFSDNS--TPPAVQSVQVGYLHAPTG 1237
Qy 1148 SGKSTKPLSPYQBKEYVLVLPNSVATTASPMKYMHATYGVNPNCYFNGKCTNTGASLT 1207
Db 1238 SGKSTKVPAAVASQYKVLVLPNSVAATLFGAYMSKAHGINPNIRTCVRTVTGDSITY 1297
Qy 1208 STYGHYLT--GACSRNDYVILCDECHADATVTLGIGKVLTEAPSKNVLVLTATATPPG 1265
Db 1298 STYKFTADGKAAGAYDIIICDECHSDVATITLIGITVLDOAETAGVRLVYVLTATATPPG 1357
Qy 1266 VIPTPHANITBIQUTDEGTIPFHGKKIEENLKKGRHLIPEATKKCHDELANELARKGIT 1325
Db 1358 TVTTPHNSNIEVALGHEGIEIPYKAIPLAIFIKGRHLIFCHSKKKCDELAAALRGWVN 1417
Qy 1326 AVSYRGCDISKIP-EGDCVVVATDALCTGYTGDVDSYDCSLMVEGTCHVDLDPFTTMG 1384

Db 1418 AVAYYRGLDSVPTQGDVVVVVATDALMTGYTGDVSDVIDCNVAISOIVFSLDPTTIT 1477
Qy 1385 VRVCGVSAIVKQORRGTRGRAGIYVYVDSGCTTPSGMVPCECNIVEAFDAKAWYGLSS 1444
Db 1478 TQVVPQDAVSQRGRGTGRGLGVYVYVSSGRRPSGMFDSVLCYCDAGAAWYELTPA 1537
Qy 1445 EAOTILDITYTQGLPAIGANLDEWADLFS-MVNPBPSFVNTAKRTADNVYLLTAAQLQL 1503
Db 1538 ETTVRLRAYENTPCLPVCQDHLFWEAVFTCLTHIDAHFLSQTQKQGENFAYLTAYQATV 1597
Qy 1504 CHQGYVAAPNDAPRWQARGLKGPCGVLRDLGDAC-----PGPEP----- 1545
Db 1598 CAR-----AKAPPPSWD-----VMWK-----CLTRLKPTLTGTPPLLYRLGAVTN 1637
Qy 1546 -----SEVTRY-----QMCFTEVNTSGTAALAVGVGVAMAYLAIDTFGATCVRRCWSITS- 1595
Db 1638 EVLTLTPVTKYIATCQADLEIMTS-SWVLAGGVLAAVAAYCLAT-----GCISIIGR 1689
Qy 1596 --VPTGATVAPVDEE-----EIVBECASFIPU-EAMVAAIDKJKSTI-----TTTSP 1640
Db 1690 LHLNDRVVVAP--DKETLYEAFDEMERCASKAALIEBQORMAEMLSKIQGLLOQATROA 1747
Qy 1641 FTLETALE-----KLNTFLGPHAATILAIIEYCCGLVTLDPNPPASCYVFAITAGITPLPH 1696
Db 1748 QDIOPAIQSSWPKLQEFWAKHMNFISGIOYLAGLSTLPGNPAVASMMAFSAULTSPLT 1807
Qy 1697 KIMFSLFGALASKLTDARGALAPMAGAAGTALGTWTSVG---FVFMGLGYYAAASS 1753
Db 1808 STTILLNIMGWLASQIAPPAGATGVVSGLVGNAV---SIGLTKLVDVLVAGYAGIS 1864
Qy 1754 TACLTFKCLMGWPTMDQLAGLVYAFNPAAGVVGVLVSACAMFALTAGDP--HWPNRLL 1811
Db 1865 GALVAFKIMGSEKPTVEDVNVLLPALSPCALVVGIVICAAILRRHVQGGEGAVQWNRLLI 1924
Qy 1812 TMLARSTVNCNEFIATDRIRKILGLEASTPWSVISACIRMLHTTEDDCGLI---AW 1868
Db 1925 AFASRGNHVAPTHYVWESDASQRTQVLSLT-----ITSLRLRLHAWITEDCPVPCSGSW 1980
Qy 1869 GLEIWOQVVCNFFVICENVLKAGVQSMVNIIPGCPYSCQKYGKPGWISGMLQARCPGAE 1928
Db 1981 LODIWDVWCILTDPKWLSS--KLPLKPMGPIPIPCQKYGKVGWAGTGMVTTCPGCA 2038
Qy 1929 LIFSVEVNGFALYKGPRTCSNYWRGAVPVNARLCSGARP-DPTDWTSLVNVYGVDRYCK 1987
Db 2039 ISGHVRMGTKMI-TGPKTCLNLMOGTFPINCYTEGCPVKPPPNYKTAIMRVAASEYVEV 2097
Qy 1988 EKMGDHIPTAVSSPNVCTQVP---PTLRAAVALDVGVQVQCYLGEKPTPTWTTACCYGP 2044
Db 2098 TQHGFSYFVTLGTSNDL---KVPQVPAPEFFSVWDGVQIHRFAPV-----GP 2143
Qy 2045 DGKGTVKLPRVDGHTPGVRMOLNLRDALETNDCNSTNTPSD---EAAVSALVFKQEL 2101
Db 2144 FFRD---EVTFTVGLNSFVVGSQLPCDPEPTEVLASMLTDPSSHITAEAAARLARSGP 2200
Qy 2102 RRTNQLLEAISA-----GVDTTKLPA----- 2122
Db 2201 SQASSASQLSAPLSKATCTTHKTAYDCDMVDANLFGDGVTRIESDSKVILVLSLDSMT 2260
Qy 2123 -----PSI-BEVVVRKROFRARTGSLTLP PPPRSPVPGVSCPSLESORSDPLEGPNLPP 2174
Db 2261 EVEDREPSVPSEYLIKKRKFPP-----ALPPMAR-----PD 2292
Qy 2175 SPVVLQALPMPILLGAGECNPFTAIGCAMTETGGPDDLPSYPPKKE----- 2221
Db 2293 YNPVLIETWRP-----GYBPPTVLGALPPT-----PQTPVPPRRRRRAKVLTDQNEGV 2343
Qy 2222 -----VSEWSESWSTATTASSYVTGPPYKPIRGK 2251
Db 2344 LREMADKVLPLQDNNDGSHGTGADTGDIVQOQPSDE--TAASEAGLSLSSMPPLEGBGD 2401
Qy 2252 DSTQ-----SAPAKR-----PTKKLKGSEFSCSMYSYTWTD-VISFKTASKV 2292

2402	PDLEFEPVGSAPSEGECEVIDSDSKSWSTVSDQEDSVICSSMSYSGWTGALITPCQPEEE	2461
2293	LSATRAITSGFLKORSUVVYTEPDAELRKQKVITINRQPLFPSPYHKQVRLAKEKASKV	2352
2462	KLPIPLNSLIMRPHNKVYSTTSRSASLRKAKVTFDRVQVLDHAHYDSVLQDVKRAASKVS	2521
2353	GVMWDYDEVAHAHPSKSAKSHITGLRGTDVRSNAARKAVIDLQCKVEAGEIPSHYR-QTV	2411
2522	ARLLTVVEEACALTPPHSAKGRY-GFGAKEVRS-LSRRAVNHIIRSVWEDLLEBHTPTIDTT	2579
2412	IVPEEYFVKTPOKFTKPPRLISYPHLEMKRCVEKMYGVAPDVVKAVMGDAYGR-VDP	2470
2580	IMAKNEVFCIDPYKGGKKPARLIYVPLGVYRCEKMALOYIAQKLPRAIMGSPYGFQYSP	2639
2471	RTRVKRLLSMW--SPDVGATCDVCPDSTITTPEDIMVETDIYSAAKLSQDHRAGIHTIA	2528
2640	AERVDFLLKAWGSKKDPMGFSYDTRCFDSTVTERDIRTEESIYQACSLPQEARTVIHSLT	2699
2529	RLIYAGGPMIAYDGREIGYBRCRSSGVYTTSSNSLTCWLKVAAAEOAGMKVPRFLICG	2588
2700	ERLYVGGPMTNSKGQSGCYGRCSRASGVFTTSMGNTMTCYIKALAAACAAAGIVDFVMLVCG	2759
2589	DDCTVIWKSAGADAKQAMRVFASWVKMGAPQDCVPQPKYSLEETSTCSSNVTSGITKS	2648
2760	DDLWVISESQNEEDENLRAFTTEAMTRYSGAPCDLPRPEYDELELITCSSNSVVALDSR	2819
2649	GKPYFYFLTRDPRIPLGRCSAEGLYNPSAAWIGYLIIHHYPCLVSVRVLAVHFMEQMLFED	2708
2820	GRRRYFLTRDPTTPIITRAAWETVRHSVPNSWLGNIIOYAPTIVRWVMIMTHFTSILLAQD	2879
2709	KLPEVTTFDVKYKNYTPVPELPSIIAGVHGIEAFSVVRYTNAEILRVSSQSLDTMTMPPPL	2768
2880	TLNQNLNFEWYGAVYSVNPDLPAIBRLHGLEAFSLHTYSPHELRSVAATLRKLGAPPL	2939
2769	RAWRKARAVLASAKRRGGAAKLARPELL-WHATSR----PLPDLDKTSIVARTTYNYCD	2823
2940	RAWKSARAVRASIIAQARAAICGRYLFNWKVKTKLPLPEASELDSLGHFT-----	2994
2824	VYSPGQDVFTTPQRRLOKFLVKYLAIVFALGLIAGLAI	2863
2995	VGAGGGDIYHVSGHARPRLL-----LLCLLLISVGVI	3027

RESULT 11
ABG30698

ABG30688
ID ABG30688 standard; protein; 3033 AA.

AC ABG30688;

DT	07-OCT-2002	(first entry)
XX		

DE Human HCV-related polypeptide.

XX Hepatitis C virus; human; virucide; gene therapy; HCV;
KW fulminant hepatitis C.
KW

XX
OS Homo sapiens.

XX PN JP2002171978-A.

XX
PD
18-JUN-2002.

01-DEC-2000: 2000JP-00367365.

PR 01-DEC-2000: 2000JP-00367365.

PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.

FA (TORA) / TORAY IND INC.
XX

DR WPI; 2002-569884/61.

DR N-PSDB; ABK88904.

PT A gene of a fulminant hepatitis C virus strain and the encoded

PT polypeptide useful in gene therapy to treat hepatitis C.

PS Claim 1; page 25-33; 36pp; Japanese.

CC The invention relates to a human polypeptide related to hepatitis C virus
CC (HCV), and the polynucleotide encoding it. The polypeptide can be used
CC for the development of gene therapy on fulminant hepatitis C. This
CC sequence represents a human HCV-related polypeptide

Sequence 3033 AA;

Query Match 21.2%; Score 3265.5; DB 5; Length 3033;

Best Local Similarity
29.8%; Pred. No. 1.6e-243;

Matches 964; Conservative 453; Mismatches 1232; Indels 583; Gaps 101;

Qy	8	TSPVPA	TRKQV	---KQTOASYP---	-----VSIKTSVERGORAKKQVOR	46	
Db	3	TNPKPQ	RKTNTNR	BEDVKFPGGGQIVGGVYLLPRGRPLRGVTRTKRTKTSERSQPRGR	62		
Qy	47	DARPRNT	KIAGI	-----HDGLOTLAQAAALP---	-----AHGWGRODPRHKHSRNILGIL	90	
Db	63	QPIPKDR	RSSTCKAWGK	PCRPWPLXGNEGLWAGWLLSPRGSRPSWGTDPDRHRSNNGVKV	122		
Qy	91	LDYPLG	WIGDVTT	PLVGLVAGAVRVPVCOIVRLLEDGNNWATG---	WFGVHILFVVCCL	147	
Db	123	IDTLTCG	FADLMGYIPVVGAP	PLSGA-ARAVAHGVRLVEDGVNYATGNLPGPFPSIFLLAL	181		
Qy	148	LS-LAC	PCSGARVTD	PDNTITILNCCORNQIVCSPSTCLHGPCVLC---	ADECWV	201	
Db	182	LSCITV	PVPSAAQVKN	-TSSSYMVTNDCSNDISITWOLEAAVLHVPVCVPCERVGNSTRCWV	240		
Qy	202	PANP--	-YISHPS	NNWTGTFDSFIADHIDFVMGALVTCDALDIGELCGACVLVGDWL	V---R	255	
Db	241	PVSNMA	VROPAL	T---OGLRTHIDMWVMSATFCSALYVGDLCGGVMLAAQVFI	VSPOY	297	
Qy	256	HWLHID	LNBTGTCYLB	VPVTGIDPGFIFGIGMAGKVEAVIFLTKLASQVPVAIATMESS	315		
Db	298	HWFQV	-----ECNCS	GIYPGTITGHRMAWDMMNWSPATMILAYVMRVEVI	DIIVSG	350	
Qy	316	VHYLGA	LVYASRGK	WYQLLLALML-----	-----	342	
Db	351	AHWGV	FGLAYFSGOGAWAK	VIVILLAAAGVDAGTTVGGAVARSTNVIAGVFSHGPOON	410		
Qy	343	-----	YIEAT	-----SGNPR	VRPTGCSIAEF-----	363	
Db	411	IQLINT	NGSWHINPTAL	CNDSLNTGFLAALFYTNRFNSSCCPGRLSACRNL	IEAFRIGW	470	
Qy	364	-----	CSPLMI	-----PCCHSYLSENV--SEVIC	SPK-----	390	
Db	471	TLQYED	NVTNPEDMR	BPCHWYPPKPCGVPARSVCGPVYCTPSPVWVGT	TDRRRGVPTY	530	
Qy	391	W-----	-----TRP	ITLEYNNISINWPTYIPGARGCMVFKNNTWGC--CRIR	---NV	433	
Db	531	WGENET	DVFLNSTRP	-----POGSWFGCTWMN	STGF-----TKTCGAPPCRT	TRADENA	579
Qy	434	PSYCTG	MTDAWNDTRNT	YEACGYTPWLT-----TAMHNGS	ALKALILQ---	YPGS	481
Db	580	STDLLC	PTCDFCERK	PDATYIKCGSGPMLTPKCLVHYPYRLWHYPCTVNTFT	FKIRMYVGG	639	
Qy	482	KEMPKH	NMWSGHLY	FEBSDPTPIVIFYDPVNSTLLP-----PERWARLP	GP	PPVWRGSMLO	537
Db	640	VE----	HRLTAACN	FTRGDRCDL---EDRDRS	QLSPLLHSTTEMAILPCT-----	682	
Qy	538	VPQGFY	DVDKDLAT	GLITKDKAWKNYQVLSATGALSITGTTKAVNLILGL	CGSKYLI	597	
Db	683	-----	YSDLPAL	STGLSLHLHQNIVDVQTYMGLSPAITKYVVRWEWV	MLFLLLADAR--	V	735
Qy	598	LAVLYLS	LCFGRASGY	PLRPLVPSQVLOAGDWLVLSKAOVAPPAL	IFFICCYLRCR	LR	656
Db	736	CACL	-WMLILL	QOEAAL	EKL-----VLHAASA	-----NCHGLL	770
Qy	657	YAALLG	FVPMAAGL	PLTFFVFAAAAAQPDYDWVRLLVAGLVLMWAGNR	GHRIALLVGPWF	716	

Db 771 YFAI-----FFVAA-----WHIRGRVVLTTYC-----LTGLMP 799
Qy 717 LVALLTLHLVTPASAFDETEIIGLTIPTPVVALVMSRFGFFAHLPRCALVNSYLQWR 776
Db 800 F-CLLLMALPRQAYADPAVHGQIGVGLLILITFLTTCYKTLGQC-----LW--W 849
Qy 777 -----ENWFNVTLRPER-----FFVLVCFPGGATYDALVTCVCHVALLCUTSS 821
Db 850 LCYLLTLGEAMIOBWPVPMQVRGDRDGIAMAVTIFCPGVVFDITKW-----LLALLGP 902
Qy 822 A-----ASFPGTDSVRARHMLVRLGKCHAMVSHVVLKFEFFLVFCE-NGVPFYKHL--HGD 874
Db 903 AYLRLAALTHVYFVRAHALIRVCAVQLAGGRYVQVALLALGRWTGTYYIDHLTMSD 962
Qy 875 VLPNDFASKLQBP--FFPEGRKARYVRNRRGLACDVTGDLVPPVARLGDVLFAGLAM 932
Db 963 WAASGLRDLAVAVEPIIFSPMEKVIWVGAEB--TAAAGDILHGLPVLSARLQOEILLG--- 1017
Qy 933 PPD-----GWAITAPFTLQCLUSERGTLSAMAVMTGIDPRTWGTIIFRLGSLATSYMGFV 987
Db 1018 PADGYTSKGWKLAPITAYAAQOTRGLLGAIVVSMTRDRTEQAGEVQILSTVSQSLGTT 1077
Qy 988 CDNVLYTAHSGSKRRRLAHPGSHPIVDAANDODIYQPCGAGSLTRCSCGETKGVLV 1047
Db 1078 ISGVLWTVYHGAGNKTLAGLURGPVTQMYSSAEGDLVGPSPGKYLSLEPCCKGAVDLYLV 1137
Qy 1048 TRLGSLVEVNSDDPYMCCVCCALPMVAKSGSAPILCSSHVTCMFTTAARNSGG---SV 1104
Db 1138 TRNADVIPARRRGDKRGALLSPRISITLKGSGGVLCPRGHVVLFPAAVCSRGVAKSI 1197
Qy 1105 SQIRVRPLVCAGYHPQVTAHATLDTKPTVPNEYSVQILIAIPTGSGKSTKJPLSVMBEKYE 1164
Db 1198 DFIPVETLDVVTRSPFSDNS--TPPAVPQYQVGYLHAPTGSGKSTKVPVYAAQGYK 1254
Qy 1165 VLVLNPSVATTASPKMYHATYGVNPNICYFNGKCTNTGASITYSTYGMWLT--CACSRNY 1222
Db 1255 VLVLNPSVAATLFGAYLSKKAHGNPNIRTVGMTGREATYSTYKFLADGGCAGAY 1314
Qy 1223 DVITCDECHADATTVLIGIGKVLTEAPSKNVLVLATATPPGVIPTPHAMITEIQLTDE 1282
Db 1315 DIILCDECHADVATISILGIVLQOAGTAGVRLVLATATPPGSVTTPHPDIEVGLGRE 1374
Qy 1283 GTIIFPHGKKIKEENLKKGRHLIFBATKXGCDLANELARKGITAVSYVYRGCDISKIP-EG 1341
Db 1375 GEIIFYGRAIPLSICKIGRHLIFCHSKKKCDLAAALRGMGLNAVYVYRGDLVDSIIPAQG 1434
Qy 1342 DCVVVATDALCTGYTGDFDSVYDCLMVGECHVDLQDPTFTMGVYVCGVSAIVKQRRGR 1401
Db 1435 DVVVVATDALMTGYTGDFDSVIDCNVAVTQAVDFSLDPTFTTITQTPQDAVSRQRGR 1494
Qy 1402 TGRGRAGIYYVVGSCPTSPGMVPECNIVEAFDAKAWYGLSSTBAQTILDTYRTPQGLPA 1461
Db 1495 TGRGRQGYRIVYSTERASGNFDSVLCEDYDAGANWYDLTPAETTVRLRAYFTPLGLPV 1554
Qy 1462 IGANLDEWADLFS-MVNPESFVNTAKRTADNYVLLTAAQOLQCHQYGAAPNDAPRWQ 1520
Db 1555 CODHLEFEAVFTGLTHIDAHFLSQTAGENFAYLVAYQATVCAR---AKAPPSPSWDA 1610
Qy 1521 -----ARLKK--PCGVLMWLDGADACPGPEPEV-----TRY-----QMCFTYVNTSG 1562
Db 1611 MWKCLARLKPFLAGPTPLLYRL-----GPITNEVTLTHPTGYKIATCMQADLEVMTS- 1662
Qy 1563 TAAAVGVGVAMAYLAIDTFGATCVRRCWSITSPTGATVAPVDEBEI-----VEECA 1616
Db 1663 TWVLAGVLAAYAVAYCLATGCVSIIGR-----LHVNQRVVVAP--DKEVLEYAFDEMECA 1716
Qy 1617 SFIFPL-EAMVAADIKLSTI-----TTSPFTLETALE-----KLNTPLGPHAATILAI 1665
Db 1717 SRAALIEBORIAEMLSKIQGLLQQAQKQADIQAPMAQSWPKVQFQWARMWNFISGI 1776
Qy 1666 EYCCGLVTLDPNPASCVAFIAGITTPPHKIKMFLSLFCGATASKLTDARGALAFMA 1725
Db 1777 QYLAGLSTLPGNPVAVASMMAFSAALTSPLSTSTTILLNIMGWLASQIAPPAGATGFVVS 1836

Qy 1726 GAAGTALGTWTSVGF---VEDMLGGYAAASSTACLTFTKCLMGBWPTMDQAGLVYSAPNP 1782
Db 1837 GLVGAAVG---SIGLGKVLVDILAGYGAGISGALVAFKIMSGEKPSMEDVINLLPGILSP 1893
Qy 1783 AAGVGVLSACAMFALTAGPD---HWPNRLLTMLARSNTVCNEYFIATDRIRKILGI 1838
Db 1894 GALVGVGI--CAAILRRHVGFEGGAVOMMRLLIAPASRGNHVAPTHVYTSDDASQRTVL 1951
Qy 1839 LEASTMSVISACIRMLHTPTEDDCGLI---ANGLEIWQYVVCNPFVFCFNVLKAGVQSMV 1895
Db 1952 LGSIT-----ITSLLRLLHNWITEDCPIPCSGSMLRDVMDVCTILITDFKNWLT--KLFP 2005
Qy 1896 NIFGCPYPYSCOKYKGPWIGSMLOARPCGABELIFSVENGFAKLYKGPRTCSNYRGAV 1955
Db 2006 KLPGLPFIQCKGYKGVWAGTGMTTRCPCGANISGNVRLGSMRI-TGPKTCMNTWQGT 2064
Qy 1956 PVNARLCGSARP-DPTDWTSLVNVYGVDRYCKYKMGDHI FVTAVSSPNVCFTQVPTLR 2014
Db 2065 PINCYTEGOCAPKPPNTNYKTAIRVAASEYAEVTHQGSYSYVTGLITTDNLKIPCOLPSPE 2124
Qy 2015 AAVAVDGVQCYLGEKPTWTTTS-ACCYGPDKGKTVKLPFRVDGHTPGVYRMQLNRDA 2073
Db 2125 FFWVDGVQIHRFAPTPKPFERDEVSCFGLNSVAVGSQLPCEPEPDADVLRSML----- 2179
Qy 2074 LETNDCNSTNTPSDEAAVSALVFKBELRTNOLLEAISAGVDTTKLPAPSIIEBVVYXR 2133
Db 2180 -----TDPHITAETAARLARGSPPEASSS---VSQLSAPSLRATCTT-- 2221
Qy 2134 QFRAPT-----CSLTLPPPPRSVPGVSCPELSQRSPLGSPNLPSPV-- 2178
Db 2222 --HSNTYDVMVDANLLMEGVAQTEPESVPLVDFLEPM-----ABEESDLEPSISEC 2274
Qy 2179 -----LQLAMP-----PLLGA---GECNPFTAIGCAMTETGGDDPLSPYPKKE 2221
Db 2275 MLPRSGFPRALPAWARPDYNPPLVESWRRPDYQPTVAGCALP----PKCAPTPPFR 2330
Qy 2222 -----VSE-----WSEDSWSTATTASSVYTGPPYKPIRGKDSOTQAP 2258
Db 2331 RTVGLSESTISEALQLAIKTFGQPPSSDGASSTGAGAAESGGTSPGEPAPSETGSAS 2390
Qy 2259 AKRPTKKLKSFEF-----CSMSYTWTD 2282
Db 2391 SMPLEGEQDPOLESQVBLQPPQGGVAPGSGSGSWSTCSEEDTTVCCSSMSYMTG 2450
Qy 2283 -VSFTKASVLSATRAITSGFLKQRLVYVTEPRDAELRKQKVTINRQPLFPSPYHKQV 2341
Db 2451 ALITCPSPEEKLPINPLSNLRYHNKYCTTSKSASQRAKVTFTQVLDHAHDSVL 2510
Qy 2342 RLAKKASKVGVVMWDYDEVAHHTPSKSAKSHITGLRGTDVR--SGAARKAVLDLQKVE 2399
Db 2511 KDIKLAASKVSARLLTLEEACQLTPPHSARSKY-GFGAKEVRSLSGRAVNHIKSWK--D 2567
Qy 2400 AGEIPSHYRQTVIVPKEEVFKTPQKTKPPLISYPHLEMRCVEKMYGOVAPDVVKA 2459
Db 2568 LLEDQPTPIPTTIMAKNEVFCVDPAPKGGKPARLIVYPDLGVRVCEKXALYDITQKLPQA 2627
Qy 2460 VMGDAYGF-VDPRTRVRLLSWMS--PDVAGTCDTVCDFDSTITPEDIMVETDIYSAKL 2516
Db 2628 VMGASYGFQSPQAQVBYLLKAWAEKDDPMGFSDTRCFDSTVTERDIRTEESIQACSL 2687
Qy 2517 SDQHRAGIHTIARQLYAGGPMIAYDGREIgyrrcrssgvvttssnsltcwlvkvnAAEQ 2576
Db 2688 PEEARTAIHSLTERLYVGGPMFNSSKGQTCGYRRCRASGVLTTSMGNTITTCVVALAACKA 2747
Qy 2577 AGMKNRPLFCGDDCTVIWISAGADADKQAMRVFASWKMVGAPQDCVPQPKYSEBELTS 2636
Db 2748 AGIVAPTMLVCGDDLVIWISQCTEEDERNLRAFTAMTRYASAPGPPRPEYDELEITS 2807
Qy 2637 CSSNVTSGITKSGKPYFLTRDPRI PLGRCSAEGLYNPAAWIGYLIHHYVCLVWSRVL 2696
Db 2808 CSSNVVALGPRGRRRYILTRDPTTLARAAWEIVRHSPINSLNGNIIOYAPTIVWRNVL 2867

Qy 712 VGPPLVALLTLHLVTPASAFDEI---IGGLTIPVVAVALVMSRRGFFFAHLPRCALV 768
Db 791 YGVNPL--LLLALLPPRAYAMDREMAASCAGVFGVGLILLTSLPHYKFLFARL-----842
Qy 769 NSYLWQWENFMNVTLRPERFEFLVLCFP-----GATYDALVTCVCHVALL--CLTSSA 822
Db 843 ---TW-----WLQYFITRAEHLQWII--PPLNVRGGRDAVILLITCAIHPLSIFITIKIL 892
Qy 823 ASFFG-----TDSRVRAHR-----MLVRLGKCHAWSHYSHYVLKFFLLVFGEANGVF 866
Db 893 LAILGLPLVMOAGITKVYFVRAHGLIRACMLVR-----KVAGGHYVQVQMALMKAALATGY 948
Qy 867 FYKHL-----HGDVLPNDFAKSLPLQEPFPFEGKARVNRNRRRLACODTVDGLPVV 919
Db 949 VYDHLTPLRDWAHAGL--RDLAVAV--EPVYFSDMETKITWGDATTAACGDIIILGLPVS 1003
Qy 920 ARLGDLVPAGLA--MPPDGMWAIAPFTLQCLSERGTLSAMAVMTGDDPRTWTCITIFRLG 977
Db 1004 ARGREIHGLPADSLEGGQWLLAPITAYSQOTRGLGCIITSLUTGRDRNVEGEVQVVS 1063
Qy 978 SLATSYMGFVCDNVLXTAHHGSKRRRLAHPGTSIHPIITVDAAN--DQDI--YQPPCGAGSL 1034
Db 1064 TATQSLATCVNGCWTVYHAGSKTLAGPKG---PITQMYTNVDQDLVGHQAPPGARSL 1120
Qy 1035 TRCSCGETGYLVTRLGSLVEVKNKSDDPYWCVCAGALPMNAKSGSGAPILCSSGHVIGMP 1094
Db 1121 TPCTCGSDLYLRHADVIIVRRRGRSGSLSPRPVSYLKGSGGGLLCPSGHAGVGF 1180
Qy 1095 TAA---RNSGGSVSQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYSVQIILIAPTGSKS 1151
Db 1181 RAAVCTRGVAKADFPVYESMETMRSVPFTDNS---SPPAVPOTFQVAHLHAPTGSKS 1237
Qy 1152 TKLPLSYMQERYEVLVNLPSVATTASMPKYNHATYGVNPNCYFNGCKTNTCASLTYSTYG 1211
Db 1238 TKVPAAYAAQGYKVLVNLPSVAATLFGCAYMSKAHGDIPNRTGVRITITGAPITYSTYG 1297
Qy 1212 MYLT-GACSRN-YDVIICDECHADTATVVLGIGKVLTEAPSKNVLVVLATATPPGVPIPT 1269
Db 1298 KFLADGGCGGAYDIIICDECHSDSTSTILGIGTVLDOAETAGARLVVLATATPPGSVTV 1357
Qy 1270 PHANITEIQLTDEGTIPHGKKIKEENLKKGRHLI FEATKKHCDLANELARKGITAVSY 1329
Db 1358 PHPNIEEVALSSTGEIPYGAIPETIKGRHLIFCHSKKKDELAUKUSGLGNNAVY 1417
Qy 1330 YRGCDISKIP-EGBCVVVATDALCTGYTDPDSYVDCSLWVEGTCHVDLDPFTFMGRVVC 1388
Db 1418 YRGLDVSVIPTSGDIVVATDALMTGTFGDFSDVDCNTCYQTQVDSLDPFTFIEITTV 1477
Qy 1389 GVSIVKQRRGRGRAGIYIYVVDGSCPTSPGMVPECNIVEAFDAKAWGLSSTBAQT 1448
Db 1478 QDVAVSRRQRGRGRGMGIYRFVTPGERPSGMFDSVLCECYDAGCAWYELTPAETSV 1537
Qy 1449 ILDTYRTQPLPAIGANLDEWADI,PS-MVNPEPSFVNTAKETADNYVLLTAQLOLCHOY 1507
Db 1538 RLRLAYLNTPLGVCCODHLFEWESVFTGLTHIDAHFLSQTQKAGDNFPYLVAIQATVCARA 1597
Qy 1508 GYAAPNDAPRMOG-ARLCKK---PCGVLMRLDGDACPGPSPSVTRYOM-CFT---EVN 1559
Db 1598 QAPPPSDQWQKILRLKPTLHGFTPLLYRL-GAVQNEVTTTHITKYIYIACMSADLEVV 1656
Qy 1560 TSGTAALAVGVGVMAYLAIDTFCATVRRCMSITSVPTGATVAPVVDDEBI-----VE 1613
Db 1657 TS-TWVLVGGVLAALAAAYCLTTGSGWIVGR-----IILSKPAIIPDREVLVREFDEME 1709
Qy 1614 ECASFIP-LEAMVAADIKL-----STIT-----TTSPFTLEALEKINTFLGPHAATI 1661
Db 1710 ECASHLPYIEQGMQLAQOFKOKATGLIQTATKQAEAAAP-YVESKWRTLFAFWAKHWNF 1768
Qy 1662 LAITEYCCGLVTLPNPNFASCVAFIAGITTPHLPHKIMFSLFPGGAIAKSLTDARGALA 1721
Db 1769 ISGLOYLAGLSTLPCNPAIASLMAFTASITSPLTQHTLLFNILGGVAAQALAPPSAASA 1828
Qy 1722 FMMAAGATALTGTWTSVGF---VFDMLGGVAAAASSTACTLTKCLMGEMPTMDQLAGLVYS 1778
Db 1829 FVGAGIAGAAVG---SIGLKVLDIAGYAGALVAFKVMGSGEMPSTEDLVNLLPA 1885
Qy 1779 AFNPAAGVGVLSACAMFALTAGPD---HWPNRLLTMLARSNTVCNEYFIATDIRRK 1834
Db 1886 ILSFALVGVVV---CAAILRRHVGEGGAVQWMMRLTAFASRGNHVPFTHVVPESDAAAR 1943
Qy 1835 ILGILEASTPMSVISACIRMLHTPTEDDCGLI---AWGLEIWOVQVNFVFICFNVLKAGV 1891
Db 1944 VTQILSLT---ITQLKRLHOWINEDCSTPCSGMLRDVMDWICT---VLTDFKTWL 1995
Qy 1992 QS---MWNIPGCPFFSCQYKGPWIGSMLOARCPGCAELIFSVENGEAKLYKGPRTCSN 1949
Db 1996 QSKLLPLPGVPFFSCQYKGVWRGDIQMOTTCPCGAQITGHVKNGSMRIV-GPRTCSN 2054
Qy 1950 YMRGAVPNARLCSARPDPT-DWTSLVNVNVRDYCKYKMGDHIIFVTAVSSPNV-CFT 2007
Db 2055 TWHGTFFINAYTTCPTSPAPNYSRALWRVAEYEVTRVGDPHYVTGHTTONTVKCPC 2114
Qy 2008 QVP-----PTLRAAVA-----VDGVQVQCYLGEKPTPMWTS 2038
Db 2115 QVPAPBPFTEVDGVRLLHRYAPACKPLLEEVTFVLVGLNQVLVGSQLP---EPB-----2165
Qy 2039 ACCVGPDKGKTVKL--PFRVDGHTPGVRMQLNRLDALETND-----CNSTNN 2084
Db 2166 ---PDVAVLTFMLTDPESHITABTAKRRLARGSPPSLASSASSASOLSAPSLKATCTTRHD 2220
Qy 2085 TPSDEAAVASALVFKQEL-----RRTNOLL-----EASAGVDTTKLPAPSIIEVVVRK 2132
Db 2221 SPDADLEALLWRQEMGNITRVESENKVVILDSFPLQAEDEBEREVSUVA--EILRRS 2278
Qy 2133 QFRARTGSLTLPPPRSVPFVSCP-----ESLQSD-----PLEGPNLPPSP 2176
Db 2279 RKF-----PRAMPWARPDPYNPLLESWKDPDYPVPVHVHGCPLP-PAKAPPIP 2325
Qy 2177 P-----VLQAMPPLLAGECNPFF-----TAIGCAMTETGGPDDL 2214
Db 2326 PRRKRTVILSESTVSSALAEAL--TKTFGSSSESAVDSGTATASPQPSDDGAGSDVE 2383
Qy 2215 SY---P---KKEVSEWSDESWSATTASSVTPGPKIRGKDSQTQSAKAPRPTKKLG 2268
Db 2384 SYSMPLEGEPGDPLDSGWSVSEAS-----2413
Qy 2269 KSEFSCMSYTWTD-VISFKTASKVLSTRAITSGFLKQRLSVYVTEPRDAELRKQKVTI 2327
Db 2414 EDVVCCMSYTWGALITPCAAEBETKLPIINALSNLLRHHNLVATTSSRSASLQKVT 2473
Qy 2328 NRQPLFPSPYHKQVRLAKEKASKVGVWMDYDEVAHAHTPSKAKSHITGLRGTVRSAA 2387
Db 2474 DRLQVLDHRYRDLVKEMKAKASTVKAKLLSVEEACKLTPPHSARSKF-GYGAKDVRN-LS 2531
Qy 2388 RKAVALDLOK---CVEAGEIPSHYRQTVIYPKBEVFVKTPQKPKPRLISYPHLEMR 2443
Db 2532 SKAVNHHSRWKOLLEDETETPI---DTTIMAKNEVFCQPEKGGKPARLIVFDLGVV 2588
Qy 2444 VERMYQVAPDVVVKAVMGDAYGF-VDPTRVRKLLSMWSPD--AVGATCDTVCDFDSTIT 2500
Db 2589 CERKALYDVVSTLPQAVMGSSYGFQVSPQORVEFLVNAWKAKKCPMGFAVDTRCFDSTVT 2648
Qy 2501 PEDIMVETDIYSAKULSDQHRAGIHTIAROLYAGGPMIAYDGREIGYRRCRSSGVYTTSS 2560
Db 2649 ENDIRVEESIYQCCLDAPEARQAIRSLTERLYIGGPLTNSKGQNGCYRRCRASGVLATSC 2708
Qy 2561 SNSITCHLVKNAAEQAGMKNPRFLICGDDCTVTKWSAGADADQAMRVFASMMKVMGAP 2620
Db 2709 GNTLTCVLAACAAACRAAKQDCTMWLVCGDLDLVICSAGTOEDASURAFTEAMTRYSAP 2768
Qy 2621 QDCVPOPKYSLEBLTSCSNVTSGITKSGPYFLTRDPRIPRIGRCSAEGLYGNPSAAWI 2680
Db 2769 PGDPPKPEYDLELITSCSNVSAHADGSKRVYLTEDPTTPLARAWEARHARHPVNSWL 2828
Qy 2681 GYLIIHYPCLWBSRVLAHVHPMEQMLFEDKLPETVTFDNYGKNYVTPVEDDLPSTIAGVHI 2740

Db 2829 GNIIMYAPTLWARMLTWHFFSILLAOBLEKALDCQIYGACYSIEPIELDPLQIQRHLGL 2888
Qy 2741 EAFSVVVTNAEILRVSOSLTDMTMPPIRAWRKARAVLASAKRGGGAHAKLARPLL-WH 2799
Db 2889 SAFSUHYSYSGEINRVASCLRKGLGVPVLRVHRARSVRALLSOGGRAATCGKLYLFNWA 2948
Qy 2800 ATSR-----PLP-----DLDKTSVARYTTFNCDVYSPEDGVFITPQRRLQKFLVKYLAVI 2850
Db 2949 VRTKLKLTPIPAASQLDLSNFWAGYS-----GGDIYHLSLRARPRW-----F 2991
Qy 2851 VFALGLIAGLAI 2863
Db 2992 MWCLLLSVGVGI 3004
RESULT 13
ID ABG32451 standard; protein; 3010 AA.
AC ABG32451;
XX
DT 15-NOV-2002 (first entry)
XX
DE Hepatitis C virus Con 1 isolate polyprotein.
XX
KW HCV; Con 1; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication; polyprotein.
XX
OS Hepatitis C virus.
XX
PN WO200259321-A2.
XX
PD 01-AUG-2002.
XX
PF 16-JAN-2002; 2002WO-EP000526.
XX
PR 23-JAN-2001; 2001US-0263479P.
XX
PA (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
XX
PI De Francesco R, Migliaccio G, Paonessa G;
XX
DR WPI; 2002-599793/64.
XX
DR N-PSDB; ABK91411.
XX
PT New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
PT ribosome entry site (IRES) region, useful in studying HCV replication and
PT expression.
XX
PS Claim 1; Page 34-36; 69pp; English.
XX
CC The invention relates to nucleic acid molecules comprising altered HCV
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC internal ribosome entry site (IRES) region coding for one or more NS3,
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations
CC are detailed in the specification. Also included are (1) an expression
CC vector comprising a nucleotide sequence coding for the altered nucleic
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
CC recombinant cell human hepatoma cell comprising the altered nucleic acids
CC ; (3) a recombinant cell produced by introducing into a human hepatoma
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
CC replicon enhanced cell or which containing a functional HCV replicon; (5)
CC an HCV replicon enhanced cells made in the method; and (6) measuring the
CC ability of a compound to affect HCV activity. The HCV replicons and HCV
CC replicon enhanced cells are useful in studying HCV replication and
CC expression, and HCV and host cell interactions, producing HCV RNA and
CC proteins, and providing a system for measuring the ability of a compound
CC to modulate one or more HCV activities e.g. to discover drugs which may
CC treat HCV mediated diseases such as liver failure, cirrhosis and
CC hepatocellular carcinoma. The present sequence is the HCV replicon Con 1
CC polyprotein (comprising the Core, E1, E2, P7, NS2, NS3, NS4A, NS4B, NS5A

CC and NS5B proteins) used as a basis for the adaptive mutations of the
CC invention
XX
SQ Sequence 3010 AA;
Query Match 21.2%; Score 3262; DB 5; Length 3010;
Best Local Similarity 29.8%; Pred. No. 2.9e-243;
Matches 970; Conservative 452; Mismatches 1183; Indels 648; Gaps 116;
Qy 8 TSPVAPRTRKNKQTQASYPVSIK-----TSVERGORAKKVKQORDARPR 51
Db 3 TNPQPKQRTKRTNRR---PODVKPGGGQGVGVYLLPRRGLRGLVTRATKRTSERSQPR 59
Qy 52 NYKIAGIHGQITLAQAALP-----AHGWGRQD 79
Db 60 GRR-----QIPKARQPEGRAWQPGYWPVLYGNEGLGWAGWLLSPGRSRPSWGPTD 111
Qy 80 PRHKSRLGILLDYPGLGWIGVTHTHPLVGLVAVAGVVRVQIVRLLLEDGNNWATG--- 136
Db 112 PRRSRLNGKVIDTLCGFADLMGYIPLVGAPLGA-ARALAHGVRVLEDEGVNATGNLP 170
Qy 137 WFGVHLFVVCLLS-LACPCSGARVTDPTNTTILTNCCQRNQVIYCSPTCLHBPCCVIC 195
Db 171 GCSFSIFLLALLSCLTIPASAYEVRNV-SGVYHVNDCSNASIVTEADMTWHTPGCCVPC 229
Qy 196 ADE-----CWVPANPYISHPSNWTGTSFLADHIDFVMGALVTCDALDIGELCGACVLVG 250
Db 230 VRENNSSRCWVALPTLA-ARNASVPITIRRHVDLLVGAALCSAMVVGDLGCSVFLVA 288
Qy 251 DMLV-----RHLIHIHDLNETGTCYLEVPTGIDPGFL--GFIGW---MAGKVEAIFLTKL 301
Db 289 QLFTFSRRHETVQ-DCN-----CSTYPGHVTGHRMAWMDMMNWSPTAALVVSOL 337
Qy 302 ASQVPIATMFSVHVYLAVALGALYASRGWYQALLALMLYIEATSNPIRVPVTCGSA 361
Db 338 L-RIPQAVVDMVAGAHGVLGALAYISMVGNWAKVLIVMLLFAGVDGGTYV---TGGTMA 393
Qy 362 E-----FCSPLMIPCPCHSYLSE 379
Db 394 KNTLGITSLFSPGSSQIKQLVNTNGSMHINTALNCNDSLNTGFLAALFY---VHKFNS 450
Qy 380 -----NVSEVICSPKWTPTILEYNNNSISWTPY-----TIPGARGC----- 416
Db 451 GCPERMASCPIDAFAGW-GPITYNESHSDORPWCWHYAPRPGGIVPAAQVCGPVYCF 509
Qy 417 -----MVKFKNT-----WGCCRIRNVPVY-----C 437
Db 510 TSPVTVVGTDRFGVPTVYSGENETDVLNLTNTPPQGNWFGCTWMNSTGFTKTCGGPPC 569
Qy 438 TWG-----TDAVMNDTRNTYEACGVTPWLT-----TAMHNGSALKLAILQ- 477
Db 570 NIGGIGNKTLCTPTDCPRKHPEATYTKCGSGPMLTPRCLVHYVYRLWHYPCVTNFTPKV 629
Qy 478 --YGSKE--MFKPHNWSG-HLIFEGSDTPIVTFYDPVNSTLLPPEWAKLPPTPVVR 532
Db 630 RMYVGGVEHREAAACNMTGRERCNLEDRD-----SELSPLLLSTTEWQVLPDS- 678
Qy 533 GSWLQVPGFFSDVKDLATGLITKDKAWKNQVLYSATGALSJTGVTTKAVVLLILGLCG 592
Db 679 -----FTTLPALSTGIHILHQNVDVQYLYGIGSAVVSFAIKWEYVLLLFELLAD 728
Qy 593 SKYLITLAVLCYLSLCFGRASGYPLRPVLPQSQYLAQGWDLVLSKAQVAPFALIFFCCYLR 652
Db 729 ARVCACTLMMMLL-----IAQEAALLENLV----- 753
Qy 653 CRLRYAALLGVFVMAAGLPLTFFVAAAQAQPDYDWWVR-LLVAGLVWAGNRGHRILL 711
Db 754 --LNAASVAG---AHGI-LSFLVFFCAA-----WYIKRLVPGAAY-----AL 790
Qy 712 VGPVPLVALLTLHLVTPASAFDTEI---IGSLTTPPVVALVWMSRFGFFAHLPRCALV 768
Db 791 YGVWPL--LLLLLAPPRAYANDREMAASCAGAVFVGILLITLSHYKFLARL----- 842

Qy	769	NSYLQWRWENFWNVTILRPFRFVLVCFP-----GATYDALVTFVCVCHVALL-CLTSSA	822
Db	843	---IW-----WLOQYFIITRAEHLQVWI--PPLNVRGGRDAVILUTCIAHPELIFITIKIL	892
Qy	823	ASFPF-----TDSRVRAHR-----MLVRLGKCHAWSYSHYVLKFLFLVPGENVF	866
Db	893	LAILGLPLVLQAGITKVPYFVRAHGLTRACHLYR----KVAGGHYVQWALMKLAALGTY	948
Qy	867	FYKHL-----HGDVLNPNDFASKLPLOEPFPFPEGKARVYRNGRRLACGDTVDGLPVV	919
Db	949	VYDHLTLPLRDWAHAGL--RDLAVAV--EPVFSDMETKVIITWGDATAACGDIILGLPVS	1003
Qy	920	ARLGDLVFAGLA--MPDGHAI TAPPTLOCLSERGTLSAMAVNVTGIDPRTWGTITIFRLG	977
Db	1004	ARRGRETHLPADSGLEGGRMLLAPITAYSQOTRGLGCIITSITGDRNQVEGEVQVS	1063
Qy	978	SLATSVMGFCDNVLVYTAHSGSKRRLLAHPITGSIHPITVDAAN--DODI--YQPPCGAGSL	1034
Db	1064	TATQSFPLATCVNGCVTIYHGAGSKTLAGPKG---PITQMTNVVDQLVGNQAPPGARSL	1120
Qy	1035	TRSCGBTKYLVTRGLSGLYVEVNSDDPYWCVCGALPMVAKGSSGAPILCSSGHVIGMF	1094
Db	1121	TPCTCGSSDLVLTVRHADVILPVRRRGDSRGSLLSPRPVSLYKSGSSGGPFLCPSGHAVGIF	1180
Qy	1095	TAA---RNSGGSVSQIRVRLPVLVCAGYHPQYTAHATLDTKTPVNEYSVQIILAPTSGSKS	1151
Db	1181	RAAVCTRGVAKAVDFVPVESMETTMRSPVEFTDS---SPPAVPQOTFOVAHLHAPTSGSKS	1237
Qy	1152	TKLPLSYMQSKYEVLNLPNSVATTASMPKYMHAATYGVNPNICYFNGKCTNGTASITYSTYG	1211
Db	1238	TKVPAAYAAQYKVLVLNLPNSVAATLFGGAYMSKAHGIDPNIRGVRTITTGAPITYSTYG	1297
Qy	1212	MYLT--GACSRN--YDVIIICDECHATDATVTLGIGKVLTEAPSKNVRLVVLATATPPGVPIPT	1269
Db	1298	KFLADGCGSGGAVDIIICDECHSDTSTTILGIGTVLQOAGTAGARLVLTATATPPGSVTV	1357
Qy	1270	PHANITBIQLTDEGTIPFHGKKIKKEENLKKGRHLIIFRATKKHCDLANELARKGITAVSY	1329
Db	1358	PHPNIEVALSSTGEIPIFYKAIPIETIKGRHLIFCHSKKKCDELAALKSLGGLNNAVY	1417
Qy	1330	YRGCDTSKIP--EGDCVVVATDALCTGTGDFDSVYDCSLMVEGTCCHVDLDPFTMGVRVC	1398
Db	1418	YRGUDVSVIPTSGDVIIVATDALMTGTFGDFDSVIDCNTCTVQTVDFPSLDPFTTETTVT	1477
Qy	1389	GVSAIKVQRRGRTGRAGIYIYVVGSCSTPSSGMVPECNITVEAFDAKAWVGLSSTEAOQ	1448
Db	1478	PQDAVSESQRGRTGRGEMGIYFVTPGERPSGMFSDSVLCECYDAGCANVELTPAETSIV	1537
Qy	1449	ILDTYRTQPLGPAIGANLDEWDLFS--MVNPEPSFVNTAKRTADNVYLLTAAQLQCHQY	1507
Db	1538	RLRAYLNTPLPCQDHLFEWESVFTGLTHIDAHFLTSQTKOAGDNFPYLVAYQATVCARA	1597
Qy	1508	GYAAPNDAPRWOG--ARLGKK---PCGVLTWBLDGNADACPGPEPEVTRYQM-CFT---EVN	1559
Db	1598	QAPPPSDQWKKCLIRUKPTLHGTPPLLYRL-GAVQNEVTTTTHPIKYIINACHMSADLEV	1656
Qy	1560	TSGETAALAVGVGVAMAYLAIDTFCATCVRCWSITTSVPTGATVAPVUDEEEI-----VE	1613
Db	1657	TS--TWLVGVLAALAAAYCILTTSVSVIVGR-----IILSGKPAIIDPREVLREFDEME	1709
Qy	1614	ECASFIP--LEAMVAADIKLK-----STIT-----TTSPTFLEALEKLNFLFGPHAATI	1661
Db	1710	ECASHLPYIEOGMLABEQFKQKAILLOATATKQAEAAAP--VWESKWRTEAFWAKHMMWF	1768
Qy	1662	LALIEYCCGLVTLPDNPFASCVFPAIAGITTPPLPHKTMFSLFPGGAIASKLTDARGALA	1721
Db	1769	ISGIQYLAGLSLTLPGNPAIASLMAFTASITSPLTQHTLLFNILGGVWAQALAPPSSAASA	1828
Qy	1722	FMWAGAGTAGLTGWTSGVF--VFDMLGGVAAASSTACLTAKCLMGEMPTMDOLAGLVYS	1778
Db	1829	FVGAGTAGAAVG---SIGLKGVLVDIILAGYGAGVAGALVAFKWSGEMPTSDLVNLLPA	1885
Qy	1779	AFNPAAGVGVGLSACAMFALLTTAGPD-----HWPNRLLTMLARSNVTWCNEYFIATDRIRRK	1834

Db	1886	ILSPGALWGV--CAAILRRHVGPGEVAVQMMNRLLIAFASRGNHVSPHYHPESDAAAR	1943
Qy	1835	ILGILEASTPWSVISACIRWLHPTTDDCGLI---AWGLEIMQYVCNFFVICFNVLKAGV	1891
Db	1944	VTQILSSLT---ITQLKRLHQMINEDCSTPCSGSMLRDVMDICT---VLTDFKTLW	1995
Qy	1892	QS--MNNIPCCPYSCQGYKGPMWIGSMLQARCPGABILISFVENGPAKLYKGPRTCSN	1949
Db	1996	QSKLLPRLPGVPFFSQRGYKGVNRGDGIMQITTCPCGAQITGHVKNGSMRIV--GPRTCSN	2054
Qy	1950	YMRGAVPVNARLCSARPDP--DWTSLVNVYGVDRYCKYKEMGDHIFVTAVSSPNV--CFT	2007
Db	2055	TWHTGTPINAYTGPCTPSAPNYSRALMRVAABEYVETRVGDHFYVGTMTTNDNVKPCP	2114
Qy	2008	QVP-----PTLRAAVA-----VDGVQVCYLGPBPKTPWTS	2038
Db	2115	QVPAPFEFFTEVDGRLHRYAPACKPLLREEYFLVGLNQYLVSQLP---EPE-----	2165
Qy	2039	ACCYGGPGKGTVKL--PFRVGHTPGVNRQMLNRDALETND-----CNSTWN	2084
Db	2166	-----PDVAVLTSMLTDPSHITAETAKRRLARGSPPSLASSASQLSAPSLKATCTTRHD	2220
Qy	2085	TPSDEAAVSALVPKQEL-----RRTNQLL-----EASISAGVDTYTKLPAPSTEEVVVRK	2132
Db	2221	SPDADIEANLLWRQEMGNITRVESENKVILDSFEPLQABEDEREVSVA--ETLRRS	2278
Qy	2133	RQFRANTGSLTPPPRSPVGVSCP-----ESLQRSD-----PLEGPSNLPPSP	2176
Db	2279	RKF-----PRMPIWAPDPNYPLESWKDPDYPVPVHGCPLP--PAKAPP1P	2325
Qy	2177	P-----VLQLAMPPLIGAGECNPF-----TAICAMTETGGGDDLP	2214
Db	2326	PPRKRTVVLSESTVSSALAEAL--TKTFGSESSAVDSGTATASDPQSDDGADGSDVE	2383
Qy	2215	SY---PP---KKVSVSWSDSSTATASYVTGPPYKIRGKDSQTQSAKAPKRTKKLG	2268
Db	2384	SYSSMPLEGEGBDPLSDGSMSTVSEAS-----	2413
Qy	2269	KSEFFCSMSYTTWD--VISFKTASKVLASATRAITSGFLKORSILVYVTEPRDAELRKOKVTI	2327
Db	2414	EDVVCMSYTTGALITPCAAEETKLPINALSNSLLRRHNLVYATTSASLRQKVTF	2473
Qy	2328	NROFLPFPYHKQVRLAKEKASKVGVGMMDYDEVAHAHTPSKAKSHITGLRGDTVRSGAA	2387
Db	2474	DRLOVLDDHYROVLKEMKAKASTVKAKLLSVEEACKLTPPHSARSKF--GVGAKDVNR--LS	2531
Qy	2388	RKAVLDLQK-----CVBAGEIPSHYROTIVUPKEEVVTKPQPTKPPRLISYPHLEMR	2443
Db	2532	SKAVNHIRSWKDLLEDDETPI---DTTIMAKNEVFCVQPEKGRXPARLIVFPDILGVRV	2588
Qy	2444	VEKMYYGQAVDPVVKAVMGDAYGF--VDPTRVRKRLLSMWSPO--AVGATCDTVCFDSTIT	2500
Db	2589	CEKNALYDVVSTLUPQAVMGSSYGFQVSPQORVEFLVNAWKAKCPMGFAYDTRCFDSTVT	2648
Qy	2501	PEDIMVETIYSAKLSQDRHAGIHTIARQLYAGGPMIAYDGREIGYRRCSSGVYTTSS	2560
Db	2649	ENDIRVEESIYQCCDLAPEARQAIRSLTERLYIGGPLTNSKQNCYGRRCRASGVLTTC	2708
Qy	2561	SNSLTCWLKVNAAAEQAGMKNRFLICGDDCTVIWKSAGADADQAMRVFASMKVMYGAP	2620
Db	2709	GNTLTCTVLAACAAACRAKQDCTMLVCGDDLVCVSSAGTQDEASLRAFTAMTRYAP	2768
Qy	2621	QDCVPQPKYSLEBLTSCSNVTSGITKSKPKPYFLTRDPRIPLGRCSAEGLVNPSAAVI	2680
Db	2769	PGDPPKPEYDLELITSCSNVSVAHDDASGRVYVLTTRDPTTPLARAAWETARHTPVNSWL	2828
Qy	2681	GYLIHHYPCILWRSRLVLAHFMEQMLPDKLPETVTFDWTYKKNYVTVVBDLPSTIAGVHGI	2740
Db	2829	GNIMYAPTILWARMILMTWFFSILLAQEQLKALDCQIYGACYSIEPLDLPQIIQRLHGL	2888
Qy	2741	EAFSVVRYTNAEILRYSQSLTDMTMPPLRAWRKBAVALASAKRRGGAHAKLARFLL--WH	2799

Db 791 YGVNPL--LLLLLAPPRAYAMDREMAASCGAVFVGLILTLSPHYKFLFARL----- 842
Qy 769 NSYLQORWENFMWNTLRPERFFLVLCFP-----GATYDALVTFVCHVALL--CLTSSA 822
Db 843 ---1W-----WLQYFTRAEAHQWLI--PPLNVRGGDAVILITCAIHPELIITYIKIL 892
Qy 823 ASFFG-----TDSRVAHR-----MLVRLGKHCHAWYSHYVLKFFLLVFGENGVF 866
Db 893 LAILGLPLVLQAGITKVPYFVRAHGLIRACMLVR---KVAGGHYVQWALMKLAALTGY 948
Qy 867 FYKHL-----HGDVLENDFAKLPLOEPFFPEFEGKARVYRNGRRLACDVTGDLVYV 919
Db 949 VYDHLTPLRDWAHAGL--RDLAVAV---BPVYFSDMETKVITWAGDAACGDIIILGLPVS 1003
Qy 920 ARLGDVLFAGLA--MPDGMATAPFTLOCLSERGTLISAMAVVMTGIDPRTWTGTIFRLG 977
Db 1004 ARGREIHLGPADSLEGGWELLAPITAYSQOTRGLGCIITSITGRDRNQVEGEVQVVS 1063
Qy 978 SLATSYMGFVCDNVLVYTAHSGSKRRLAHPTGSIHPITVDAAAN--DQDI--YQPPCGAGSL 1034
Db 1064 TATQSFATLCVNGCWITVYHAGSKTLAGPKG---PITQMYTNVDQLVGNQAPPGARSL 1120
Qy 1035 TRCSGGETKYLVTRELGLSLVEVNSDDPYWCVCALPMAVAKSGSGCAPILCSSHVIGMP 1094
Db 1121 TPCCTGSSDLVYTRHADVIVPVRERGDSRGSLLSPRPVSYLKGSSGGPFLCPSGHAVGIF 1180
Qy 1095 TAA---RNSGGSVSQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYSVQIIAPITGSGKS 1151
Db 1181 RAAVCTRGVAKADVFPVESHETWRSVPFTDNS---SPPAVPQTQVAHLHATPGSGKS 1237
Qy 1152 TKLPLSYMQEYEVLLVNLNPSVATTASMPKYMHATYGVNPNPCYFNKGCTNTGASITYSTYG 1211
Db 1238 TKVPAAYAAQYKVLVNLNPSVAATLFGAYMSKAHGDIPNIRTGVRTITTCGAPITYSTYG 1297
Qy 1212 MYLT-GACSRN-YDVIICDECHADTATVILGKVLTEAPSKNVLVVLATATPPGVIPT 1269
Db 1298 KFLADGGCSGGAYDIIICDECHSDTSTILGIGTVLQDAETAGARLVVLATATPPGSVTV 1357
Qy 1270 PHANITELQTDGTIPPHGKKIKEENLKKGRHLIIFEATKKHCDLANELARKGITAVSY 1329
Db 1358 PHNIEVALSSTGEIIPYGKAIPIETIKGRHLIFCHSKKKCDLAKLSGLGLNAVAY 1417
Qy 1330 YRGCDISKIP-EGDCVVVATDALCTGYTGDPSVYDCSLMVEGTCHVDLDPFTFMGRVRC 1388
Db 1418 YRGLDVSVIPSGDVIIVATDALMTGTDGDFSDVIDCNTVQTQVDFSLDPTFTIETTV 1477
Qy 1389 GVSALVKGQRGRGRAGIYVYVDSCTPSGMVPECNIVEAFDAKAWTGLSSTEAQT 1448
Db 1478 PQDAVRSQRGRTRGRMGTYRFVTPGERPSGMDSSVLCCEYDAGCAWYELTPAETSV 1537
Qy 1449 ILDTYRTQPLPAIGANLDEWADLFS-MVNPERFSFVNTAKRTADNYVLLTAAQLQCHOY 1507
Db 1538 RLRAYLNTPLPVCODHLEFVESFTGLTHIDAHFLSQTKAGDNFPYLVAYQATVCARA 1597
Qy 1508 GYAAPNAPRQW-ARLGKK---PCGVLRULDGADACPGPBPSEVTRYQM--CFT---EVN 1559
Db 1598 QAPPSWDQMKCLIRLKPTLHGPPTLLYRL-GAVQNEVTTTHITKYIMACMSADLEV 1656
Qy 1560 TSGTAALAVGVAMAYLAIDTFCATCVRRCWTSITSVPTGATVAPVUDEBI-----VE 1613
Db 1657 TS-TWVLVGGVLAALAAAYCLTTGVSIVIGR-----IILSGKPAIIPDREVLRYEPDEME 1709
Qy 1614 ECASFIP-LEAWAAIDKX-----STIT-----TTSPTLETALEKNTFLGPHAATI 1661
Db 1710 ECASHLPYIEGQMQLAEQFKQKAILGLQTATKQABAAAP-VVESKRTLEAFWAKHWNF 1768
Qy 1662 LAIIEYCCGLVLPDNPSPASCVAFIAGITTPPLPHKIMFLSLFGGAIAASKLTDARGALA 1721
Db 1769 ISGJOYLAGLSTLPCNPALIASMAFTASITSPLTQHTLLFNILGGWVAAQALAPPSAASA 1828
Qy 1722 PMAGAGATGALTWTSVGF-----VDFMLGGYAAASSTACLTFKCLMGEPWMDQLAGLVYS 1778
Db 1829 FVGAGIAGAAVG---SIGLGRVLDIILAGYGAGVAGALVAFKVMGSGEMPSTEDLVNLLPA 1885

Qy 1779 AFNPAAGVGVGLSACAMFALTTAGPD-----HWPNRLLTMLARSNTVCNEYFIATRDIRR 1834
Db 1886 ILSFGALVGVV--CAAILRRHVGPGGAVQVMNRLIAFASRGNHVSPTHVVPESDAAA 1943
Qy 1835 ILGILEASTPWSVISACIRMLHTPTEDDDCGLI---ANGLEIWQVVCNFFVICFNVLKAGV 1891
Db 1944 VTQILSLT-----ITQILKRLHOWINEDCSTPCSGSLRDVMDWICT-----VLTDFTKWL 1995
Qy 1892 QS--MNNIPGCPFFVSCOKYKGPWIGSMLOARCPGAEILIFSVEENGFAKLYKGPRTCSN 1949
Db 1996 QSKLLPLRPGVPFFPSCORGKYGWRGIGIMQTTCCGCAQITGHVNGSMRIV--GPTCSN 2054
Qy 1950 YMRGAVPVNARLCSARPDP--DWTSLVNVYGRDYCKYKMGDHIIFVTAVSSPNV--CFT 2007
Db 2055 TWHGTFFINATYTGCTPSPAPNYSRALWRVAABEYVEVTRVGDVPHVYVTGMTDNNVKPC 2114
Qy 2008 QVP-----PTLRAAVA-----VDGVOVQCYLGEKPTPTWTS 2038
Db 2115 QVPAPEFFTEVDGVRLLHRYAPACKPLLRBEVTVLVLGNQYLVGSQLP---EPE----- 2165
Qy 2039 ACCYGPDPKGTVKL--PFRVDGHTPGVRMQLNLRDALETND-----CNSNN 2084
Db 2166 ---PDVAVLTSMLTDPSHITAETAKRARGSPSLTSSASQLSAPSLKATCTTRHD 2220
Qy 2085 TPSDEAAVSALVFKQEL-----RRTNQLL-----EASAGVDTTKLPAPSIBEVVVRK 2132
Db 2221 SPDADLLEALLWRQEMGNITRVESENKVILDSFEPLOAEEDEREVSVA--EILRRS 2278
Qy 2133 RQFRARTGSLUTLPPPRSVPGVSCP-----ESLQSD-----PLEGPNLPPSP 2176
Db 2279 RKF-----PRAMPIWARPDYNPPLLESKDPDYVPPVHVHGCPLP--PAKAPDIP 2325
Qy 2177 P-----VLQAMPMPLLGAGECNPF-----TAIGCAMTETGGGPDOLP 2214
Db 2326 PPRKRTVIVSESTVSSALAEAL--TKTFGSSBSSAVDSGTATASPQPSDDGAGSDVE 2383
Qy 2215 SY---PP---KKEVSEWSDESWSATTAFTASSVVTGPPYKIRGKDSOTOSAPAKRPTKKLG 2268
Db 2384 SYSSMPLEGEPCGDDSLDGSWSTVSEAS-----2413
Qy 2269 KSEFSCMSYTWTD-VISFTASKVLSATRAITSGFLKQKSLVTVTPRDELRKQKVTI 2327
Db 2414 EDVVCCSMSYTWGALITPCAABETKLPINALSNLRLHNLVYATTSRSASLRKQKVT 2473
Qy 2328 NRQPLFPYSYHKQVRLAKEKASKVGVWMDYDEVAHTPSKASHITGLRGTVRSAA 2387
Db 2474 DRLOVDDHRYDVLKEMKAKASTVKALLSVBEACKLTPHSARSKF-GYGAKDVRN-LS 2531
Qy 2388 RKAVIDLQK---CVEAGEIPSHYRQTVIVPKBEVFVKTPQKPKPRLISYPHLEMR 2443
Db 2532 SKAVNHIRSVWKOLLEDETETPI---DTTIMAKNEVFCVQPEKGGKPARLIVFPDLGVV 2588
Qy 2444 VEKMYGQVADPVVKAVMGDAYGF--VDPTRVRKRLLSMWSPD---AVGATCDTVCFDSTIT 2500
Db 2589 CEKMALYDVVSTLPQAVWSSYSGFQVSPQORVEFLVNAWAKKCPMGFPAYDTRCFDSTV 2648
Qy 2501 PEDIMVETDIYSAKLSQDRAGHTIARQIYAGGPMIAYDGRIGYVRCBSSGVYTTSS 2560
Db 2649 ENDIRVEESIYQCCDLAPEARQAIRSLTERLYIGGLPLTNSKGQNCYRRCRASGLVITSC 2708
Qy 2561 SNSLTCWLKYNAAAEQAGMKNPFLICDDCTVTIWKSGADADAKQAMRVFASMMKVMGAP 2620
Db 2709 GNTLITCYLKAACRAAKLODCTMLVCGDDLVLVICSAGTQEDASLRAFTEMTRYAP 2768
Qy 2621 QDCVPQPKYSLEELTSCSNVTSIGTSKXPYYFLTRDPRIPRLGRCSAEGLGYNPSAAWI 2680
Db 2769 PGDPKPEYDLELITSCSNVSVVAHDASGRVYVLTDRPTTPLARAAWETARHTPVNSWL 2828
Qy 2681 GYLIIHYFCLVWSVLAHFHMEQMLFEDKLPETVTPDWYKGNVTVPVEDLPSIAGVHI 2740
Db 2829 GNIIMYAPTLMARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIQLRHL 2888

Db 2832 IMYAPTLWARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIQRLHGLSAP 2891

Qy 2744 SVWRYTNAEILRVQSOLTDMTPPLRAWKKAVALASAKRRGGGAHAKLARFLL-WHATS 2802

Db 2892 SLHSYSPGEINRVASCLRLKLGVPPLRVWRHRARSVRARLLSQGGRAATCGKYLFWNAVRT 2951

Qy 2803 R-----PLP-----DLDKTSVARYTTFNDCVYSPGVDVITPQRRLOKPLVKYLAVIVFA 2853

Db 2952 KKLTFIPAAQQLDSSWFVAGYS-----GGDIYHLSLRARPRW-----FWMC 2994

Qy 2854 LGLIAVGLAI 2863

Db 2995 LLLLSVGVGI 3004

Search completed: October 27, 2005, 15:41:35
Job time : 318 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2005, 15:33:26 ; Search time 73 Seconds
(without alignments)

3774.860 Million cell updates/sec

Title: US-10-009-002-2

Perfect score: 15376

Sequence: 1 MPVISTQTSPVPAPRTRKNK.....KYLAVIVFALGLIAVGLAIS 2864

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3273.5	21.3	3033	1 GNVJ38	genome polyprotein
2	3262	21.2	3033	1 JQ1303	genome polyprotein
3	3237	21.1	3010	1 GNVJTW	genome polyprotein
4	3232	21.0	3010	1 A45573	genome polyprotein
5	3224.5	21.0	3011	1 S40770	genome polyprotein
6	3223	21.0	3010	1 GNVVCJ	genome polyprotein
7	3218	20.9	3010	1 GNVVTC	genome polyprotein
8	3204.5	20.8	3011	1 GNVVC3	genome polyprotein
9	3161	20.6	3010	1 S18030	genome polyprotein
10	3126.5	20.3	3011	1 GNVVCH	genome polyprotein
11	3119	20.3	3014	1 J55620	genome polyprotein
12	2055	13.4	3005	2 T08841	polyprotein - dour
13	2029.5	13.2	2970	2 T08839	polyprotein - marm
14	1028.5	6.7	1435	2 T01075	polyprotein - hepa
15	871	5.7	386	2 S68016	ATPase/RNA helicase
16	811.5	5.3	876	2 PC2219	polypeptide - hepa
17	698.5	4.5	874	2 JQ0883	genome polyprotein
18	688	4.5	874	2 JQ0881	genome polyprotein
19	649.5	4.2	365	2 JQ0879	NS5 protein - hepa
20	645.5	4.2	216	2 S21337	genome polyprotein
21	634.5	4.1	365	2 JQ0880	NS5 protein - hepa
22	530	3.4	492	2 P50326	polyprotein - hepa
23	416	2.7	782	2 S18032	genome polyprotein
24	415	2.7	3988	1 GNVVBV	genome polyprotein
25	412	2.7	782	2 S19875	genome polyprotein
26	406.5	2.6	3898	1 A44217	genome polyprotein
27	406.5	2.6	3898	2 S58295	polyprotein - hog
28	406	2.6	782	2 S19876	genome polyprotein
29	406	2.6	782	2 S18031	genome polyprotein

ALIGNMENTS

RESULT 1

GNVJ38

Genome polyprotein - hepatitis C virus (strain HC-J8)

N:Contains: capsid protein C; envelope protein M; Hepacivirin (EC 3.4.21.98) (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C:Species: hepatitis C virus

C>Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004

C:Accession: A40250; PQ0397; PQ0559

R:Okamoto, H.; Kurai, K.; Okada, S.I.; Yamamoto, K.; Lizuka, H.; Tanaka, T.; Fukuda, S.;

Virology 188, 331-341, 1992

A:Title: Full-length sequence of a hepatitis C virus genome having poor homology to repo:

A:Reference number: A40250; MUID:92230232; PMID:1314459

A:Accession: A40250

A:Molecule type: genomic RNA

A:Residues: 1-3033 <OKA>

A:Cross-references: UNIPROT:P26661; GB:D0121; NID:g221608; PIDN:BAA01761.1; J.Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Feutheuer, J.F.; Follett, E.; Yap, P.L.

J. Gen. Virol. 73, 1131-1141, 1992

A:Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to e>

A:Reference number: PQ0393; MUID:92268871; PMID:1316939

A:Accession: PQ0397

A:Molecule type: genomic RNA

A:Residues: 2678-2754 <CHA>

A:Cross-references: DDBJ:D10134

A:Experimental source: isolate E-b12

R:Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno,

Biochem. Biophys. Res. Commun. 181, 279-285, 1991

A:Title: Distribution of plural HCV types in Japan.

A:Reference number: PQ0554; MUID:92068204; PMID:1720309

A:Accession: PQ0559

A:Molecule type: mRNA

A:Residues: 2678-2729 <KAT>

A:Cross-references: GB:D10562; GB:D90518; NID:g221523; PIDN:BAA01418.1; PID:g221524

C:Superfamily: hepatitis C virus genome polyprotein

C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural

F:1-115/Product: capsid protein C #status predicted <CPC>

F:116-191/Product: envelope protein M #status predicted <EPM>

F:192-389/Product: major envelope protein E #status predicted <MEE>

F:390-733/Product: nonstructural protein NS1 #status predicted <NS1>

F:734-1010/Product: nonstructural protein NS2 #status predicted <NS2>

F:1011-1619/Product: hepatitis C virus #status predicted <NS3>

F:1234-1241/Region: nucleotide-binding motif A (p-loop)

F:1316-1321/Region: nucleotide-binding motif B

F:1320-1323/Region: DEXH motif

F:1620-1866/Product: nonstructural protein NS4a #status predicted <NS4a>

F:1867-2017/Product: nonstructural protein NS4b #status predicted <NS4b>

F:2018-2033/Product: nonstructural protein NS5 #status predicted <NS5>

F:196, 209, 233, 299, 305, 417, 423, 430, 448, 477, 534, 542, 558, 578, 627, 649, 1091, 1217, 1259, 2038, 231

Query Match

Best Local Similarity 21.3%; Score 3273.5; DB 1; Length 3033;

Matches 980; Conservative 436; Mismatches 1185; Indels 679; Gaps 106;

Db 467 VGMGALQYEDVNTNPNEDMRPYCMHYPRRCQGVVSASSVCGPVYCFTPS---PVVVGTTDR 523

Qy 403 ISWPTYTPGARGCMVKFNNT-----WGC-----CRIR---NVPSY 436

Db 524 LGAPYTW-GENETDVFLNSTRPPQGSWFGCTWNNSTGYTKTCGAPPCRIRADPNASMD 582

Qy 437 CTMGTDVAMNDRNTYEACGVTPLT-----TAWHNGSALKLAILQ---YPSKEM 484

Db 583 LLCPTDCFRKHPDPTYIKCGSGPMLTPCLIDYPVRLWHYPCVTNYTIFKIRMVGVGB- 641

Qy 485 FKPHNMWGHLYFEGSDPTPIVIFYDPVNSTLLP-----PERWARLPGETPPVVRGSLWQVPQ 540

Db 642 ---HRLTAACNFTRGDRCNL---EDRDRSQSLPLHSTTEWAILPCT----- 682

Qy 541 GFYSDVKDLATGLITKDAWKNYQVLYSATGALSJLTGVTTKAVLILLLGCGSKYLILAY 600

Db 683 --YSDLPALSTGLLHLHQNIYDVQPMYGLSPALTKYIVRWEWVLLFLLLADAR--VCAC 738

Qy 601 LCYLSLCFRASGYPLRPVLPFSQSLQAGWDVLSKAQVAPFALIPFICCYLRCRLRYAAL 660

Db 739 LWWLIL-----LQQAEEALEKLVVLHAA-----SAASC 766

Qy 661 LGFVPMAGLPLTFVFAAAAAQPDYDWWVRLLVAGLVWAGNRGHRITALLVGPWPLVAL 720

Db 767 NGFLYF-----VIFFAA-----WYIKGRVVPATYS-----LTGLMSFG-- 801

Qy 721 LTLHLVTPASAFDEIIGGLTIPPVVALVMSRFGFFAHLLPRCALVNSVLMQRW---- 776

Db 802 LLLALPOQAVAYDASVHGQIGAULLVLITLFTLPGYKTLRS-----FLW--WLCYL 853

Qy 777 -----ENFMWNVTLRPER---FFVLVCPFGATYDALVTFVCVCHVALLCLTSSAASF 825

Db 854 LTLAEAMVQEWAPPQVGRGDGIWAVAI PCGVVFDITKW-----LLAVLGPVLL 906

Qy 826 FGTDSR-----VRAHRML-----VRGKCHAMVSHVYLFLLVFOE-NGVFFYKHL--HG 873

Db 907 KGALTRVPYFVRAHALLRMCTMR---HLAGGRYV-QWVLLALGRWGTGYIDHLTPMS 961

Qy 874 DVLNDFASKLPQEP--FFPEGKARYVRNEGRLACGDTVDGLPVVARGLDILVFAGLA 931

Db 962 DWAANGRLDLAVAVEPIIIPSPMEKKVIVWGAE--TAACGDILHGLFVSARLGREVLLG-- 1017

Qy 932 MPPD-----GWAITAPFTLOCLSERGTLISAMAVVMGTGIDPRTWTGTIFRLGSLATSYMGF 986

Db 1018 -PADGYTSKGSLLAPIAYAAQTRGLLGTIVVSMTRGDKTEQAGEIQVLSVTVQSFLT 1076

Qy 987 VCDNVLYTAHSGSKRRRLAHPGSIHPITVDANDODIYQPPCGAGSLTRCSGKTKYL 1046

Db 1077 TISGVLWTVYHGAGNKTLAGSRGPVTQMYSSAEGDLVGPWPPGPKSLEPCTCGAVIDLYL 1136

Qy 1047 VTRLGSLVEVNSDDPYVCVCGALPMVAKGSSGAPILCSSGHVIGMFTAARNSGG---S 1103

Db 1137 VTRNADVTPARRRGDKRGALLSPRLSTLKGSSGGPVLCPRGHVGVPRAAVCSRGVAKS 1196

Qy 1104 VSQIRVRLPVCAGYHPQYTAHATLDTKTPVNEYSVQILIAPTGSGKSTKLPLSYMOEKY 1163

Db 1197 IDFPVETLIDIVRSPTSDNS---TPPAVQTYQVGYLHAPTGSKSTKVPVYAAQGY 1253

Qy 1164 EVLVLPNSVATTASMPKYMHAITYGVNPNCFYNGKCTNTGASLTYSTYGMILT-GACSRN- 1221

Db 1254 KVLVLPNSVAATLGFAGVLSKAHGINPNIRTGVRTVTVTGAPITYSTYKFLADGGCAGGA 1313

Qy 1222 YDVLICDSCHATDATVTLGIGKVLTEAPSKNVLNVLATATPPGVIPTPHANITELQTD 1281

Db 1314 YDIIICDSCHAVDSTIIIGITGLDQAEATAGVRLTLVLATATPPGVTTPHPNIEBALGQ 1373

Qy 1282 BGTIPFHGKKIKEENLKKGRHLIFEATKKHCDLANELARKIGITAVSYRRGCDISKIP-E 1340

Db 1374 EGEIPFYGRAIPLSYIKGRHLIFCHSKKCKDELAALRGMLNAVAYRGLDVSIVPTQ 1433

Qy 1341 GDCVVVATDALCTGYTGDFDSYDGLSVMEFGCHVDLDPFTFTMGVVRVCGVAIVKGQRRG 1400

Db 1434 GDVVVVVATDALMTGTGDFDSYDIDCNVAVTQVVDPSLDPTFTITTTQVTPQDAVSRQRG 1493

Qy 1401 RTGRGRAGIYVYVYDGSCTPSGMVPECNIVBEAFDAAKAWYGLSSTEAQITILDYRTOPGLP 1460

Db 1494 RTGRGLGIYRYVSTGERASGMDSVLCECYDAGAAMYELTPAETTVRLRAYENTGCLP 1553

Qy 1461 AIGANLEWADLFS-MYNBPESFVNTAKRTADNVLLTAAQLQLCHQYQVAAPNDAPRWQ 1519

Db 1554 VQDHLFEWAEVFTGLTHIDAHFLSQTQSGENFAYLTAYQATVCAR-----AKAPPSWD 1609

Qy 1520 GARLGKPKGVGLWFLDGDAC-----PGPEP-----SEVTRY---Q 1552

Db 1610 -----VMMK-----CLTRLKPTLVGPTPLLYRLGSVTNEVTLTHPVTKIATCM 1653

Qy 1553 MCFTEVNTSGTAALAVGVGVAMAYLAIDTFGATCVRRCWSITSVPTGATVAPVVUDEBEI- 1611

Db 1654 QADLEVWTS-TWVLAGGVLAAYAAVCLAT- GCVCII--IGRLHVNRQAVAP--DKEVLY 1706

Qy 1612 -----VEECASFPL- EAMVAAIDKLKSTI-----TTTSPTTLETALE-----KLNTPLG 1655

Db 1707 EAFDEMEECASRAALIEEGORIAEMLKSKIQGLLQQAASKQAQDIQPAVQASWPKVEQFWA 1766

Qy 1656 PHAATILAIIEYCCGLVTLPDNPASCVFAFIAGITTPLPKHKIKWFLSLFGGATASKLTD 1715

Db 1767 KHMNFISGIOYLAGLSTLPGNPAVASMMAFSAALTSPLSTSTTILNLILGGWLASQIAP 1826

Qy 1716 ARGALAFWMAAGATGALTWTSTVSGF---VFDMLGGYAAASSTACLTFFKCLMGWPTMDQL 1772

Db 1827 PAGATGFVSGLVGAAGV---SIGLGKVLVDILLAGYCGISGALVAFKIMSGEKPSMEDV 1883

Qy 1773 AGLVYSAPNPAAGVVGVLSSACAMPALTAGPD-----HWPNRLLTMLARSNTVCNEYFIAT 1828

Db 1884 WLLPGILSPCALVVGVI--CAAILRRHVGPGEAGVQMMNRLLIAFASRGHNHVAPTHVTE 1941

Qy 1829 RDIRKILGILEASTPMSVISACIRWLHTPTEDDCGLI---ANGLEITWQYVCFNFFVICFN 1885

Db 1942 SDASQRYTQLLSLT-----ITSLLRLHNNWITEDCPIPCSGSWLRDWDVWCTILTDFKN 1997

Qy 1886 VLKAGVOSMVNI PCFPYSCQKYGKPGWIGSMLOARCPQCAELIFSVEGFAKLYGKPR 1945

Db 1998 WLTS--KLFPKPGFLPISQKYGKVGWAGTGIMTTRCPCGANISGNVRLGSMRI-TGPK 2054

Qy 1946 TCSNYRGAVPVNARLCSGARPDP-TDWTSLVNVYGVDRYCKYKMGDGHIFVTAVSSPNV 2004

Db 2055 TCNNIWGTFPINCYTEGQCQVCPKPAFPKFAIWRVAASEYAEVTHGSHYHITGLTTDNL 2114

Qy 2005 CFTQVP---PTLRAAVADGVQVQCYLGEBKPTWTTTS-ACYCG-----PD 2045

Db 2115 ---KVPQOLSPSEFFSWVDGVQIHRFAPIPKPFPRDEVSCVGLNSFVVGSQLPCDPEPD 2171

Qy 2046 GKGTVKL--PFRVDGHTPGVRMQLNRDALETNDCNSTNNTPSDEAAVSALVFKEQLRR 2103

Db 2172 TDVLTSMLTPSHITAEAAARL-----ARGSPPEASESSASQLSAPSLRA 2217

Qy 2104 T-----NQLLEA-ISAGVDTTKLPAPISEBVVVRKQFRARTGSLTLPPPPRSVPG 2153

Db 2218 TCTTHGRKAYDVMVDANLFMGDDVTRIESES--KVVV----- 2252

Qy 2154 VSCPESLQSDPL-EGSNSLPPS-----PPVLQL-AMP---MPLLGA---GEC 2193

Db 2253 -----LDLSDPMVEERSDLEPSIPSEYMLPKKRPFPALPAWARPDYNNPPLVESWKRPDY 2306

Qy 2194 NPFTAICAMTETGGGDDPLPSYPPKKE---VSEMS-----DES 2229

Db 2307 QPATVACALPP-----PKTPTPPPPRRRTVGLSESIADALQQLAKTSFCQPPSPGDSG 2362

Qy 2230 WST-ATTASSYVTGPP-----YPKIRKGDOSTQAPAKRPTKKKL----- 2267

Db 2363 LSTCADAADSGSRTPPDELALSETGISSSMPPLEGEPCD---PDLEQEQVELQPPPOGGV 2419

Qy 2268 -----GKSEFS-----CSMSYTWTD-VLSFKTASKVLSTRAITSGFLKQSRSLV 2310

Db 2420 VTPGSGSGMSWSTCSEEDSDSVCCMSMSYSWTGALITPCSPBEELPINPLSNLSLRYHNKV 2479

1790 LMAFTAAVTSPLTTSQTLLENLGGVAAQAAPGAATAFVSGSLAGAAGV---SVGLGR 1846
1741 -VFDMLGYYAASSTACUFTKCLMGWETMDQAGLVYSAPNPAAGVGVVLSACAMFALT 1799
1847 VLVDFILAGYAGVAGALVAFKIMSGELPSTEDLVNLLPAIILSPGALVGVV---CAAIIIR 1904
1800 TAGPD-----HWPNNRLLTWLARSNTVCNEYFFATRDIRKILGILEASTPWSVISACIRWL 1855
1905 HVGEGEGAVQMMNRLLIAPASRGNHVSPTHYPESDAAARVTAISSLVTTQLLRRLHQWL 1964
1856 HTPTEDDCGLIANGLEIWOYVYCNFFVICFNVLKAGVQSMWNIIPGCFYSCQKGYKGPWIG 1915
1965 SSESTTPCS-GSWLRDIWDWICEVLSDFTWLK--TKLMPHLPGIPFVSCQHYGKGVWRG 2021
1916 SGMLOARPCGAELIFSVEGFAKLYKGPRTCSNYWRGAVPVNARLCSGARPDPFT-DWTS 1974
2022 DGIHMTCHCAEITGHVKNGTMRIV-GPKTCRNWMSGTFPINAVTTGCTPLPAPNYTF 2080
1975 LVVNYGVDRDYCKYKMGDHI FVTAVSSPNV-CFTQVP-----PT 2012
2081 ALNRVSAEYVEIRVGVDFHYVTGTTNLLKPCQCVPSPEFTELDGVRLHRFPCKPL 2140
2013 LRAAVAVD-----GVQVOCYLGEPTKPTMTTSACCYCPGDKGKTVKL--PFRVDGHTP 2062
2141 LREEVFRVGLHDYVPGSQLPC---EPB-----PDVAVLTSMLTDPSHITAAAA 2186
2063 GVRM-----QLNRDALETNDGNTNNTSPSDEAAVSALVFKQEL----- 2101
2187 GRRLARGSPPEASASSQLSAPLSKAT--CTINHDSDAELIEANLLWRQEMGNITRV 2244
2102 RRTNOLL-----EALSAGVDITKLPAPSLIEVVVRKROFRARTGSLTL-----PP--- 2146
2245 ESENKWLDFDPLVAEDEREISVPA--ETLRKSRF---TQALPFWARPDPVNPPLIE 2299
2147 ---PPRSVPGV--SCPESLQSRDPLEGSPNLPSPPP-----VL---QLAMPPLLGA- 2190
2300 TWKKNYEPVPPVHGCLP-----PPQSPVPPPRKRTVTLTESTLTALAEALAK 2350
2191 -----GECNPTFAICAMETCGGPD-DLPYSY---PP---KKEVSEWSEDSSTATT 2235
2351 SFGSSSTSGITGDNTTTSSEAPSGCSPDSEYSSMPPLLEGEPDPLSDGWSSTVSS 2410
2236 ASSVYTGPPYKIRCKDSTQAPAKRPTKKLKGSEFSCSMTYTD--VISFKTASKVL 2294
2411 EAG-----TEDVCCSSMTYTGALITPCAAEEQKL 2441
2295 ATRAITSGFLKORSIVVYVTEPRDAELRKQKVTINRQPLFPSPSYHKQVRLAKEKASKVGV 2354
2442 PINALSNSLLRHHNLVYSTSRACORQKVTDFRLQVLDSDHYQDVLEKVAASAKVKAN 2501
2355 MWDYDEVAHPTPSAKASHITGLRQTDVRSAGAKAVLDL----QKCVAEGEIPISHYRQT 2410
2502 LLSVEEACSLTPPHSAKSKF--GYGAKDVRC--HARKAVNHINSVMKDLLEDSVTPT--QT 2556
2411 VIVPKEEVFTKPKPTKPRLLISYPHLEKRCVEKYYGVQAPDVVKAVMGDAYGF-VD 2469
2557 TIMAKNEVFCVQPEKGRKPARLIVFDLGVRCVKEMALYDVSKLPFAVMGSSYGFQYS 2616
2470 PRTRVKRLLSWSP--DAVGATCDTVCFDSTITTPEDIMVETDIYSAAKLSQHRAGIHTI 2527
2617 PGQVFEVLVQAWKSKRTPMGFSYDTRCFDSTVTESDITREAIYQCCDLDPQARVAIRSL 2676
2528 ARQLYAGGPMIAYDREITGYRRCRSGSVYTTSSNSLTCWLKVNAAAEQAKGNKPRFLIC 2587
2677 TERLYVGGPLTNSRGENCGYRRCRASGLVLTSSCGNTLTACYIKARAAACRAAGLQCTMLVC 2736
2588 GDDCTVIWKSAGADAKAMRVFASMMKVMGAPQCVQPKYSLELTSCSNSTSGITK 2647
2737 GDDLVIICESAGVQDAASLAKRAFTAMTRYAPPQDPQPEYDLELTSCSNVSVAHDG 2796
2648 SGKPYFYFLTRDPRIPLGRCSAEGGLGNFNSAAMIGYLIHHYFCLMWSRYLAVHFMQMLFE 2707

2797 TGRKVVYLTDRPTTPLARAAWETARHTPVSNLGNIIMFAPTLWARMLMTHFPFSVLIR 2856
2708 DKLPETVTFDYGKNTVPVEDLPSIIAGVHGIEARSVVRVYNAEILRVOSLDTMTMP 2767
2857 DQLEQALDCDIYGACYSIEPLDUPPIIQRHLGSAFSLHSYSGEINRVAACLRKKGVP 2916
2768 LRAWRKARAVLASAKRGGNAHAKLAFLL-WHATSR-----PLDLDKTSVARTTYNYC 2822
2917 LRAWRHARSVRARLLSRGGRAICGKYLFWAVRTKLTPIAAGRLDLSGFTAGYS 2976
2823 DVYSPGDDVITPORRLOKFLVKYLVIVFALGLIAVGLAI 2863
2977 G-----GDIYHSVSHARPRW-----FWFCLLLLAAGVGI 3005

RESULT 6
GNWVCJ
genome polyprotein - hepatitis C virus (strain J)
N:Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructural
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A39253; PS0086
R:Kato, N.; Hijikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimoto
Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990
A:Title: Molecular cloning of the human hepatitis C virus genome from Japanese patients v
A:Reference number: A39253; MUID:91088550; PMID:2175903
A:Accession: A39253
A:Molecule type: genomic RNA
A:Residues: 1-3010 <KAT>
A:Cross-references: UNIPROT:P26662; GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
R:Kato, N.; Ohkoshi, S.; Shimotohno, K.
Proc. Jpn. Acad. 65B, 219-223, 1989
A:Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence vari
A:Reference number: PS0085
A:Accession: PS0086
A:Molecule type: genomic RNA
A:Residues: 2650-2707 <KA2>
A:Experimental source: Japanese isolate
C:Comment: The cleavage sites of this polyprotein have not been determined.
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serine
P-2-115/Product: capsid protein C #status predicted <CPC>
F:116-191/Product: envelope protein M #status predicted <EPM>
F:192-389/Product: major envelope protein E #status predicted <WEE>
F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F:1007-1615/Product: hepatitis C virus #status predicted <NS3>
F:1230-1237/Region: nucleotide-binding motif A (P-loop)
F:1312-1317/Region: nucleotide-binding motif B
F:1316-1319/Region: DEXH motif
F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
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Query Match 21.0%; Score 3223; DB 1; Length 3010;
Best Local Similarity 30.2%; Pred. No. 4.8e-192;
Matches 977; Conservative 439; Mismatches 1206; Indels 614; Gaps 117;

QY 8 TSPVAPRTRKNKQTOASYPVSIK-----TSVERGORAKRKVORDARPR 51
DB 3 TNPFRQTKENTNR---FQDVFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPR 59
QY 52 NYK-----IAGHDGLQTLAQAALP-----AHWGRODPRHKSRN 86
DB 60 GRRQPIPKARRPEG-RTWAQPGYWPPLYNEGMGAGWLLSPRGSPPSWGPTDPRRRSRN 118
QY 87 LGILLDPLGHWIGDVTHTPLVGLVAGAVRVCQIVRLLEDGVNWTG---WFGVHLF 143
DB 119 LGRVIDTLTCGFADLMGYIPLVGLAPLGA-ARALAHGVRLVEDGVNATGNLPGCSFSIF 177
QY 144 VVCLLS-LACPCSGARVTDPTNTTILTNCCORNQVIYCSPTCLHBEPCVICADE---- 198

178 L L A L L S C L I T P A S A Y E R N V - S G I Y H T N D C S N S S I V E A A D M I M H T P G C V P C V R E S N F S 236
199 - C W P A N P Y I S H P N W G T O S F L A D H I D F V M G A L V T C D A L D I G L C C A C V L G D M L V - - - 254
237 R C W A L T P T L A R N S S I P T T - I R R H V D L L V G A A L C S A M T V G D L C G S V F L V S O L F T F S P 295
255 R H W I H I D L N E T G T C Y L E V P T G I D P G F L G - - F I G W - - - M A G K V B A V I F L T K L A S Q V P Y A I 309
296 R R Y E T V Q D C N - - - - C S I Y P G H V S G H R M A D M M N W S P T T A L V V S Q L L - R I P Q A V 344
310 A T M E S S V H Y L A V G A L I Y Y A S R G K Y Q L L A L M L Y - - - - - 343
345 V D M V A G A H G W L A G L A Y S Y M G N W A K V L I V M L L P A G V D G H T H V T G R V A S S T Q S L V S W L S 404
344 - - - - - I E A T - - - - - S G N R P R V P T G C S I A E 362
405 Q G P S Q K I Q L V N T N G S W H I N R T A L N C N D S L Q T G F T A A L F Y A H R F N A S G C P E R M A S C R I D E 464
363 P C - - - - S P L M I P C P - - - - - C H S Y - - - - - L S E N V S E V I C Y S P K W T R P I T L E Y N N - 401
465 P A O G W G P I T H D M P E S S D Q R P Y C H Y A P R C G I V P A S Q V C G P V Y C F T F S - - - P V V U G T T D R 521
402 - - - - - S I S H Y P T I P G A R C M W K F K N N T - - - - - W G C C R I R N V P S Y - - - - - C T M G - - - 440
522 F G A P T Y S W - - - - - G E N E T D V L L S N T R P P O G N W F G C T W M N S T G F T K T C G G P P C N I G G V G 575
441 - - - - - T D A W N D T R N T Y E A C G V T P M L T - - - - - T A H N G S A L K A I L Q - - - - - Y P G S 481
576 N N T L V C P T D C R K H E A T Y T K C G S G P M L T P R C M W D Y P R L M H Y P C T V N F T V F K R V M Y V G G 635
482 K E - - - - M F K P H N M S G - H L Y F E G S D T P I V Y F D P V N S T L L P P E R W A R L P C T P P V R G S W L Q V 538
636 V E H L N A A C N W T R C E R C D E D R D R - - - - - S E L S P L L S T T E M O I L P C S - - - - - 678
539 P Q G Y S D V K O L A T G I T K D K A W K Y Q V L Y S A T G A L S I T G V T T K A V I L L G L C S K Y L I L 598
679 - - - - - F T T L P A L S T G L I H L R I N V D Q V L Y G I G S A W S F A I K W E Y I L L L L L A D A R V C A C 734
599 A Y L C Y L S I C F G R A S G Y P L R P V L P S Q S Y L O A G M D V L S K A Q V A P P A L I F F I C C Y L R C L R Y A 658
735 L M M L L - - - - - I A Q A E A T L E - N L V L N A A S V A - - - - - G A H 763
659 A L L G F V P M A G L P L T F F V A A A A Q P D Y D W V R - L L V A G L V L W A G R N R G H R I A L V G P W P L 717
764 G L L S F - - - - - L V F F C A A - - - - - W I K G R L V P G A Y - - - - - A L Y G W P L 796
718 V A L L T L H L V T P A S A F D T E I I G G T I P P V A L V M S R F G F F A H L L P R C A L V N S Y L M O R W E 777
797 - - - - - L L L L L A L P P R A V A M D R E M A A S C G G A V F V G L V L L T L S P Y K V F L A R L I M W L Q Y F I T R A E 854
778 N - - - - - W F N V T L R P E R F L V L V - - - - - C P G A T Y D A L V T F C V C H V A L L C I L T S S A A S - - - - - P F G 827
855 A H L Q W V P P L N V R G R D A I L L T C A V H P E L I F D I T K L L A L G L P M V L Q A G I T R V P V F V R 914
828 T D S R V A R H M L V R L G K H A W T S H V L F F L A V F G E N G V F F K H L - - - - - H G D V L P N D F 880
915 A O G L I R A - C M L V R - - - - - K V A G H V Q M A F M K L A A L T G T Y V Y D H L T P L R D W A H A G L - - - - - R D L 967
881 A S K L P L O E P P P F F G K A R V Y N E G R L A C G T V D G L P V A R L G D L V F A G L A M P P D - - - - - 935
968 A V A V - - - - - E P V V F S D M E T K L I T W G A D T A A C G D I I S G L P V S A R R G K E I L L G - - - - - P A D S F G E Q 1021
936 G W A I T A P T L O C L E R G T L S A M A V M T G I D P R T W T G I F I R L G S L A T S Y M G V C D N V L Y T A 995
1022 G W R L L A P I T A V S Q O T R G L L G C I I T S L T G R D K N Q V D G E V Q V L S T A T Q S F L A T C V N G V C M T V 1081
996 H G S K G R R L A H P T G S I H P I T V D A A N - D O D I - - - - - Y O P P C A G A S L T R C S C E T K G Y L V T R L G S 1052
1082 Y H G A G S K T L A G P K G - - - - - P I T O M Y T N V D Q D L V G W P A P P A G A R S M T P C T C G S S D L Y L V T R H A D 1138
1053 L V E Y N K S D D P Y W C V G A L P M A V A K S G A P I L C S G H V I G M F T A A - - - - - R N S G G S V S Q I R V 1109

1139 V P V R R R D S R G S L L S P R P I S Y L K G S G G P L L C P S G H V G V I F R A A V C T R G V A K A V D I P V 1198
1110 R P L V C A G Y H P Q Y T A H A T L D T K P T V P N E Y S V Q I I A P T G S G K S T K L P S Y M Q E Y E V L V L N 1169
1199 E S E T T M R S P V F T D N S - - - - - S P P A V P Q T F Q V A H L H A P T G S G K S T K V P A A Y A A Q G Y K V L V L N 1255
1170 P S V A T T A S M P K Y M H A T Y G V N P N C Y F N G K C T N T G A S L T Y S T Y G M Y L T - G A C S R N - Y D V I I C 1227
1256 P S V A A T L G F A Y M S K A H G I E P N I R T G V R T I T T G P I T Y S T Y C K F L A D G G S G G A Y D I I C 1315
1228 D E C H A T D A T T V L G I G K V L T E A P S K N V R L V L A T A T P G V I P T H A N I T E I O L T D E G T I P F 1287
1316 D E C H S T D S T I L G I T G V L D Q A E T A G A R L V L A T A T P G S I T V P H P N I E E V A L S N T G I P F 1375
1288 H G K I K E E N L K G R H L I F E A T K K H C D E L A N E L A R K G I T A V S Y R G C D I S K I P - E G D C V V V 1346
1376 Y G R A I P E A I K G R H L I F C H S K K C D E L A A K L T C L G L N A V A Y R G L D V S V I P T S G D V V V V 1435
1347 A T A L C T G Y T G D F D S V Y D C S L M V E G I T C H V D L D P T F T M G V R V C G V S A I V K Q R R G T O R G R 1406
1436 A T D A L M T G T G D F D S V I D C N T C V T Q T V D F S L D P T F T I E T T L P Q D A V S R A Q R R G T O R G R 1495
1407 A G I Y Y Y V D G S C T P S G M V P E C N I V E A F D A A K A W Y C L S T E A Q T I L D T Y R T O P G L P A I G A N L 1466
1496 S G I Y R F V T P E R P S G M P D S S V L C E Y D A G C A W Y E L T P A E T S V R L A Y L N T P G L P V C O D H L 1555
1467 D E W A D L F S - M V N P E P S F V N T A K R T A D N Y V L L T A A Q L Q L C H Q Y G Y A A P N D A P R M O G - A R L G 1524
1556 E F W E S V T G T H I D A H F L S O T K A G D N L P Y L V A Y Q A T V C A R A Q A P P P S W D M W K C L I R L K 1615
1525 K K - - - - - P C G V L M R L D G A D A C P G P S E V - - - - - T R Y O M - C F T - - - - - E V N T S G T A A L A V G V G 1571
1616 P T L H G P T P L L Y R L - - - - - G A V Q N E V T L T H P I T K Y I M A C S A D L E V V T S - T W L V G S V L 1667
1572 V A M A Y L A I D T F G A T C Y R C H S I T S V P T G A T A P V D D E E I - - - - - V E E C A S F T P - L E A M 1624
1668 A A L A A Y C L T T G S V V I V G R - - - - - I L S G R P A V I P D R E V L Y Q B E D E M E C A S H U P I E Q G 1721
1625 V A A I D K L K - - - - - S T I T - - - - - T T S P T L E T A L E K L N T F L G P H A A T I L A I B Y C C G L V T 1673
1722 M Q L A E Q F K A L G L Q T A T K Q A E A A P - V V E S K W R A L E V F W A K H M N F I S G I Q I A G L S T 1780
1674 L P D N P F A S C V F A T I G T T P L P H K I M F L S L F G A I A S K L T D A R G A L A F M M A G A A G T A L G 1733
1781 L P G N P A L A S M A F T A S I T S P L T T Q N T L L F N I L G W A A Q L A P P S A A S A F V C A G I A G A A V G 1840
1734 T W T S V G F - - - - - V F D M L G C Y A A A S T A C L T F K C L G E M P T M D Q L A G L V Y S A F N A P A G V V G V L 1790
1841 - - - - - S I G L G K V L V D I L A G Y G A G A L V A F K V M G E M P E S T E D L V N L L P A I L S P G A L V G W 1897
1791 S A C A M P A L T T A G P D - - - - - H W P N R L L T M L A R S N T V C N E Y F I A T R I R K I L G I L E A S T P W S 1846
1898 - - - - - C A I L R H V G G E G A V Q M N R L I A F A S R G N H V S P T H Y V P E S D A A A R V T Q I L S S L T - - - - 1952
1847 V I S A C I R M L H T P T E D D C G L I - - - - - A W G L E I W Q Y C N F F V I C F N V L K A G V S - - - - - M Y N I P G C P 1901
1953 - I T O L L K R L H O W I N E D C S T P C S G S W L K D V M D W I C T - - - - - V L S D F K T W L Q S K L L P R L P G L P 2007
1902 P Y S C Q K Y G P W T G S M L O A R C P C G A B L I F S V E N G F A K L Y K G P R T C S N Y R G A V P V N A R L 1961
2008 F L S C Q R G Y K G W R G D G I M O T T C P C G A Q I T G H V K X G S M R I V - G P K T S N T W H G T P I N A Y T 2066
1962 C G S A R P D P T - D W T S L V V N Y G V R D Y C K Y E K M G D H I F V T A V S S P N V - C F T Q V P - - - - - 2010
2067 T G P C T P S P A P N Y S R A L W R V A A E V E V T R V G D P H Y V T G M T T D N V K C Q P A P E F F T E V D 2126
2011 - - - - - P T L R A A V D - - - - - G V Q V C Y L G P K T P W T T S A C C Y G P D G K G T 2050
2127 G V R L H R V A P C K P L L R E E V V F V G L N Q Y L V G S O L P C - - - - - E P E - - - - - E D V A V L T 2172
2051 V K L - - - - - P R V D G H T P V M Q L N L R D A L E T N D - - - - - C N S T N T P S D E A A V S A L V 2096
2173 S M L T D P S H I T A E T A K R L A R G S P P S L A S S A S Q L S A P S L K A T C T T H D S P D A D I E A N L L 2232

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QY 2097 FKQEL-----RRTNQL-----EASAGVDTTKLPAPSTEEVVVRKQFRARTGSLTL 2144
D 2233 WRQMGGNITRVESKNKVIILSDPPIRAVDEBEISVPA--EIURKPKPPALPIWAR 2290
QY 2145 P---PP-----PRSVPGV--SCPESIQSDPLEGPS-NLPPGPP-----VLQLAMP 2184
D 2291 PDYNPLLESKMDPDYVPVVGCP-----PSTKAPPIPPRRKRTVLTSTV 2340
QY 2185 MPLLAGECNFPTALGCANTETG---GGPD-----DLPST---PP---KKEVSEW 2225
D 2341 SSALAEATKTFGSGSAVDSGTATGPDQASDDGDKGSDVESYNNPPEGEFGDPDL 2400
QY 2226 SDGSWTATTASSVYTPPKIRKGDSTQSAKAPKPTKKLKGSEKSCMSYTWTD--VI 2284
D 2401 SDGSWT-----VSG-----EAGEDVCCSMSTYWTGALI 2430
QY 2285 SFKTASKVLSATRAITSGFLKQSLVYVTEPRDAELRKQKVTINRQPLFPFSPYHKQVRLA 2344
D 2431 TPCAEESEKLPINPLNSLLRHSMVYSTTSRSASLRQKVTDFDLQVLDHHDYDLVKEM 2490
QY 2345 KEKASKVGVWMDVDEAAHTPSKSAKSHITGLRGTDIRSGAARKAVLDL-----QKCVEA 2400
D 2491 KAKASTVKARLLSIEACKLTPPHSAKSKF-GYGAKOVRSLSSR-AVNHIRSVMEDLLED 2548
QY 2401 GEIPSHYRQTVIVPKEEVFKTPQKPTKPPRLISYPHLEMRCKVEKMYGQVAPDVVKAV 2460
D 2549 TETPT---DTTIMAKNEVFCVQPEKGRKPARLIVFPDLGVRCBKALYDVVSTLPQAV 2605
QY 2461 MGDAYGF-VDRPTRVKRLLSMSPD--AVGATCDTVCDFDSTITPBDIMVETDIYSAAKLS 2517
D 2606 MGPSYGFQYSPQORVEFLVNTWKSCKPMGFSYDFRCFDSVTENDIRTESSIQCCDLA 2665
QY 2518 DQIRAGIHTIAROLYAGPMIAYDREIYGRRCRSSGYVTTSSNSLTCWLKVNAAEQ 2577
D 2666 PEARQAIRSLTERLYVGGFLNSKGQNGCYRCRASGVLTTSCGNLTLCYLKATAACRAA 2725
QY 2578 GMKPRPLICGDDCTVIWKSAGADAKAMVFAFSWKMVGAPQDVCPPQKYSLEELTSC 2637
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QY 2698 VHFMEQMLFEDKLPETVTFDHYKNYTVVEDLPSIIAGVHIEAFSVVRYTNABILRVS 2757
D 2846 THFFSILLAQSQLEKALDCQIYGACYSIEPLDLPQIIBRLHGLSAFSLHSYSPGEINRVA 2905
QY 2758 QSLTDMTPPLRAWRKARAVLASAKRRGGAHAKLARFL--WHATSR---PLP-----D 2807
D 2906 SCLRLKLVFPPLRVHRHARSVRAKLLSQGRAATCGKYLFWNAVTKLKLTPIPNASQLD 2965
QY 2808 LDKTSVARYTTFNVCVSPGDFEITPQRRLQKFLVKYLAIVIPALGLIAVGLAI 2863
D 2966 LSGWFWACYN-----GGDIVHLSLRAPRW-----FMLCLLLSVGVGI 3004

RESULT 7
GNWTC
Genome polyprotein - hepatitis C virus
N:Contains: capsid protein C; envelope protein M; hepatitis C virus genome polyprotein
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: A38465
R:Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E.;
J. Virol. 65, 1105-1113, 1991
A:Title: Structure and organization of the hepatitis C virus genome isolated from human
A:Reference number: A38465; MUID:91140698; PMID:1847440
A:Accession: A38465
A:Molecule type: Genomic RNA
A:Residues: 1-3010 <TAK>
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A;Cross-references: UNIPROT:P26663; EMBL:M58335; NID:G329770; PIDN:AAA72945.1; PID:G3297;
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural
F:2-115/Product: capsid protein C #status predicted <CP>
F:116-191/Product: envelope protein M #status predicted <EPM>
F:192-389/Product: major envelope protein E #status predicted <MEE>
F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F:11007-1615/Product: hepatitis C virus genome polyprotein #status predicted <NS3>
F:1230-1237/Product: nucleotide-binding motif A (P-loop)
F:1312-1317/Region: nucleotide-binding motif B
F:1316-1319/Region: DEXH motif
F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
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Query Match 20.9%; Score 3218; DB 1; Length 3010;
Best Local Similarity 29.8%; Pred. No. 9.8e-192;
Matches 968; Conservative 448; Mismatches 1192; Indels 642; Gaps 116;

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QY 8 TSPVAPRTRKNKQTOASYPVSIK-----TSVERGORAKKVVORDARPR 51
D 3 TNPQPKQTKRNTNR---PDQVKFGGQIVGVYLLPRRGRPLGVRAPKTSESRQPR 59
QY 52 NYK----IAGIHGLOTLAQALP-----AHGWGRQDPRHKS RN 86
D 60 GRRQIPKARRPEG-RTWAQPGVPWPLYGNEGLGWAGWLLSPGSRPSWGTDPRRSRN 118
QY 87 LGILLDPLGHWIGDVTTHPLVGPLVAGVVRVPCQIVRLLEDGVNWTG---WFGVHLF 143
D 119 LGKVIDTLTCGFADLMGYIPLVGAFLPGA-ARALAHGVRLVEDGVNVTALGNLPGCSFIF 177
QY 144 VVCLLS-LAPCSGARVTDPTNTTILTCQCORNOVYICSPSTCLHPGCVICADE---- 198
D 178 LLALLSCLTTPASAYEVHNY-SGIYHVNTDCSNASIVYEADLIMHTPGCVPCREGNSS 236
QY 199 -CWVPANPYLSHPNSWNTGDSFLADHDFVMGALVTCDALDIDGELGACVLVGDWLRVH 257
D 237 RCWALVTPLA-ARNVTIPTTIRRHVDLLVGAFAFCSAMYVGLDGSFVLSQFTFSP 295
QY 258 LIHIDLNETGTCLYEPTGIDPGFLG--FIGW---MAGKVEAVIFLTKLASQVPAIATM 312
D 296 RRVTLQDCN-----CSIVPGHVSHRMAWDMMNWSPPTALVWSQLL-RIQAVVDM 347
QY 313 FSSVHYLVAGALIYASRGWYQLLLALMLY-----LEATSGNPI----- 352
D 348 VAGAHWGVLAGLAYYSWAGNNAKVLIVMLLFAGVGDGTHVTGGAQAKTNNRLVSNFASGP 407
QY 353 -----RVPTGCSIAEF-----CSPLMIPCP----- 372
D 408 SQKTLINTNGSWHINTALNCNDSLOTGFLAALFYTHSNSSCCPERMACQRTIDKFDQ 467
QY 373 -----CHSY-----LSENVSEVICSPKTRPITLEYNNSISW 405
D 468 GWGPITVAESSRSQRPYCVHYPPOCTIVPASEVCGPVYCFYPS---PVVVGTTDR--- 521
QY 406 YPTIP---GARGCWKFKNT-----WGCCRIRNVPSY-----CTMG----- 440
D 522 --FGVPTYRWGENETDVLNNTNRPQGNWFGCTWMNSTGFTKTCGGPPCPCNIGVGNNTL 579
QY 441 --TDVAVNDTRNTYEACGVTPLT-----TAWHNGSALKLAILQ---YPGSKB-- 483
D 580 TCPTDCFRKPEATYTKCGSGPWLTPRCMVDPYPRLWHYFCTVNTFTFKVRMYVGVGEHR 639
QY 484 MFKPHNMSG-HLYFEGSDTPIVVFYDPVNSTLLPPERWARLPCTPPVVRGSLQVPGF 542
D 640 LNAACNTRGECDEDRDP-----ELSPLLSTTEWQVLPDS----- 678
QY 543 YSDVKDLATGLITKDAKWKYQVLYSATGALSGLTGTVTTKAVVLLLLGLCGSKYLLAYLC 602
D 679 FTTLPALSTGLIHUHQINVDVQVLYIGSAVSPAIKWEYVLLFLFLDLADARVACALMM 738
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```
Db 2712 LTCYLKASAAACRAAKLQDCTMLVNGDDLWVICESAGTQEDAAASLRVFTTEAMTRYSAAPGD 2771
Qy 2624 VPQPKYSLEELTSCSSNVTSGITKSGKYYELTRDPRIPLGRCSAEGLYNPSAAWIGYL 2683
Db 2772 PPQPEYDLELTSCSSNVSVAHADSGKRYVYELTRDPTTFLAARAWETARHTFVNSWLGN 2831
Qy 2684 IHHPVCLWVSRLVAVHFMQMLFEDKLPETVTFWYGNKYVTPVBDLPSIIAGVHIGIAF 2743
Db 2832 IMYAPTLLWARMILMTHFFSILLAQBQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAF 2891
Qy 2744 SVRYTNAEILRVOSQLTDMTPPLRAWKARAVLASAKRRGGAHAKLARPLL-WHATS 2802
Db 2892 SLHSPGEINRVASCLKGLGVPPLRVWRHARSVRRLSQGGRAATCGKYLFWNAVKT 2951
Qy 2803 R----PLP-----DLDKTSVARYTTFNCDVYSPGDFVITPQRLQKFLKYLAVIYFA 2853
Db 2952 KLKUTPIPAASRLDLSGFWFAGYS-----GGDIYHLSLRAPRW-----FMLC 2994
Qy 2854 LGLIAVGLAI 2863
Db 2995 LLLLSVGVI 3004

RESULT 8
GNWVC3
Genome polyprotein - hepatitis C virus (strain HCV-1)
N:Contains; capsid protein C; envelope protein M; hepatitis C virus (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A39166; PQ0403; PQ0404
R:Choo, Q.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, C.; Coi
Proc. Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991
A:Title: Genetic organization and diversity of the hepatitis C virus.
A:Reference number: A39166; MUID:91172826; PMID:1848704
A:Accession: A39166
A:Molecule type: mRNA
A:Residues: 1-3011 <CHO>
A:Cross-references: UNIPROT:P26664; GB:M62321; NID:G329873; PIDN:AAA45676.1; PID:G329874
R:Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.I
J. Gen. Virol. 73, 1131-1141, 1992
A:Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to e
A:Reference number: PQ0393; MUID:92268871; PMID:1316939
A:Accession: PQ0403
A:Molecule type: genomic RNA
A:Residues: 1577-1633 <CHA>
A:Cross-references: DBJ:D10128
A:Experimental source: isolates E-b16
A:Accession: PQ0404
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1577-1633 <CH2>
A:Experimental source: isolates E-b17
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural
F:1-115/Product: capsid protein C #status predicted <Cpc>
F:116-191/Product: envelope protein M #status predicted <ERM>
F:192-389/Product: major envelope protein E #status predicted <MEE>
F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F:1007-1615/Product: hepatitis C virus #status predicted <NS3>
F:1230-1237/Region: nucleotide-binding motif A (P-loop)
F:1312-1317/Region: nucleotide-binding motif B
F:1316-1319/Region: DEXH motif
F:1616-1862/Product: nonstructural protein NS4a #status predicted <NAA>
F:1863-2013/Product: nonstructural protein NS4b #status predicted <NAB>
F:2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F:196, 209, 234, 305, 325, 417, 423, 430, 448, 476, 532, 540, 556, 576, 623, 645, 1213, 1255, 2041, 2077, 22
Query Match 20.8%; Score 3204.5; DB 1; Length 3011;
Best Local Similarity 29.7%; Pred. No. 6.8e-191;
Matches 962; Conservative 442; Mismatches 1215; Indels 621; Gaps 110;
```

```
Qy 8 TSPVAPRTRKNKQTOASYPVSIK-----TSVERGORAKRKVQDARPR 51
Db 3 TNKP-----QKNGKNTNRQDVKFPGGGOIVGGVYLLPRGPRLGVRATKTSERQPR 59
Qy 52 NYK-----IAGHDGLQTLAAALP-----AHGWRQDPRHRSRN 86
Db 60 GRRQPIKARRPEG-RTWAQPGYPWPPLYGNEGCGWAGWLLSPRGRPSMGPTDPRRSRN 118
Qy 87 LGILLDYPLGWIGDVTHTPLVGLVAGAVRVCQIVRLLEDGNWATG---WFGVHLF 143
Db 119 LGRKVIDTLTCGFADLMGYIPLVGAPLGA-ARALAHGVRVLEDDGNVATGLPGCSFIF 177
Qy 144 VVCLLS-LACPCSGARVTDPTNTTILTNCCQRNQVIYCSPTCLHFPQGVIC-----AD 197
Db 178 LLALLSCLTPASAYQVN-STGLYHVNTDCPNSSIVVEAADAILHTPGCVPCVREGNAS 236
Qy 198 ECWVPANPYI-SHPSNNWTGDSFLADHIDFVMGALVTCDAIDIGELCGACVVLGVDWL-- 254
Db 237 RCWVAMTPTVATRDGKLPATQ--LRRHIDLLVGSATLCSALYVGLDCCSVFLVGLQFTFS 294
Qy 255 --RHMLIHDILNETGTCYLEVPTGIDPGFLGFGW---MACKVEAVIFLTKLASQVPAI 309
Db 295 PRRH-----TTQGCNCSYIPGHIIGHR--MAWMMMNWSPPTALVMAQLL-RIPQAI 344
Qy 310 ATMESSVHVLAVGALIYYASRGKMYQLLLALMLY--IEA----- 346
Db 345 LDMTAGAHGVLAGIAVFSWGNWAKVLLVLLLPAGVDAETHVTGGSAGHTVSGFVSLLA 404
Qy 347 -----TSGNPRVPTGCSIAE 362
Db 405 PGAKQNVQLINTNGSWHLNLTALNCNDSLTGMLAGLFYHHKFNSSGCGPERLAS----- 458
Qy 363 FCSPL-----MPCPCHSVLSENV-SEVICYSKPTRPI 395
Db 459 -CRPLTDFDQGWGPISYANGSGPQRPYCWHPKPCGI VPAKSVCGFVYCTFS---PV 514
Qy 396 TLENN-----SISWYPTTPGARGCMVKFNNT-----WGCCRIRNVPSY----- 436
Db 515 VVGTTDRSGAPTYSW-----GENDTDVFLVNNTRPPLGNWFGCTWMNSTGTFKVCGAPP 568
Qy 437 CTMG-----TDVMDNTRNTYBACGVTPWLT-----TAWHNGSALKLAILQ 477
Db 569 CVIGGAGNNTLHCPTDCFRKHPDATYSRGSGPWITPRCLVDYPRYLWHYCTINYTIK 628
Qy 478 ---YPSKE--MFKPHNMWSG-HLYFGSDTPIVYFVDPVNSTLLPERRWARLPGTPPV 531
Db 629 IRMTVGGVHRLEAACNWTGERCDLEDRD-----SELPLLTTTQWVLFCS----- 678
Qy 532 RGSMLQVPQGFYSVDKDLATGLITKDKAWKNYQVLYSATGALSITGVTTKAVVILILGLC 591
Db 679 -----FTTLPALSTGLIHLHQNVIVDVQVLYGVGSSIASWAIKWEYVVLFLLLA 727
Qy 592 GSKYLIILAYLCYLSCLCFGRASGYPLRPVLPQSQSYLQAGWDVLSKAQVAPFALIFCICYL 651
Db 728 DARVCSCLMWMML-----ISQAEALENLVI----- 753
Qy 652 RCLRYAALIGFVPMAGLP--LTFVVAASAAQPDYDMVYVLLVAGLVLAGNRGRHRIA 709
Db 754 ---LNAASLAG-----THGLVSLVLFVCFCA-----WYLK-----GKWVPGAVY 788
Qy 710 LLVGFPMPLVALLTLHLVTPASAFDTEI---IGLTIPTVVVALVVMRSRFGFAHLPRCA 766
Db 789 TFYGMWPL--LJLLALLPQRAYALDTEVAASCGGVLL---VGLNALTLSPYKYISWCL 843
Qy 767 LVNSYLWQRMEN-----WFMNVTLRPERFELVLCFPGATYDALVTCFCHVALLC-LTSS 821
Db 844 WMLQYFLTRVEAQLHVMVPLNVRGGRDAVILL-----MCAVHPTLVFDITKL 891
Qy 822 AASEFGTDSRVRAHRMLV-----RLGKCHAMYSHYVLKFFLLVFGEN 863
Db 892 LLAVFGPLWILQASLLKVPYFVRVQGLLRCALARKMIG-----GHVQVQVILKIGALT 945
Qy 864 GVFFYKHLH--GDVLPNDFASKLPLQBPFFFPFEGKARVYRNEGRRLACGDTVDGLPVVVAR 921
```


Db 1310 YDIIICDECHSTDSTSILGIVLDAQETAGARLVVLAAATPPGCVTVVPHNPNEEVALPN 1369
Qy 1282 EGTIPFHGKIKKENLKGRLHIFEAATKKGCHDELANELARKGIIATAVSYRGCDISKIP-E 1340
Db 1370 TGEIPFYGKALPLETIGRHLIFCHSKKCDLAAKLSALGVNAVAYRGLDVSVIPTS 1429
Qy 1341 GDCVVVATDALCTGYTGDFDSVDCSLMWGEGTCHVDLPDPTFMGVRVCGVSAIVKGORRG 1400
Db 1430 GDVVVATDALMTGYTGDFDSVDCNTCVTQTVDFSLDPTFTIETTLTPQDAVSRSORRG 1489
Qy 1401 RTGRGAGIIVYVDGSCTPSGMVEPCNIVEAFDAAKAWGLSSFEAQITILDYRTQGLP 1460
Db 1490 RTGRGCGIITRVTPGRPSGMPDSSVLCEDYAGCAWYELTPAIVTSRLAYLNTGCLP 1549
Qy 1461 AIGANLDEWADLFS-MYNPBPFSVNTAKRTADNTVLLTAAQLQCHQYGAAPNDAPRWQ 1519
Db 1550 VCVHLEFWSVFTGLTHIDAHFLSQTQAGENFPYLVAVQATVCARAQAPPPSMDQMK 1609
Qy 1520 G-ARLGKK---PCGVLRLOGDACPGEPESEV-----TRYQM-CFT---EVENTGTAA 1565
Db 1610 CLIRLKPTRLGPTPLLYRL-----GAVQNEVTLTHPIITKIFMACMSADLEVVTSTW 1661
Qy 1566 LAVGVGAMAYLAIDTGTACVRCWISITSVPTGATVAPVUDEEI-----VEECASF 1619
Db 1662 LVGGVLAALAAAYCLTGSVVIVGR-----IILSGRPAIIDREVLYQBFDEMBECASHL 1715
Qy 1620 P-LEAMVAADKDKL-----STITTSPTLETALKLNTFLGPHAAITLAIIEYC 1668
Db 1716 PYIEQGQLAEQFKQKALGILLQATSKQAEAAAPVVESSKWQALEAFWAKHWNFISGLYL 1775
Qy 1669 CGLVTLDPNPPASCVFAGIITPLPHKIMFISLFGGAIASKLTDARGALAPMMAGAA 1728
Db 1776 AGLSTLPGNPAIVSLMAFTASITSPLTQHTLLFNILGWWAAQLAPPSAASAFVAGAGIA 1835
Qy 1729 GTALGTWISGCF---VDFMLGYYAAASSTACTLTKCLMGEMPTMDQLAGLVYSAFNAAG 1785
Db 1836 GAAVG---SIGLGKVLVDILAGYGAGVAGALVAFKMGSGEMPTSDLVNLLPAILSPGAL 1892
Qy 1786 VVGVLSCAMFALTAGFD---HWPNRLLTMLARSNTVCNEYFIATRDTRRKILGILEA 1841
Db 1893 VGVVV---CAALLRHVPGEGAVQMMNRLIAFASRGHVSPTHVVPESDAAARVTKILSS 1950
Qy 1842 STPMSVISACIRWLHTPTEDDCGLI---AMGLEIYWQVYCNFFVFCFNVLKAGVQS---MVN 1896
Db 1951 LT-----ITQRLRLRHQWINECDSTPCSGSWLRDWDWICT-----VLTFDKTQLQKLLPR 2002
Qy 1897 IPGCPFFYSCQYKGPWIGSMQLQACPCGNAELIFSVEGFAKLYKGPRTCSNYYWRAVP 1956
Db 2003 LPGDFFFSQYRGYRGGVWGDGMQTTCPGCAQITGHVKNGSMRIV-GPKTCSNTMWHGTFP 2061
Qy 1957 VNARLCSARPDPPT-DWTSLVVNYGVDRDYCKYKMGDHI FVTAVSSPNV-CFTQVPPTLR 2014
Db 2062 INAYTTGCTPSFAPNYSRALRWRAEYVEYTRVGDFHYVTGTTDNNVKPCQVPAP-E 2120
Qy 2015 AAVAVDGVQVQCY-----LGEPTKPTWTSACCY-GPDGKGKTVKL--PFR 2056
Db 2121 FFTEVDGVLLHRYAPACKPLLRDEVTQVGLNQFPVGSQLPCEPEPDVTVLTSLMTDPSH 2180
Qy 2057 VDGHTPGVRQMLNRDALETND-----CNSTNWTSPDEAAVASLVFKQEL--- 2101
Db 2181 ITAETAKRRLARGSPPLSSASSQSALGAPSLKATCTTRHDSPADLIEANLLMRQENGGN 2240
Qy 2102 ----RRTNOLL-----BAISAGVDTTKLPAPSIIEVVVRKQRPARTGSLTLP---PP-- 2147
Db 2241 ITRVESENKVVILDSFPLRAEEDEREVSVA--EILKRKRPALPIIWARPSYNPPLL 2298
Qy 2148 -----PRSVFGV--SCPESLQRSPLGEGSNLPPSP-----VLQAMPMLPLLGAGEC 2193
Db 2299 ESWKDPDYPVPVHGCPLP-----PTMAPPIPPRRKRTVTVLTSTVSSALAEAT 2349
Qy 2194 NPFTAICAMTETG--GGPDDL-----SYPP-----KKEVSEWSDESWSSTAT 2234
Db 2350 KTFGSSGSSAVDSGTATAPPDQPSDDGDRGDDDESYSMPPEGEPPDLSLDCGWSVTS 2409

Qy 2235 TASSYVTGPPYPKIRGKDSQTSAPAKRPTKKKLGKBEFSCSMYSMTWTD-VISFKTKASKVL 2293
Db 2410 EEAS-----EDVACCMSYMTGTALITPCAABESK 2439
Qy 2294 SATRAITSGFLKORSLSVYVTEPRDAELRKOKVTINRQPLFPSPSYHKQVRLAKEKASKVVG 2353
Db 2440 LPINPLSNSLLRRHHNMVYATTSRAGLRQKVTDFRLQVDPDDHRYDRVLKEMKAKASTVKA 2499
Qy 2354 VMVDYDEVAHAHTPSKSAKSHITGLRGTDVRSAGAKAVLDL-----QKCVAGEIPSHYRQ 2409
Db 2500 KLLSVEAEACKLTTPHSARSKF-GYGAKDVN-LSSKAVNHIHSVMKOLLEDETETP1---D 2554
Qy 2410 TVIVPKEEVFKTPQKPTKPPPLISYPHLEMRCEVQYQVADPVVVKVMGDAYGP-V 2468
Db 2555 TTIMAKNEVFCVQPEKGRKPARLIVPELGVRCERKVALYDVVSTLPQAVMGSSYGFQY 2614
Qy 2469 DPRTRVKRLLSMW--SPDAVGATCDTVCFDSTITPEDIWVETDIYSAAKLSDDHAGIHT 2526
Db 2615 SPQORVEFLVNAWKSXKNPMGFAYCTRCFDSTVTESDIRVEESIYQCCDLAPEARQVIRS 2674
Qy 2527 IARQLVAGGPMIAYDGREIGYRRCSRSGVYTTSSNSLTCWLKVNAAAEQAMKNPRFLI 2586
Db 2675 LTERLYIGGPLTNSKGQNGYRCRAGSVLITTCGNTLITCYLKASACRAAKLODCTMLV 2734
Qy 2587 CGDDCTVIWKSAGADADQAMRVFASWMMYMGAPQDCVQPKYSLEBLTSCSSNVTSGIT 2646
Db 2735 CGDDLVCICESAGTQEDAAASLRVFTTEAMTRYSPAPPDPPQPEYDLELITSCSSNVSAHD 2794
Qy 2647 KSGKPYFLTRDRIPLGRCSAEGLVNPSAANIGYLIIHHYPCLVWSRVVLAVHMEQWLF 2706
Db 2795 ASGRVYLLTRDPTTPLARAAAWETARHTPVNSWLGNIIIMYAPTLWARMILMTWFFSILLA 2854
Qy 2707 EDKLPEVTVDWYGNKVTVPVEDLPSIIAGVHGIEAFSVVRYTNAEILRVYSQSLTDMTP 2766
Db 2855 QOELEKALGCOIYQATYFIEPLDPLQIIQRHLGLSAFSLHSYSGEINRVASCRLKLGVP 2914
Qy 2767 PLRAWRKARAVLASAKRGGAGHAKLARPLL-WHATSR-----PLP-----DLDKTSVARY 2816
Db 2915 PLAVWRHRARSVRAKLSQCGRAATCGKYLFNWAVRTKLTPIPAASQLDLSGWFVAGY 2974
Qy 2817 TTFNYCDVYSPGDFVITPORRLOKFLVKYLVAVIFALGLIANGLAI 2863
Db 2975 S-----GGDIYHLSLRARPRW-----FMWCLLLLSVGVI 3004

RESULT 10

GNWVCH

genome polyprotein - hepatitis C virus (strain H)
N:Contains: capsid protein C; envelope protein M; hepatitis virin (EC 3.4.21.98) (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5)
C:Species: hepatitis C virus
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A36814; A41546
R:Inchauspe, G.; Zebedes, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M. submitted to GenBank, July 1992
A:Description: Genomic structure of the human prototype strain H of hepatitis C virus: cc
A:Reference number: A36814
A:Accession: A36814
A:Molecule type: genomic RNA
A:Residues: 1-3011 <INC>
A:Cross-references: UNIPROT:P27958; GB:M67463; NID:G329737; PIDN:AAA45534.1; PID:G329738
R:Inchauspe, G.; Zebedes, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991
A:Title: Genomic structure of the human prototype strain H of hepatitis C virus: comparif
A:Reference number: A41546; MUID:92052256; PMID:1658800
A:Contents: annotation
C:Note: neither amino acid nor nucleotide sequence is given
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; glycoprotein; hydrolase; nonstructural
F:1-115/Product: capsid protein C #status predicted <CP>
F:116-191/Product: envelope protein M #status predicted <EP>

F:192-389/Product: major envelope protein E #status predicted <ME>
F:390-729/Product: nonstructural protein NS1 #status predicted <NS2>
F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F:1007-1615/Product: hepatitis B virus surface antigen #status predicted <NS3>
F:1230-1237/Region: nucleotide-binding motif A (P-loop)
F:1312-1317/Region: nucleotide-binding motif B
F:1316-1319/Region: DEXH motif
F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F:2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F:196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,2338,2340,2341,2342,2343,2344,2345,2346,2347,2348,2349,2350,2351,2352,2353,2354,2355,2356,2357,2358,2359,2360,2361,2362,2363,2364,2365,2366,2367,2368,2369,2370,2371,2372,2373,2374,2375,2376,2377,2378,2379,2380,2381,2382,2383,2384,2385,2386,2387,2388,2389,2390,2391,2392,2393,2394,2395,2396,2397,2398,2399,2400,2401,2402,2403,2404,2405,2406,2407,2408,2409,2410,2411,2412,2413,2414,2415,2416,2417,2418,2419,2420,2421,2422,2423,2424,2425,2426,2427,2428,2429,2430,2431,2432,2433,2434,2435,2436,2437,2438,2439,2440,2441,2442,2443,2444,2445,2446,2447,2448,2449,2450,2451,2452,2453,2454,2455,2456,2457,2458,2459,2460,2461,2462,2463,2464,2465,2466,2467,2468,2469,2470,2471,2472,2473,2474,2475,2476,2477,2478,2479,2480,2481,2482,2483,2484,2485,2486,2487,2488,2489,2490,2491,2492,2493,2494,2495,2496,2497,2498,2499,2500,2501,2502,2503,2504,2505,2506,2507,2508,2509,2510,2511,2512,2513,2514,2515,2516,2517,2518,2519,2520,2521,2522,2523,2524,2525,2526,2527,2528,2529,2530,2531,2532,2533,2534,2535,2536,2537,2538,2539,2540,2541,2542,2543,2544,2545,2546,2547,2548,2549,2550,2551,2552,2553,2554,2555,2556,2557,2558,2559,2560,2561,2562,2563,2564,2565,2566,2567,2568,2569,2570,2571,2572,2573,2574,2575,2576,2577,2578,2579,2580,2581,2582,2583,2584,2585,2586,2587,2588,2589,2590,2591,2592,2593,2594,2595,2596,2597,2598,2599,2600,2601,2602,2603,2604,2605,2606,2607,2608,2609,2610,2611,2612,2613,2614,2615,2616,2617,2618,2619,2620,2621,2622,2623,2624,2625,2626,2627,2628,2629,2630,2631,2632,2633,2634,2635,2636,2637,2638,2639,2640,2641,2642,2643,2644,2645,2646,2647,2648,2649,2650,2651,2652,2653,2654,2655,2656,2657,2658,2659,2660,2661,2662,2663,2664,2665,2666,2667,2668,2669,2670,2671,2672,2673,2674,2675,2676,2677,2678,2679,2680,2681,2682,2683,2684,2685,2686,2687,2688,2689,2690,2691,2692,2693,2694,2695,2696,2697,2698,2699,2700,2701,2702,2703,2704,2705,2706,2707,2708,2709,2710,2711,2712,2713,2714,2715,2716,2717,2718,2719,2720,2721,2722,2723,2724,2725,2726,2727,2728,2729,2730,2731,2732,2733,2734,2735,2736,2737,2738,2739,2740,2741,2742,2743,2744,2745,2746,2747,2748,2749,2750,2751,2752,2753,2754,2755,2756,2757,2758,2759,2760,2761,2762,2763,2764,2765,2766,2767,2768,2769,2770,2771,2772,2773,2774,2775,2776,2777,2778,2779,2780,2781,2782,2783,2784,2785,2786,2787,2788,2789,2790,2791,2792,2793,2794,2795,2796,2797,2798,2799,2800,2801,2802,2803,2804,2805,2806,2807,2808,2809,2810,2811,2812,2813,2814,2815,2816,2817,2818,2819,2820,2821,2822,2823,2824,2825,2826,2827,2828,2829,2830,2831,2832,2833,2834,2835,2836,2837,2838,2839,2840,2841,2842,2843,2844,2845,2846,2847,2848,2849,2850,2851,2852,2853,2854,2855,2856,2857,2858,2859,2860,2861,2862,2863,2864,2865,2866,2867,2868,2869,2870,2871,2872,2873,2874,2875,2876,2877,2878,2879,2880,2881,2882,2883,2884,2885,2886,2887,2888,2889,2890,2891,2892,2893,2894,2895,2896,2897,2898,2899,2900,2901,2902,2903,2904,2905,2906,2907,2908,2909,2910,2911,2912,2913,2914,2915,2916,2917,2918,2919,2920,2921,2922,2923,2924,2925,2926,2927,2928,2929,2930,2931,2932,2933,2934,2935,2936,2937,2938,2939,2940,2941,2942,2943,2944,2945,2946,2947,2948,2949,2950,2951,2952,2953,2954,2955,2956,2957,2958,2959,2960,2961,2962,2963,2964,2965,2966,2967,2968,2969,2970,2971,2972,2973,2974,2975,2976,2977,2978,2979,2980,2981,2982,2983,2984,2985,2986,2987,2988,2989,2990,2991,2992,2993,2994,2995,2996,2997,2998,2999,3000,3001,3002,3003,3004,3005,3006,3007,3008,3009,3010,3011,3012,3013,3014,3015,3016,3017,3018,3019,3020,3021,3022,3023,3024,3025,3026,3027,3028,3029,3030,3031,3032,3033,3034,3035,3036,3037,3038,3039,3040,3041,3042,3043,3044,3045,3046,3047,3048,3049,3050,3051,3052,3053,3054,3055,3056,3057,3058,3059,3060,3061,3062,3063,3064,3065,3066,3067,3068,3069,3070,3071,3072,3073,3074,3075,3076,3077,3078,3079,3080,3081,3082,3083,3084,3085,3

Db 1773 QYLAGLSTLPGNPAIASLMAFTAAVTSPLTTGQTLLFNILGQWAAQLAAPGAATAFVGA 1832
Qy 1726 GAAGTALGTWTSVGF---VFDMGLGYAAASSTACILTKCLMGEMPTQDQLAGLVYSANP 1782
Db 1833 GLAGAL---DSVGLGKVLVDILAGYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSP 1899
Qy 1783 AAGVVGVLSSACAMFALTAGDP---HWPNRLLTWLARSNTVCNEYFIATDIRKKILGI 1838
Db 1890 GALAVGVVFASIL---RRRVGPEGAVQMMNRLIAFASRGNHVSPTHYVVPESDAAARVTAI 1947
Qy 1839 LEASTPWSVISACIRWLHTPTEDDGLIAGLEIWOVYCNFFVICFNVLKAGVQSWNIP 1898
Db 1948 LSSUTVQLRLRLHQWISSECTTPCS--GSLWRDIDMWICEVLSDFKTLWKA--KLMQLP 2004
Qy 1899 GCFYSCQKYGKPMWIGMLQARCPGAEILFVSNGFAKLYKGPRTCSNYMRGAVPVN 1958
Db 2005 GIPFVSCQRYGVWRGDMHTRCHCGAEITGHVKNGTMRIV-GPRTCKMWSGTFFIN 2063
Qy 1959 ARLCGSARPDP--DWTSLVNVYGRDYCKYKEMGDHIFVTAVSSPNV-CFTQVP----- 2010
Db 2064 AYTGPCTFLPAPNYKFAIMRVSAEYVEIRRVGDFHYVSGMTTDLNLCPCQI1SPSPFT 2123
Qy 2011 -----PTLRAAVAND-----GVQVQYLGEKPTPWTTSACCVGPDGK 2047
Db 2124 ELGVLRLHRFAPCKPLREBSFRVLGHEYPVGSQLP-----EPE-----PDVA 2169
Qy 2048 GKTVKL--PFRVDGHTPCVRMLNRLDALEND-----CNSNTNTPSDEAAVS 2093
Db 2170 VLTSMITDPSHITAEAGRLARGSPSPMASSASQSLKATCATANHDSPLAEIEA 2229
Qy 2094 ALVPKQEL-----RRTNQLL-----EASAGVDVTKLPAPSIEVVVRKQFRATGS 2141
Db 2230 NLLWRQEMGNNITRVESKNVILDSFDPLVAEEDEREVSFPA--EILRKSRRFAPALPV 2287
Qy 2142 LTLF-----PPRSVP----- 2152
Db 2288 WARDYNPLLVETWKKPYEPVPHVGHGCLPPRPSPVPPPRKKTIVLTSTLPTALAE 2347
Qy 2153 -----GVSCPELQSRDPLEGNSLPPPPVQLAMPPLQAGECNPFATIGC 2201
Db 2348 ATKFGSSSTGICDNTTSSP--APSGCPDSDVESYSMPLEG----- 2393
Qy 2202 AMTETGGPDLPSYPKKEVSEWSDSWATATTASSVVTGPPYKIRKDGSTOSAPAKR 2261
Db 2394 ----EPGDPD-----LSDGSWSVTSS-----GADT----- 2414
Qy 2262 PTKKLKSEFSCMSYTTVDVIFSKTASVLS-ATRAITSGFLKORSLLVYTPRDAEL 2320
Db 2415 -----EDVVCCSMYSMTGALVTPCAAEQKLPINALSNLRLHHNLVYSTTSRACQ 2467
Qy 2321 RKQVTINRQPLFPSPYHKQVRLAKEKASKVGVWMDYDEAAHTPPSKSAKSHITGLRG 2380
Db 2468 RKKVTFPRLQVLDVSHYQDVLEKVAASKVYKANLLSVEEACSLAPPHSAKSKF-GYCAK 2526
Qy 2381 DVRSGAARKAVLDL-----QKCVBAGEI1PSHYRQTVIVPKBEVFKVTPKQTKPRLISY 2436
Db 2527 DVRC-HARKAVAHVSNVKKLSDSVTPI---DTTIMAKNEVFCVQPEKGRKPKARLIVF 2582
Qy 2437 PHLEMRCKEYMGVGOVADPVKAVMGDAYGF-VDPRTFVKLLSNW--SPDAVGNATCDTV 2493
Db 2583 PDLGVRCERKALVDVWSKPLAVNGSSYGFQYSPGQRVFLVQAWKSKTKTPMGLSYDTR 2642
Qy 2494 CFDSITPDEDI1WETDIYSAKLSQHRAGHTTARQLYAGGPMIAVDGREIGVRRCRSS 2553
Db 2643 CFDSITVSDIRTEAIIYQCCDLDPQARVAIKSLITERLYVGGPLTNSGENCGYRRCBAS 2702
Qy 2554 GYTTSSNSITCWLKVNAAAEQAKMKNRFLICGDDCTVI1WKSAGADADQKMRVFASW 2613
Db 2703 RVLTSCGNTLTRYIKARAAACRAAGLQDCTMLVCGDDLLWICESAGVQEDAASLRAFTEA 2762
Qy 2614 MKWGAPODCVPOPKYSLEELTSCSSNVTSIGTSKGPYFLTRDPRIPLCRCSAEGLY 2673
Db 2763 MTRYSAPPDPQPPDEYDLELITSCSSNVSVAHGDGAGKRVYVLTTRDPTTPLAARAAWETARH 2822

RESULT 11

JC5620

Genome polyprotein - hepatitis C virus (isolate EUH1480)

N:Contains: capsid protein C; envelope protein M; hepatitis C virus (EC 3.4.21.98) (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C:Species: hepatitis C virus

C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C:Accession: JC5620

R:Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.

Biochem. Biophys. Res. Commun. 236, 44-49, 1997

A:Title: The complete coding sequence of hepatitis C virus genotype 5a, the predominant

A:Reference number: JC5620; MUID:97366593; PMID:9223423

A:Accession: JC5620

A:Molecule type: mRNA

A:Residues: 1-3014 <CHA>

A:Cross-references: UNIPROT:O39928; GB:Y13184

A:Experimental source: genotype 5a, which predominates in South Africa

A:Note: the translation of the nucleotide sequence is not complete in this paper

C:Superfamily: hepatitis C virus genome polyprotein

C:Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serine

F:2-115/Product: capsid protein C #status predicted <CPC>

F:116-191/Product: envelope protein M #status predicted <EPM>

F:192-389/Product: major envelope protein E #status predicted <ME>

F:384-408/Region: hypervariable #status predicted

F:390-730/Product: nonstructural protein NS1 #status predicted <NS1>

F:731-1007/Product: nonstructural protein NS2 #status predicted <NS2>

F:1008-1616/Product: hepatitis C virus #status predicted <NS3>

F:1231-1238/Region: nucleotide-binding motif A (P-loop)

F:1313-1318/Region: nucleotide-binding motif B

F:1317-1320/Region: DEXH motif

F:1617-1863/Product: nonstructural protein NS4a #status predicted <N4A>

F:1864-2014/Product: nonstructural protein NS4b #status predicted <N4B>

F:2015-3014/Product: nonstructural protein NS5 #status predicted <NS5>

F:2210-2249/Region: interferon sensitivity determining #status predicted

Query Match 20.3%; Score 3119; DB 1; Length 3014;

Best Local Similarity 29.4%; Pred. No. 1.5e+185;

Matches 945; Conservative 448; Mismatches 1251; Indels 574; Gaps 105;

Qy 8 TSPVAPRTRKNKQTOASYPVSIK-----TSVERGORAKRKVQDARPR 51

Db 3 TNPQPKTKNTNRR---FQDVKPGGGQIVGGVYLLPRGPKLGVATRKNSERSQPR 59

Qy 52 NYKIAGHDGLQTLQAALPA-----HWGRQD 79

Db 60 GRR-----QPIPKARRPTRGSMGQYWPVLYANEGLGWAGWLLSPRSSRPNWGNPD 111

Qy 80 PRHKSRLG-----ILLDYP--LGWIGDVTHTPLVGLVAGVVRPCQIVRLLEDGVN 132

Db 112 PRKSPNLGRVHTLTGCFPHLMGYI-----PLVGGPV--GGVSRALAHGVKVLLEDGIN 163

Qy 133 WATG---WFGVHLFVCLL--SLACPCSGARVTDPTNTT---ILTNCCORNOVYCSPT 185

Db 164 YATGNLPGCPSPSIFVLALLMCLTVPASAV-----PYRNASGVYHTNDCPSNIVYEADNL 219

Db 2216 CTIOGHHPDADLIKANLLWQCMGNTRVEAENKVBILDCFKPLKEEDDDREISVSADC 2275
Qy 2166 -LEGPSNLPSPVQLAMP---MPLLA---GECNPFATIGCAWMTGTGGPDPLPSYPP 2218
Db 2276 FKKGPA-FPPALPV--WARGYDPLLETWKRPDYDPQVWGCPPIAGPPVPLPR--R 2330
Qy 2219 KKEVSEWSDSWSTATTASSVVTGPPY----PKIRGHKST-----QSAPAKR- 2261
Db 2331 KRKPMELSD---STVSQVMDADLADARFKVDTPSIEGQDSALGTSQSDSGPEEKRDONS 2387
Qy 2262 -----PTKKKLGKSEFS-----CSMSYTWTD-VISFKTASKVLSATR 2297
Db 2388 AASVSNHPPIEGEPDPLDGGSGSWTSVSGEDNVCCSMSTWTCALTPCSAEEKLPIN 2447
Qy 2298 AITSGFLKQSLVYVTPRDAELRQKVTINRQPLFPSPSYHKQVRLAKEKASKVGVWMD 2357
Db 2448 PLSNTLLRHNLVYSTSRSLAQKQVTPDLQVLDDHYREVVDKMLASKVKARLLP 2507
Qy 2358 YDEVAHTPSKSAKSHITGLRGTVRSGAARKAVLDL----OKCVAEGETPSHYRQTVIV 2413
Db 2508 LEEACGLTPPHSARSKY-GYGAKEVRS-LOKALKHIEGVWQDLDSDTP---LPTTIM 2562
Qy 2414 PKEVEPVKTPQKPKPKPLISYPHLEWRCVEKMYGQVAPDVVYKVMGDAYGF-VDPR 2472
Db 2563 AKNEVFAVEPSKGGKPARLLVYDPLGVRCEKALYDVAQKLPALMGSPSYQYSPAQ 2622
Qy 2473 RVKELLGMSWSPDAV--GATCDTVCFDSTITPEDIWVETDIYSAAKLSDQHRAGIHTIARQ 2530
Db 2623 RVDPLLAWSKKIPMAFSYDTRCFDSTITEHDIMTEESYQSCDLQPEARVAIRSLQR 2682
Qy 2531 LYAGGPMIADGRIGYRRCRSSGVYTTSSNSLTCWLKVNAAEQAGMKNRPLICGDD 2590
Db 2683 LYCGPMYNSKQCGYRRCRASGVFTTSMGNTMTCYIKALASCRAAKLRDCTLLVCGDD 2742
Qy 2591 CTVWKSAGADADQARVPSMWMKMGAPQDCVQPKYSLEELTSCSNVTSIGITSKG 2650
Db 2743 LVALICESQGHDEASRLATEATRYTSAPPDPVPAYDLELVTSCSNVSVARDASGN 2802
Qy 2651 PYVELTRDPRIPILGRCSAEGIGNPSAAWIGYLTHYPCLVWVSVLAVHMEQMLPBDKL 2710
Db 2803 RIYYLTRDPQVPLAKAAWEAKHSPVNSLGNIIWYAPTLLWARIVLWTHFVSVLQSQEL 2862
Qy 2711 PETVTFPMYGNVTPVEDLPSIIAGVHGIEAFSVRYTNABILRVQSGLTDMTMPPLRA 2770
Db 2863 EKTAFEMYSVSVYVPLDPAIQRHLGLSAFSLHSYSPSEINRVASCLRLKGLVPLRA 2922
Qy 2771 WRKARAVLASAKRGGNAKLARFL-WHATSR----PLPDLDTSVARYTTFYCDVY 2825
Db 2923 WRHRAVARAKLIAQGGRAAICGYILFNWAVKTKRLTPLADADRLDLSNFT-----VG 2977
Qy 2826 SPEGDVFTTPORRLOKFLVKYLAVIVFALGLIAVGLAI 2863
Db 2978 AGGDDIYHMSRAPRNL-----LILCLLLSVGVGI 3008

RESULT 12

T08841
polyprotein - douroucouli hepatitis GB virus A
C;Species: douroucouli hepatitis GB virus A
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T08841
R;Erker, J.C.; Desai, S.M.; Leary, T.P.; Chalmers, M.L.; Montes, C.C.; Mushahwar, I.K.
J. Gen. Virol. 79, 41-45, 1998
A;Title: Genomic analysis of two GB virus A variants isolated from captive monkeys.
A;Reference number: Z16486; MUID:98120818; PMID:9460920
A;Accession: T08841
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3005 <ERK>
A;Cross-references: EMBL:AF023425; NID:g2828599; PIDN:AAC40502.1; PID:g2828600
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein

Query Match 13.4%; Score 2055; DB 2; Length 3005;
Best Local Similarity 25.7%; Pred. No. 4.1e-119;
Matches 820; Conservative 401; Mismatches 1237; Indels 736; Gaps 122;
Qy 169 LTNCCQNRQVYICSPSTCLHEPCGVCICACDCWVPANPYIS----HPSN-----WTGTD 217
Db 33 LTNCCSDSEITACDGGCLVSVGCTVCDGRCDWLYRPGVATRRPGHPOGGELEFGALMSTSSP 92
Qy 218 SFLADHIDFVWGAIVTCDALDIGELCGACVILVG-----DWLVRHHLIHLIDNETGTCTYLE 272
Db 93 AVVAAYVAGITG-----LGEPSAAALLAALARVENTPR-----PNVTCLMD 134
Qy 273 VPTGIDPGFLGFTGW-MAGKVEAVIFLTKLASQVPA--IATWFSVHYLAVGALIYYAS 329
Db 135 CDLALOSE-----AWDLVEDMRDTFTVWVMTLPWRLWYGLVMSFALMVVVLLLEQ 189
Qy 330 RGKMYQLLLALMYIEA-----TSGNPIRV-----TGCSIAEFCSPMLIPC 371
Db 190 RVNVLIVLWAGSVEPPTGCGCHVNGSIVAIIPGAKPEDRPNATQVCVCPFGQMYWLP 249
Qy 372 PCH--SYLSENS-----EVICY--SPKTRPITILEYNNNSISWYPT 409
Db 250 LCAGLAWRNGDVSGTTRDLVPCRPESMHGRGSMVWGSAAHWSRLATEVR---LW-EQ 304
Qy 410 IPGARGC-----MVFKNTWGCCIRINVPISYCTMGTDVANDTRN--- 450
Db 305 LPGSALCHFPVAGTTRDHPHATDVLSTHGIPCASCVVDRRASWCGNCTRCWEKTNKRL 364
Qy 451 TYEACGVTPWLTW-AW-----HNGSALKLAI-----LQYPGSKEMFKPHNMMSGHLYPEGS 500
Db 365 SFEACGLGSLTAEWAHVVDGGTESKIVTDGERPRIYPSHGVGTHHTAVVAARNVTVS 424
Qy 501 D-----TPIVFYDPVNSTLLPPEPWAL-----PG---TPPVVRG 533
Db 425 DIGYWHAIACPNPPSPSALPKLIPGRPVNACTICKEKGLNTAWQAPGXPAPIFTEC 484
Qy 534 SW-----LQVPOQFSDVKDLATGLITKAKMKNYQVLYSATGALSUTGVTK--AVVLI 586
Db 485 NWPRSGVRVCEGYAFDFPGSKTGFI---RSRAGFQOIARAGSMHPHRLWLLTDYLFILLV 541
Qy 587 LLGLCGSKYLILAYLCVLSLCFGRASGYPLR---PVLPSQSYLQAGWDVL-----SK 635
Db 542 LMKLAERLPLVAVALYWFNMAEANTLRIHPVNNITTAAPMTWPAALPVPVTCPTK 601
Qy 636 AQVAPFALIFFICYLRCRLRYAALLGFVPMAGLPLTFFVAAAAAQPDYDMW--VRLLV 693
Db 602 AGAVGDAL-----YMAACLGNATLGVSSVWG--GAYGAEEAGAGLWRWVGGRSFC 653
Qy 694 AG-----LVLWAGNR-----GHR 708
Db 654 AGLAWLTNUGAYLPVVEAAVGPBFVSAPLLVMAWEDSIAVFILMAANIWAYSDHLGVKL 713
Qy 709 ALLV-----GPWPLVALLTLHLVTPASAFDTEIIGGL-----TIPPVVALV 750
Db 714 AGLVAHAHLAKGALPLVLLVAAAXVTRHRHVLGFEVCVSLDADASPSDMSWMAALAAVWSVC 773
Qy 751 VMS-----RFQFFA-----HLLPRCALVNSYLWQWENWFNNVTLRPERFFLVL 794
Db 774 LLTILGLTHGRLKLEFYCYWCFHQAVRMLLCSKVGRGRDM-----RVTAIV 824
Qy 795 VCFPGATYDALVTFVCHVALCLCTSSAAFFGTG-----SRVRAHRM---LVR 840
Db 825 VA-AGIIFPREVVRCSA-----ALTALAALDSIDYLETILTLTAQAAPARAARLDSLTF 878
Qy 841 LGKCHAWYSHYVLKFFLLVFGENGVPFYKHLGDLVLPNDEFASKLPLQEPFFPFSGKAR-- 898
Db 879 LGDAD-----LTRAPVRRLERRGVTLFQHC-GQVSXGAAAILKDLGVALEPVSVTARD 931
Qy 899 -VYRNEGRRLACGTDVLDGLPVARLGLDVLFAGL-----AMPPGWAITAFPTLOCLSERG 952
Db 932 YIVRDAARTLACGVRGEGVLVVARRGDEVLVGVPPSVRALPP-GFVTPAPVVM---QRG 987
Qy 953 T--LSANAVVMTGIDPRWTGTIFRLGSLATSYMGFVCDNVLYTAHSGSKRRRLAHPGTS 1010

Db 988 LGFFSVKTSMLGRDEREHEGSIVVLGTSITRSMGTGVNGWYITTFHGSNARTLAGVGP 1047
Qy 1011 IHPITVDAANDODIYQPPCGAGSLTRCSGETKGVLVT-----RLGSLVEVKNKSDP 1062
Db 1048 VNCRWSPSDVAVYPLPSGASLEPCKCGTQSVMCIRNDGALCHGKLSKLVELD----- 1102
Qy 1063 YWCVGALPMAVA--KGSSGAPILCSSGHVIGMFTAARNSGGSVSOIR-VRPLVCAGYHP 1119
Db 1103 -----LPTISDFRSGSGPILCDEGHVGMVSVLHRGVKVTGVRYVWPWETLPKDS 1155
Qy 1120 QYTAHATLDTRPTVNE--YSVQILIAPTGSGKSTKLPLSYMOEKIYEVLLNPNVATTAS 1177
Db 1156 QVKSEA-----PPVPGKTGFTEAPLYLPTGSGKSTRIPLEYTKAGHKVLVNLPSIATVRA 1210
Qy 1178 MPKWHATYGVNPNCFNGKCT-----NTGASLITYSYTKMYLTGACSRNY-----DVIIODE 1229
Db 1211 MGPYMEKLSGQHPSIYCGHDTTAYSRITGSLPTCYTGRFM--ANPRRYLRGADIVIODE 1268
Qy 1230 CHATDATTVLGIGKVLTEAPSKNVLVLATATPPGVITPHANITEIQLTDEGTIPFHG 1289
Db 1269 CHVTDPISVLGMRARLLARCGVRLLLFATATPPGAFLAQHESIKEVPLGVGDGEVAFYG 1328
Qy 1290 KKIKEENLKKGRHLIFEATKKHCDLANELARKGITAVSYRGCDISKIPBGDCVVVATD 1349
Db 1329 HKLPVERVRTGRHLLFCHSKVECNRLHAALSTAGCNVAVYRGNE-QEIPAGDVCVCATD 1387
Qy 1350 ALCTGYTGDFOSVDCSLMWEGTCHVDLDPFTMGVRVCGVSAIVKGORRGRTGRAGI 1409
Db 1388 ALSTGYTGFGFTVTDGCLMWEEVVEVTLDPITITISVRTTPAPAEIRAQRRCRGSGQT 1447
Qy 1410 YYYVDGSGTSPSGMPECNIVAFDAAKAWYGLSSTEAOITLDTYRTQPLPAIGANLDEM 1469
Db 1448 YYYAMTAGAGTLRSGPLWAAVEAGVAYNLEPDMTDIILRAYDACPYTAITASVGEA 1507
Qy 1470 ADLFSMVNPERSF--VNTAKRTADNYVLLTAQLOLCHQYGYAAPNDAPRQW-ARLGKK 1526
Db 1508 INFPSGLVPMRNPQVAVAKSHQHNWPLLVQRTMCQENAVAGPDGPEWAGLAGTGP1 1567
Qy 1527 PCGVLRWLDGADACGPPSE-----VTRYQMCFTEVNTSGTAAALAVGVGVAMA 1575
Db 1568 PLLCRW--GARPPSPVAPHHWDDLOARLGAEGYSPCY-----AGPILLVGLALAGG 1618
Qy 1576 YLAIDTFGATCVRRCWSI-----TSVPTGATVAP-----VVDE 1608
Db 1619 AVLAWHTGSLVVTSWRVNGNPNLIQOSTRGVTSISAPYLITVCVEGQTPADGKCAEA 1678
Qy 1609 BEIVEECASFIPLEA-----MVAADKLSKSTITTSPTFLETALEKLTFLGPHAATIL 1662
Db 1679 VOLXESTCGWGPMAASFDACAGMKGVLDGSMRTTAA-----AAVEKSDSLWRSFCAN-- 1728
Qy 1663 AIIEYCCGLVTLDPNPPFASCFAPFAGITTP-----LPHKIMKFLSLFGGAIAASKLT 1714
Db 1729 ---NYC-----PPGGGATSASAFPASLDTKFAQAWDAIFTNGRSLLVGLVAGYGAREN 1779
Qy 1715 DARGALAFMMA-----GAAGTALGTWTSVGF----- 1740
Db 1780 PLGVNAALFMGMSAGHQVHVRLLAALLLGVGTMLGT-PSVGLAMGAYFAGSGTSSWL 1838
Qy 1741 --VFDMLGGYAAASSTACLTFKCLMGEMPTDQLAGLVYSAFNPAAGVYGVLSACAMPAL 1798
Db 1839 SAIVAVLGSGWEGAXNAASLTDFLTGRAELKD-MWFLVSCXASPCASVAGVALGILLWSM 1897
Qy 1799 TTAGDPHVPNRLLLTMLARNTVCNRYPIATDIRKILGILEASTPWSVISACTRWLHT- 1857
Db 1898 KKGVEDWVNRIITLLPRGSLVPDGGFFVKS--EFTERVSTILRK-----MSLSRWNTL 1949
Qy 1858 -----PTEDDCLLAWGLETWQYVNCFFVICFNVLKAGVOSMWNIPGCPFFVSCQKGYKG 1911
Db 1950 VERRELDLETCCSMLWOLIDW-----LVRFGRYIGRRLKGMVPSVRVPLVGCTPGWGG 2003
Qy 1912 PWIGSGMLQARCPGGAELIFSVEG--FAKLYKGPRTCNSYWRGAVPVNARLCGSARPDP 1970

Db 2004 SWVGEGHIEARCAACGCIITADVBEGKLVLDVHYSSRLCSNYLKGTVPVSAAGSGDABEVP 2063
Qy 1971 DWTSLVNVYGRDYCKYEKMGDHIFTAVSSPNVCFQV-----PPTLRAAIVADGVQV 2024
Db 2064 AGPAL-YOIGVAEMVOLVRKDKTLVVGASSVYHLDHLLRAIRGPPMFVGGV---GVSW 2119
Qy 2025 QCYLGEPEKTPWTTTACCYCPDGKGKTVK-----LPFRVDGHT-----PGVRM- 2066
Db 2120 EAPLQOQPLVYRA-----GQSVRFDDVRYSLP-----HTLALPPPPPPPLAMP 2164
Qy 2067 -----QMLNRD-----ALETDCNNTNTPSPDEAAVSALVFQOELRTRTQLL 2108
Db 2165 PPPPPQVWTEBEADLREARARAIEA--VNERLPVPNPEAAQAAL----- 2209
Qy 2109 EATSAGVDTTKLPAPSTEEVVVRKQFRARTGSLTLPPPRSVPG--VSCPES-----LQ 2161
Db 2210 -----DALEEAIV-----SLPHVCAILGDDCCSESPGGHFIP 2243
Qy 2162 RSDPLEGPSNL-----PPSPPVQLAMPPLLGA-----GECNPFPTAIGCAMTETGGP 2210
Db 2244 EPDAVDVPIGMVEVQVGLRDQARDLGDRLAVLGARLESAAHPEASLATERRTMGLI 2303
Qy 2211 DDLPSYPPKKEVSWSDSWSTATTASSYVTP-----PYPKIRKO----- 2252
Db 2304 DTLADVQARLDVTCRSDTSGSSPEQISLSDSEPETIVEGGLKLEVRPQP--VRFKDLIRP 2362
Qy 2253 -----STQSAKAPRPTKKLGL----- 2268
Db 2363 GEGAKRLVTVRQSCCARSATRAPALSPLIAAVTATLSFLDTHTVSDSTGRVLDPLELL 2422
Qy 2269 -----KSEFSCSMYSYTWTDVISFKTASKVLSATRAITSGFLKORSYLYVTEPR 2316
Db 2423 QNAVGDLLIVACRSESSVSYYIWSGAPLNTGRHPAPMTRPIGTHITADTKYVYVDPN 2482
Qy 2317 DAELRKQKVTINR--QPLFPSPYHKQVRKAKEKSKVGVWMDYDEVAHAHTPSKSAKSHIT 2375
Db 2483 QAGERAAKVTIWRGSRVYDAHYRGVWSEVLQOAKTIKSPGWTYDEATAKVHSRAAGFGS 2542
Qy 2376 GLRGTDVRSNAARKAVLD-LQKCEAGEIPSHYRQTVIVPKEEVFVKTPOKTKKPPRLI 2434
Db 2543 KVTYGNMTTFAARAENVNMLAKIKTKOEV-----FTLVTKREVF--OKTTRKPPRFI 2594
Qy 2435 SYPHLEMRCEKMYGVQVAPDVV--KAVMGDAYGF-VDPRTVRKRLLSMW-----SPDVA 2488
Db 2595 CFPPLDFRIAEKMLGD--PGLVAKGILGKSYLFOYTPNQVRVQLWDLWRQKHPRAI-- 2650
Qy 2489 TCDTVCFDSTITPEDIWETDIYSAAKLSQHRAGIHTIARQL---YAGGPMIAYDGREI 2545
Db 2651 TVDATCFDSSIDERDMAVETEVEFAAASPND-----LVRALGSYYAEGPMVSPKGVP 2703
Qy 2546 GYRECRSSGVYTTSSNSLTCWLKNAAABQAGMKNPRFLICGDDCTVIWKSAGAD-ADK 2604
Db 2704 GVRKCRSSGVLTTSSANSITCYIKKAAARAVGLVDPDFLIAGDDCVIIYEDDGEDHAD- 2762
Qy 2605 QAMEVFASWKKVMGAPDCVQPPKYSLSEELTSCSSNVTSGITTSKGPYFYFLTRDPRPLG 2664
Db 2763 -ALRV-----ALGNVGYDCPKTHASLDTAESCSSYLAE--CNVCTERVWMLSTDMRPLA 2815
Qy 2665 RCSAEGLY-NPSAAWTGYLIHHYPCLW---VSRVLAVHFMEQMLFBDKLP-ETVTFDWMY 2719
Db 2816 RAASE---YSDPVSSALGTIL-MYP--WHPIVRVULLPHILIMAFRGGGTDDDLVVCEVQ 2869
Qy 2720 GKNTYVPEVDLPSIIAGVHGIEAFSVVRYTNAETLRVYSQSITDMTMTPLRAWRKKARAVL 2779
Db 2870 GNHYSPFLRVLPVELVSLHGPRCLURVTADSTKTQNEGAALURDLGMMHTLAFYRRAGNVR 2929
Qy 2780 ASAKRRGGAHAKLARFLMLWHATSPLDLOKTSVARYTTFNYCDVSPGEGVFITPQRL 2839
Db 2930 TRLLRGKGWGRALARALLMHPGLKEHP-----PSIKSIPGFQWATPYEHHTVWISGKPP 2985
Qy 2840 QKFLVKYLAIVFA 2853
Db 2986 WYMDVKCLFGLVCA 2999


```

Db 390 LVLSPNNSGTTTTLNRLTLTPRSSCIPDSYF--QADYCDKVKSAMLRRLSLRTVVALV 448
Qy 1853 RWLHTPTEDDGLLAWGLEIWQYVCNFFVICFNVLKAGVQSMVNI PCGPFVSCQKGYKGP 1912
Db 449 N--REPKNDEV-QVGYVWDLWEMIRQVRVVISLRA-----LCPVSLPLMHCEGWSGE 501
Qy 1913 WIGSGMLQARCPGCAELIFSVEYFAK--LYKGPRTCSNTYWRGAVPVNARLCSGARDPPT 1970
Db 502 WLLDGHVESRCLCGCVITGDVLNGQLKDPVY-STKLCRHYYMGTVPVNMMLGYGSETSPLLA 560
Qy 1971 DWTSLVNYGVDRDYCKYEKMGDHLFVTAVSSPNVCFQVPTPLRAAVA-----VDCVQVQC 2026
Db 561 SDTEPKVVPFGTSGMAEYVVVTHVIVIRTSCYKLLRQOI---LSAAVAEPYIVDGIPIVS- 616
Qy 2027 YLGPCKPTWTTTACCYGP-----DGGKTKVKLPRFDGHTPG--VRQLNLRDALETNDC 2079
Db 617 WEADARAP-----AMVYGPQGVQVITDGERYTLPQLQRMNVAPSEVSEVSIETETEDS 672
Qy 2080 NSTN-NTPSDEAAVSALVFKQELRRTNQLLEAISAGVDYTTKL-----P 2121
Db 673 ELTEADLPAAALQAI--ENAAIRILEPHIDVIMEDCSTPSLCGSSREMPWBEIDIRTP 730
Qy 2122 APSIEEVVRKQPRATGSLTLPSPRSVPGEVSCPSLQRSDDPLEGPSNL----- 2172
Db 731 SPALISVTESSSDEKTPSASSQSDTFS-----DSFEVIOESDTAESSESVFNALSVLK 786
Qy 2173 ---PPSPVQLAMPPLLGAGECNPFTAIGCAMTETGGGDDLLPSYPPKPESEWSDS 2229
Db 787 ALFQSOATRKLTVRMCCVEKSVTRFSLGLTVA-----DVASLCME 830
Qy 2230 WSTATASSVYVTPPYPKIR---GKDSQSAKAPRTKKLKGKSEFSCSMSYTTVDVISF 2286
Db 831 IQNHTAVCDKVRTLELQVGLVGNELTFEC-----DKEARQETLASFSYIWSGVLPT 884
Qy 2287 KTASKVLSATRAIISGFLKQSLVYVTEPRDAELRKQKVTINRQPLPFPSPY-HKQVRLAK 2345
Db 885 RATPAKPPVVRPVGSLLVADTKVYVTPNDVNGRRVDKVTFWRAPRVHDKFLVDSIERAK 944
Qy 2346 EKASKVGVMMVDYDEVAHAHTPSKAKSHITGLRGTDVRSGAARKAVLD-LQKCEAGEIP 2404
Db 945 KSAQACLSMGVITYBEARTVRPHAMGWSKVSKVDLATPAKRWAVHDLRQELIEGTPVP 1004
Qy 2405 SHYRQTIVPKEEYFVKTPQKTKPRLLISYPHLEMCVEKMYQVAPDVVKAVMGDA 2464
Db 1005 --FLLTV---KKEVFFK--DRKEEKAPRLIIVFPPLDFRIAEKILGDPG-RVAKAVLGA 1056
Qy 2465 YGP-VDPRTVRKRLLSMW-SPDVGATC-DTVCFDSTITPEDIWVETDIYSAAKLSQOHR 2521
Db 1057 YAFQVTPNQRVREMLKLWESKKTPCAICVDATCFDSSITERDVALETLYA---LASDHP 1113
Qy 2522 AGIHTIARQLYAGGPMIAYDGREIGYRCRSSGVYTTSSNSLTCWLKVNAAAEQAGMKN 2581
Db 1114 EWRVALGK-YFASGTMTVPEGVGERYCRSSGVLTTTSASNCLTCYIKVKAACDRVGLKN 1172
Qy 2582 PRFLICGDDCTVIWKSAGADADQAMRVFASWMKVMGAPODCVPQPKYSLBELTSCSSNV 2641
Db 1173 VSLIAGDDCLLICERPMPDSEALGRALASY-----GYACEPSYHASLDTAPFCSTWL 1226
Qy 2642 TSGITKSKPYFYFTRDPRIPLGRCSAEGLGY-NPSAAWIGYLIIHHYPCLMVSR-VLAVH 2699
Db 1227 AB-CNADGKRHFLLTDFRRPLARMSSE--YSDPMASAIGYIL-LYPWHPITRWVIIPH 1281
Qy 2700 FMEQWLFEDKLP-ETVTFDWGKNYVVPVEDLPSTIAGVHGIEAFSVVRYTNAILRVSQ 2758
Db 1282 VLTCAFRGGGTSPDPVMQCQVHNGNYKFLDKLPNII VALHGPAAURVADTKTKTMEAGK 1341
Qy 2759 SLTDWMTPEPLRAWRKRAVILASAKRRGGAHAKLARFLMLHATSR-PLPDL 2808
Db 1342 VLSDLKLPGLAVHRKKAGA-LRTRMLSRGRWAEALARGLLWHFGLRPPPEI 1391
```

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S68016
ATPase/RNA helicase - hepatitis C virus (fragment)
C:Species: hepatitis C virus
C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C:Accession: S68016
R:Jin, L.; Peterson, D.L.
Arch. Biochem. Biophys. 323, 47-53, 1995
A:Title: Expression, isolation, and characterization of the hepatitis C virus ATPase/RNA
A:Reference number: S68016; MUID:96019946; PMID:7487072
A:Accession: S68016
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-386 <JIN>
A:Cross-references: UNIPROT:Q04045
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; nonstructural protein; nucleotide binding; P-loop; polyprotein
E:24-31/Region: nucleotide-binding motif A (P-loop)
F:86-91/Region: nucleotide-binding motif B
F:90-93/Region: DEHX motif

Query Match 5.7%; Score 871; DB 2; Length 386;
Best Local Similarity 46.3%; Pred. No. 1.5e-46;
Matches 187; Conservative 55; Mismatches 132; Indels 30; Gaps 8;

Qy 1119 PQYTAHATLDTKPTVPNEYSVQILIAPTSGSKSTKLP LSLYMOEKYEVLVNPSVATTASM 1178
Db 1 PVFTDNSS--SPPVVPOSFQVAHLHAPTSGSKSTKVPAAVAAQGYKVLVLPNSVAATLGF 58
Qy 1179 PKYMHATYGVNPNCFNGKCTNTGASLTSTYGYWLT-GACSRN-YDVIICDECHATDAT 1236
Db 59 GAYMSKAHGVN-----YGFADGGCGGAYDIIICDECHSDAT 98
Qy 1237 TVLIGIGKVLTEAPSKNVLVVLATATPPGVIPTPHANITEIQLTDEGTIPPHGKKIKEEN 1296
Db 99 SILGIGTVLQDAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIIPFYKAIPLA 158
Qy 1297 LKGRHLIFPATKXHCDELANELARKGITAVSYVRGCDISKIP-EGDCVVVATDALCTGY 1355
Db 159 IKGRHLIFCHSKKKCCDELATKLVALGINAVAYVRGLDVSVIPSSGVDVVVVATDALMTGF 218
Qy 1356 TGFDFSYYDCSLMVEGTCHVDLQPTFTMGVRCVSAIVKQGRGRTGRGRAGIYVYVDG 1415
Db 219 SGDFSDVIDCNTCTVTQVDFSLDPTFTIETTLTPQDAVSRQRRGRTGRGKPGIYRFVAP 278
Qy 1416 SCTPSGMVPECNIVEAFDAKAWGLSSTEAQITLDTYRTQPLPAICANLDEWADLFS- 1474
Db 279 GERPSGMFDSVLCCECYDAGCANVELTPAETTVRLRAYMNTPGLPVCDHLEFWEGVFTG 338
Qy 1475 MVNPEPSFVNTAKRTADNYVLLTAAQLQCHQYGYAAPNDAPRW 1518
Db 339 LTHIDAHFLSQTQSGENFPYLVAYQATVCAR-AHAPP---PSW 378

Search completed: October 27, 2005, 15:49:25
Job time : 115 secs
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2005, 15:29:48 ; Search time 316 Seconds
(without alignments)

4641.123 Million cell updates/sec

Title: US-10-009-002-2

Perfect score: 15376

Sequence: 1 MPVISTQSPVPAPTRKNK.....KYLAVIVFALGLIAVGLAIS 2864

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15376	100.0	2864	2 Q9QW5	Q9QW5 hepatitis g
2	15366	99.9	2864	2 Q999T0	Q999T0 hepatitis g
3	15317	99.6	2864	2 Q69422	Q69422 hepatitis g
4	10238	66.6	1925	2 Q6JKE4	Q6JKE4 hepatitis g
5	3310.5	21.5	3033	2 Q7T710	Q7T710 hepatitis g
6	3306.5	21.5	3033	2 Q7T716	Q7T716 hepatitis c
7	3303.5	21.5	3033	2 Q7T7H9	Q7T7H9 hepatitis c
8	3303.5	21.5	3033	2 Q7T714	Q7T714 hepatitis c
9	3303.5	21.5	3033	2 Q9IZA1	Q9IZA1 hepatitis c
10	3300.5	21.5	3033	2 Q7T7J1	Q7T7J1 hepatitis c
11	3296.5	21.4	3033	2 Q9QAX1	Q9QAX1 hepatitis c
12	3293.5	21.4	3033	2 Q7T7J2	Q7T7J2 hepatitis c
13	3292.5	21.4	3033	2 Q68801	Q68801 hepatitis c
14	3289.5	21.4	3033	2 Q7T7H7	Q7T7H7 hepatitis c
15	3289.5	21.4	3033	2 Q7T717	Q7T717 hepatitis c
16	3288.5	21.4	3033	2 Q9IZA2	Q9IZA2 hepatitis c
17	3287.5	21.4	3033	2 Q7T711	Q7T711 hepatitis c
18	3286.5	21.4	3033	2 Q7T7H6	Q7T7H6 hepatitis c
19	3285.5	21.4	3033	2 Q9DHD6	Q9DHD6 hepatitis c
20	3284.5	21.4	3033	2 Q7T7H8	Q7T7H8 hepatitis c
21	3283.5	21.4	3033	2 Q7T718	Q7T718 hepatitis c
22	3282.5	21.3	3033	2 Q7T712	Q7T712 hepatitis c
23	3282	21.3	3033	2 Q991B6	Q991B6 hepatitis c
24	3281.5	21.3	3033	2 Q7T713	Q7T713 hepatitis c
25	3281	21.3	3021	2 Q68870	Q68870 hepatitis c
26	3277.5	21.3	3033	2 Q9QF35	Q9QF35 hepatitis c
27	3276	21.3	3021	2 Q81258	Q81258 hepatitis c
28	3275	21.3	3008	2 Q9J3F4	Q9J3F4 hepatitis c
29	3273.5	21.3	3033	1 POLG_HCVJ8	P26661 h genome po
30	3273	21.3	3010	2 Q9QP06	Q9QP06 hepatitis c
31	3271.5	21.3	3033	2 Q7T7H3	Q7T7H3 hepatitis c

RESULT 1

ID	Q9QW5	PRELIMINARY;	PRT;	2864 AA.
AC	Q9QW5;			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Polyprotein.			
OS	Hepatitis GB virus B.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.			
OX	NCBI_TaxID=39113;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	BUKH J., Apgar C.L., Yanagi M.,			
RA	"Toward a surrogate model for hepatitis C virus: An infectious			
RT	molecular clone of the GB virus-B hepatitis agent."			
RL	Virology 262:470-478(1999).			
DR	EMBL; AF179612; AAF01368.1; -			
DR	HSP; P26664; 1HEI.			
DR	MEROPS: S29.002; -			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0019028; C:viral capsid; IEA.			
DR	GO; GO:0019031; C:viral envelope; IEA.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:008026; F:ATP-dependent helicase activity; IEA.			
DR	GO; GO:0003723; F:RNA binding; IEA.			
DR	GO; GO:000368; F:RNA-directed RNA polymerase activity; IEA.			
DR	GO; GO:0008236; F:serine-type peptidase activity; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	GO; GO:0006350; P:transcription; IEA.			
DR	GO; GO:0019079; P:viral genome replication; IEA.			
DR	GO; GO:0019087; P:viral transformation; IEA.			
DR	InterPro; IPR000345; CytC_heme_BS.			
DR	InterPro; IPR001410; DEAD.			
DR	InterPro; IPR011545; DEAD/DEAH_N.			
DR	InterPro; IPR002521; HCV core.			
DR	InterPro; IPR002519; HCV env.			
DR	InterPro; IPR000745; HCV_NS4a.			
DR	InterPro; IPR001490; HCV_NS4b.			
DR	InterPro; IPR002868; HCV_NS5a.			
DR	InterPro; IPR002166; HCV RdRp.			
DR	InterPro; IPR004109; Peptidase_S29.			
DR	InterPro; IPR009003; Pept_Ser_Cys.			
DR	InterPro; IPR002518; Rept_U39_HCV_NS2.			
DR	InterPro; IPR007095; RNA_pol_DS_PS.			
DR	InterPro; IPR007094; RNA_pol_PSVir.			
DR	Pfam; PF01542; HCV core; 1.			
DR	Pfam; PF01539; HCV env; 1.			
DR	Pfam; PF01538; HCV_NS2; 1.			
DR	Pfam; PF02907; HCV_NS3; 1.			
DR	Pfam; PF01006; HCV_NS4a; 1.			
DR	Pfam; PF01001; HCV_NS4b; 1.			

32	3265.5	21.2	3033	2	Q991B8	Q991B8 hepatitis c
33	3264.5	21.2	3032	2	Q991B2	Q991B2 hepatitis c
34	3264.5	21.2	3033	2	Q7T7H5	Q7T7H5 hepatitis c
35	3263.5	21.2	3033	2	Q7T7H4	Q7T7H4 hepatitis c
36	3263.5	21.2	3033	2	Q91ZA6	Q91ZA6 hepatitis c
37	3263	21.2	3010	2	Q9J3H9	Q9J3H9 hepatitis c
38	3262	21.2	3010	2	Q9WMX2	Q9WMX2 hepatitis c
39	3262	21.2	3033	1	POLG_HCVJ6	P26660 h genome po
40	3261	21.2	3012	2	Q9WIK7	Q9WIK7 hepatitis c
41	3260	21.2	3010	2	Q68826	Q68826 hepatitis c
42	3259	21.2	3010	2	Q9DTE6	Q9DTE6 hepatitis c
43	3258	21.2	3010	2	Q9DTE4	Q9DTE4 hepatitis c
44	3257	21.2	3010	2	Q02829	Q02829 hepatitis c
45	3256.5	21.2	3010	2	Q9QP61	Q9QP61 hepatitis c

Db 1981 VRDYCKYKMGDHFVTA VSPNVCFQVPPTLRAAVAVDGVQVCYLGPBKPTWTSAC 2040
Qy 2041 CYGPDGKGTVKLPFRVDGHTPGVRMQLNRDALETNDCNSTNTPSDEAAVSALVFKQE 2100
Db 2041 CYGPDGKGTVKLPFRVDGHTPGVRMQLNRDALETNDCNSTNTPSDEAAVSALVFKQE 2100
Qy 2101 LRTNQLLEAISAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLPPLPPRSVPVGCSPESL 2160
Db 2101 LRTNQLLEAISAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLPPLPPRSVPVGCSPESL 2160
Qy 2161 QRSDPLEGSNLPSPVLQAMPLGLGAGECNPFTAIGCAMTETGGGDDLPSPVPPK 2220
Db 2161 QRSDPLEGSNLPSPVLQAMPLGLGAGECNPFTAIGCAMTETGGGDDLPSPVPPK 2220
Qy 2221 EVSEWSDSHSTATTASSYVTGPPYKIRGKDSQSAPAKRPTKKLGKSEFSCSMSTY 2280
Db 2221 EVSEWSDSHSTATTASSYVTGPPYKIRGKDSQSAPAKRPTKKLGKSEFSCSMSTY 2280
Qy 2281 TDVISFTKSVLSATRAITSGLFKQSLVYVTEPRDAELRKQVTINRQPLFPPSPYHKQ 2340
Db 2281 TDVISFTKSVLSATRAITSGLFKQSLVYVTEPRDAELRKQVTINRQPLFPPSPYHKQ 2340
Qy 2341 VRLAKEKASKVGVMMWDYDEVAHTPSKSAKSHITGLRGTDVRSGAARKAVLDLQKCEA 2400
Db 2341 VRLAKEKASKVGVMMWDYDEVAHTPSKSAKSHITGLRGTDVRSGAARKAVLDLQKCEA 2400
Qy 2401 GEIPSHYRQTVIVPKEEVFKTPKPKPRLISYPHLEMRCEKMYGQVADPVVKA 2460
Db 2401 GEIPSHYRQTVIVPKEEVFKTPKPKPRLISYPHLEMRCEKMYGQVADPVVKA 2460
Qy 2461 MGDAYGPDVPRTRVKRLLSMWSDAVGATCDTVCDFSTITPEDIMVETDIYSAKLSDQH 2520
Db 2461 MGDAYGPDVPRTRVKRLLSMWSDAVGATCDTVCDFSTITPEDIMVETDIYSAKLSDQH 2520
Qy 2521 RAGIHTTARQLYAGGPMIADGRIEYRCRSGSVYTTSSNSLTCWLKYNAAEQAGMK 2580
Db 2521 RAGIHTTARQLYAGGPMIADGRIEYRCRSGSVYTTSSNSLTCWLKYNAAEQAGMK 2580
Qy 2581 NPRLICGDDCTVTKSAGADADQAMRVFASWMMKMGAPQDCVPQKYSLEELTSCSN 2640
Db 2581 NPRLICGDDCTVTKSAGADADQAMRVFASWMMKMGAPQDCVPQKYSLEELTSCSN 2640
Qy 2641 VTSGITKSGKPYFLTRDRIPLGRCSAEGLYGNPSAAWIGYLIIHYPCLWVSRVLAVHF 2700
Db 2641 VTSGITKSGKPYFLTRDRIPLGRCSAEGLYGNPSAAWIGYLIIHYPCLWVSRVLAVHF 2700
Qy 2701 MEQMLFEDKLPEVTTFDYGKNTYVPVEDLPSIIAGVHGIEAFSVRYTNAEILRVQS 2760
Db 2701 MEQMLFEDKLPEVTTFDYGKNTYVPVEDLPSIIAGVHGIEAFSVRYTNAEILRVQS 2760
Qy 2761 TDMTPPLRAWRKKARAVLASAKRRGGAHAKLARFLWHATSRLPDLDKTSVARYTTFN 2820
Db 2761 TDMTPPLRAWRKKARAVLASAKRRGGAHAKLARFLWHATSRLPDLDKTSVARYTTFN 2820
Qy 2821 YCDVYSPGDDVFIPTQRRLQKFLVKYLAVIIVFALGLIAGLAIS 2864
Db 2821 YCDVYSPGDDVFIPTQRRLQKFLVKYLAVIIVFALGLIAGLAIS 2864

RESULT 2

Q999T0 ID Q999T0 PRELIMINARY; PRT; 2864 AA.
AC Q999T0; 17 (Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE Polypeptide.
OS Hepatitis B virus B.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
OX NCBI_Taxid=39113;
RN SEQUENCE FROM N.A.
RP MEDLINE=21446677; PubMed=11562537;
RX

RA Sbardellati A., Scarselli E., Verschoor E., De Tomassi A., Lazaro D.,
Traboni C.;
RT "Generation of infectious and transmissible virions from a GB virus B
full-length consensus clone in tamarins.";
RL J. Gen. Virol. 82:2437-2448 (2001).
DR EMBL; AJ277947; CAC33083.1; -.
DR HSSP; P26664; IHEI.
DR MEROPS; U39.001; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR002521; HCV_core.
DR InterPro; IPR002519; HCV_env.
DR InterPro; IPR000745; HCV_NS4a.
DR InterPro; IPR001490; HCV_NS4b.
DR InterPro; IPR002868; HCV_NS5a.
DR InterPro; IPR002166; HCV_RdRP.
DR InterPro; IPR004109; Peptidase_S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF01506; HCV_NS5a; 1.
DR Pfam; PF00998; Viral_RdRP; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOMN 1.
KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
SQ SEQUENCE 2864 AA; 312814 MW; 795E4E6F9DBAA749 CRC64;

Query Match 99.9%; Score 15366; DB 2; Length 2864;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2860; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPVISTQTSVPAPRTRKNKQTOASYPVSIKTSVERQAKRKVQDARPRNYKIAGIHD 60
Db 1 MPVISTQTSVPAPRTRKNKQTOASYPVSIKTSVERQAKRKVQDARPRNYKIAGIHD 60
Qy 61 GLQTLQAALPAHGWGRQDPRHKSRNLGILLYPLGWIQDVTTHTPLVGLPVAGAVRPV 120
Db 61 GLQTLQAALPAHGWGRQDPRHKSRNLGILLYPLGWIQDVTTHTPLVGLPVAGAVRPV 120
Qy 121 CQIVRLLEDGWNWATGFWGVLHVVCLLSLACPCSGARVTDPTNTTILTNCCQORNIY 180
Db 121 CQIVRLLEDGWNWATGFWGVLHVVCLLSLACPCSGARVTDPTNTTILTNCCQORNIY 180
Qy 181 CSPSTCLHGPCVCICADECWPNANPYISHPSNWTGTSFLADHIDFVNGALVTCDAIDIG 240
Db 181 CSPSTCLHGPCVCICADECWPNANPYISHPSNWTGTSFLADHIDFVNGALVTCDAIDIG 240
Qy 241 ELGCACVLVGDMLVRHWHLIHIDLNETGTCYLEVPTGIDPGFLGFMGAKVAVIFLTK 300
Db 241 ELGCACVLVGDMLVRHWHLIHIDLNETGTCYLEVPTGIDPGFLGFMGAKVAVIFLTK 300

Qy 301 LASQVPAIATFSSVHYLVAGALIYYASRGKWYQLLIALMLYIEATSGNPIRVPTGSI 360
Db 301 LASQVPAIATFSSVHYLVAGALIYYASRGKWYQLLIALMLYIEATSGNPIRVPTGSI 360
Qy 361 AEFCSPLMIPCPCHSYLSENSEVICYSPKWRTRPITILEYNNISISWYPYTIIPGARGCMVKF 420
Db 361 AEFCSPLMIPCPCHSYLSENSEVICYSPKWRTRPITILEYNNISISWYPYTIIPGARGCMVKF 420
Qy 421 KNNWTGCCRIIRNVSICYTGMGTDAVWMDTRNTYEACGVTPLTTTAWHNGSALKLAILQYPG 480
Db 421 KNNWTGCCRIIRNVSICYTGMGTDAVWMDTRNTYEACGVTPLTTTAWHNGSALKLAILQYPG 480
Qy 481 SKEMFKPHNMNSGHLIFEGSDTPIVYFYDPVNSTLLPPERWARLPPTPVVVGSGMLQVPQ 540
Db 481 SKEMFKPHNMNSGHLIFEGSDTPIVYFYDPVNSTLLPPERWARLPPTPVVVGSGMLQVPQ 540
Qy 541 GFYSDVKDLATGLITKDKAWKNYQVLYSATGALSITGVTTTAKAVLILILGLCGSKYLIILAY 600
Db 541 GFYSDVKDLATGLITKDKAWKNYQVLYSATGALSITGVTTTAKAVLILILGLCGSKYLIILAY 600
Qy 601 LCYLSLCFGRASGYPRLRPVLPQSQYLOAGWDVLSKAQVAPFALIFFICYLRCLRUYAAL 660
Db 601 LCYLSLCFGRASGYPRLRPVLPQSQYLOAGWDVLSKAQVAPFALIFFICYLRCLRUYAAL 660
Qy 661 LGFVPMAGLPLTFEFAAAAAQPDYDMWVRLLVAGLVWAGNRGHRITALLVGPWPLVAL 720
Db 661 LGFVPMAGLPLTFEFAAAAAQPDYDMWVRLLVAGLVWAGNRGHRITALLVGPWPLVAL 720
Qy 721 LTLHLVTPASAFDTEIIGGLTIPPVVALVMSRFGFPAHLLPRCALVNSYLWQRWENWF 780
Db 721 LTLHLVTPASAFDTEIIGGLTIPPVVALVMSRFGFPAHLLPRCALVNSYLWQRWENWF 780
Qy 781 WNVTLRPERFELVLCFPGATYDALVTEFCVCHVALLCLTSSAASPFGDTSVRABMLVR 840
Db 781 WNVTLRPERFELVLCFPGATYDALVTEFCVCHVALLCLTSSAASPFGDTSVRABMLVR 840
Qy 841 LGKCHAWTSHVLYKFLFLVFGENGVFYFKHLHGDVLPNDFASKLPLOBPFPFPFGKARVY 900
Db 841 LGKCHAWTSHVLYKFLFLVFGENGVFYFKHLHGDVLPNDFASKLPLOBPFPFPFGKARVY 900
Qy 901 RNEGRRLACGDTVGLPVVARLGDVLVAGLAMPDPGWAITAPFTLQCLSERGTLSAMAVV 960
Db 901 RNEGRRLACGDTVGLPVVARLGDVLVAGLAMPDPGWAITAPFTLQCLSERGTLSAMAVV 960
Qy 961 MTGIDPRTWTGTIFRLGSLATSYMGFCVDNVLVYTAHSGSKRRLAHPGTGSHIPTVDAAN 1020
Db 961 MTGIDPRTWTGTIFRLGSLATSYMGFCVDNVLVYTAHSGSKRRLAHPGTGSHIPTVDAAN 1020
Qy 1021 DQDIYQPPCGAGSLTRCSCGETKGVLVTRLGLSLVEVNSKDDPYMVCVCGALPMAVAKGSSG 1080
Db 1021 DQDIYQPPCGAGSLTRCSCGETKGVLVTRLGLSLVEVNSKDDPYMVCVCGALPMAVAKGSSG 1080
Qy 1081 APILCSSGHVIGMFTAARNSGSGSVQIRVRPLVCAGYHPQYTAHATLTKPTVPNEYSVQ 1140
Db 1081 APILCSSGHVIGMFTAARNSGSGSVQIRVRPLVCAGYHPQYTAHATLTKPTVPNEYSVQ 1140
Qy 1141 ILIAPTSGSKTKLPLSYMOKEYVLVNLPSVATTASMPKYMHAITYGVNPNCFNGKCTN 1200
Db 1141 ILIAPTSGSKTKLPLSYMOKEYVLVNLPSVATTASMPKYMHAITYGVNPNCFNGKCTN 1200
Qy 1201 TGASITYTYGMYLTGACSRNVDVILCDCHATDATTVLGIGKVLTEAPSKNVLVLVILAT 1260
Db 1201 TGASITYTYGMYLTGACSRNVDVILCDCHATDATTVLGIGKVLTEAPSKNVLVLVILAT 1260
Qy 1261 ATPPGVITPPIHANTIEIQLTDEGTTIPFHGKKIKEENLKKGRHLIPEATKKGHCELANELA 1320
Db 1261 ATPPGVITPPIHANTIEIQLTDEGTTIPFHGKKIKEENLKKGRHLIPEATKKGHCELANELA 1320
Qy 1321 RKGITAVSYRGCDLSKIPGEGCVVATDALCTGYTGDPDFDSVYDCSLMVEGTCHVDLDPT 1380
Db 1321 RKGITAVSYRGCDLSKIPGEGCVVATDALCTGYTGDPDFDSVYDCSLMVEGTCHVDLDPT 1380
Qy 1381 FTMGVRVCGVSAIVKGQRRGRTGRAGIYYVVDGSCTPSGMVPBCNIVEAFDAAKAWYG 1440

Db 1381 FTMGVRVCGVSAIVKGQRRGRTGRAGIYYVVDGSCTPSGMVPBCNIVEAFDAAKAWYG 1440
Qy 1441 LSSTEAQTILDTYRTQPLPAIGANLDEWADLFSMVNPEPSFVNTAKRTADNYYLLTAAQ 1500
Db 1441 LSSTEAQTILDTYRTQPLPAIGANLDEWADLFSMVNPEPSFVNTAKRTADNYYLLTAAQ 1500
Qy 1501 LQLCHOXYGAAPNDAPRWQGRARLKGKPCGVLWRLDGADACPGPEPSEVTRYQMCFTEVNT 1560
Db 1501 LQLCHOXYGAAPNDAPRWQGRARLKGKPCGVLWRLDGADACPGPEPSEVTRYQMCFTEVNT 1560
Qy 1561 SGTAAALAVGVGANAYLAIDTFGATCVRRCWSITSVPTGATVPVDEEIEIIEVECSAFIP 1620
Db 1561 SGTAAALAVGVGANAYLAIDTFGATCVRRCWSITSVPTGATVPVDEEIEIIEVECSAFIP 1620
Qy 1621 LEAMVAIDKLSITITTSPTTLETALEKNTFLGPHAATILAIIEYCCGLVTLTPDNPPFA 1680
Db 1621 LEAMVAIDKLSITITTSPTTLETALEKNTFLGPHAATILAIIEYCCGLVTLTPDNPPFA 1680
Qy 1681 SCVFAFIAGITTPPHKIKMFLSLFGGAIASKLTLDARGALAFMMAGAGTALGTWTSVGF 1740
Db 1681 SCVFAFIAGITTPPHKIKMFLSLFGGAIASKLTLDARGALAFMMAGAGTALGTWTSVGF 1740
Qy 1741 VFDMLGYYAAASSTACLTFFKCLMGWPTMDQLAGLVYSAPNPAAGVGVJUSACAMFALT 1800
Db 1741 VFDMLGYYAAASSTACLTFFKCLMGWPTMDQLAGLVYSAPNPAAGVGVJUSACAMFALT 1800
Qy 1801 AGPDHWNRLTLMARSNTVCNEYFIATDIRRILGILEASTPWSVISACIRLWHTPTE 1860
Db 1801 AGPDHWNRLTLMARSNTVCNEYFIATDIRRILGILEASTPWSVISACIRLWHTPTE 1860
Qy 1861 DDCLLIANGLEIWOYVCNFFVICFNVLKAGVQSVMNIPGCPFFYSCQKGYKGPWJGSGMLQ 1920
Db 1861 DDCLLIANGLEIWOYVCNFFVICFNVLKAGVQSVMNIPGCPFFYSCQKGYKGPWJGSGMLQ 1920
Qy 1921 ARCPGCAELIFSVEBNGFAKLYKGPRTCSNWRGAVPVNARLCSGARPDPTDWTSLVNVYG 1980
Db 1921 ARCPGCAELIFSVEBNGFAKLYKGPRTCSNWRGAVPVNARLCSGARPDPTDWTSLVNVYG 1980
Qy 1981 VRDYCKYEKGMDHIFVTAVSSPNVCFQVPTTLBAAVAVDGVQVQCYLGEBKPTWTTTASAC 2040
Db 1981 VRDYCKYEKGMDHIFVTAVSSPNVCFQVPTTLBAAVAVDGVQVQCYLGEBKPTWTTTASAC 2040
Qy 2041 CYGPDGKGKTVKLPFRVDGHTPGVVRMQLNRDALETNDCNNTNTPSDEAAVSALVFKQE 2100
Db 2041 CYGPDGKGKTVKLPFRVDGHTPGVVRMQLNRDALETNDCNNTNTPSDEAAVSALVFKQE 2100
Qy 2101 LRRTNQLLEAISAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLPPPPRSVPGVSCPESL 2160
Db 2101 LRRTNQLLEAISAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLPPPPRSVPGVSCPESL 2160
Qy 2161 QRSPLSGPSNLPBSPVLQALAMPPLLGAECNPPPTAIGCAMTETGGPDPLSPYBPK 2220
Db 2161 QRSPLSGPSNLPBSPVLQALAMPPLLGAECNPPPTAIGCAMTETGGPDPLSPYBPK 2220
Qy 2221 EVSWSDESSTATTASSYVTGPPYKIRGKDSQSAKAPAKRPTKKLCKSFSCSMSTYW 2280
Db 2221 EVSWSDESSTATTASSYVTGPPYKIRGKDSQSAKAPAKRPTKKLCKSFSCSMSTYW 2280
Qy 2281 TDVISFKTASKVLASATRAITSGFLKQRSLVVYVTEPRDAELRQKVTINRQBLFPSPSYHKQ 2340
Db 2281 TDVISFKTASKVLASATRAITSGFLKQRSLVVYVTEPRDAELRQKVTINRQBLFPSPSYHKQ 2340
Qy 2341 VRLAKEKASKVGVWMDYDEVAHAHTPSKASHITGLRGTDVRSGAARKAVLDLQKCVEA 2400
Db 2341 VRLAKEKASKVGVWMDYDEVAHAHTPSKASHITGLRGTDVRSGAARKAVLDLQKCVEA 2400
Qy 2401 GEIPSHYRQTVIVPKEEVFKTPKPTKPPRLISYPHLEMRCEVEMKYGOVADPVVKAV 2460
Db 2401 GEIPSHYRQTVIVPKEEVFKTPKPTKPPRLISYPHLEMRCEVEMKYGOVADPVVKAV 2460
Qy 2461 MGDYGFVDPRTVRKRLLSMSPDAGATCTVCFDSTITPEDIWETDIIVSAAKLSQDH 2520

Db 2461 MGDAYFVDPRTRVRLLSMWSPPAAGATCDTVCDFDSTITPEDIMVETDIYSAAKLSDQH 2520
Qy 2521 RAGIHTIARQLYAGPMIAYDGRBIGYRRCRSSGVTYTTSSNSLTCWLKVNAAAEEQAGMK 2580
Db 2521 RAGIHTIARQLYAGPMIAYDGRBIGYRRCRSSGVTYTTSSNSLTCWLKVNAAAEEQAGMK 2580
Qy 2581 NPRELICGDDCTVTKSAGADADQAMRVFASWKMVGAPQDCVPQPKYSLEELTSCSSN 2640
Db 2581 NPRELICGDDCTVTKSAGADADQAMRVFASWKMVGAPQDCVPQPKYSLEELTSCSSN 2640
Qy 2641 VTSIGTSGKPYVFLTRDPRIPLCRCSAEGLYGNPSAAWIGYLIIHYPCLWVSRLVAVHF 2700
Db 2641 VTSIGTSGKPYVFLTRDPRIPLCRCSAEGLYGNPSAAWIGYLIIHYPCLWVSRLVAVHF 2700
Qy 2701 MEQMLFEDKLPETVTFDYGKNTVTPVEDLPSIIAGVHGIEAFSVRYTNAEILRVQSLS 2760
Db 2701 MEQMLFEDKLPETVTFDYGKNTVTPVEDLPSIIAGVHGIEAFSVRYTNAEILRVQSLS 2760
Qy 2761 TDMTPPLRAWRKARAVLASAKRGGAHAKLARFLWHATSRLPDLDKTSVARYTTFN 2820
Db 2761 TDMTPPLRAWRKARAVLASAKRGGAHAKLARFLWHATSRLPDLDKTSVARYTTFN 2820
Qy 2821 YCDVYSPGDFVITPQRLQKFLVKYLAVIVFALGLIAGLAIS 2864
Db 2821 YCDVYSPGDFVITPQRLQKFLVKYLAVIVFALGLIAGLAIS 2864

RESULT 3
Q69422 ID Q69422 PRELIMINARY; PRT; 2864 AA.
AC Q69422;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DR 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polypeptide.
OS Hepatitis GB virus B
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
OX NCBI_TaxID=39113;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95241511; PubMed=7724574;
RA Simons J.N., Pilot-Matias T.J., Leary T.P., Dawson G.J., Desai S.M.,
RA Schlauder G.G., Muerhoff A.S., Erker J.C., Buijk S.L., Chalmers M.L.,
RA van Sant C.L., Mushahwar I.K.;
RT "Identification of two flavivirus-like genomes in the GB hepatitis
RT agent.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:3401-3405 (1995).
DR EMBL; U22304; AAC54059.1; -;
DR HSSP; P26664; lHEI.
DR MEROPS; S29.002; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent RNA polymerase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed helicase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR000745; HCV NS4a.
DR InterPro; IPR001490; HCV NS4b.
DR InterPro; IPR002868; HCV_NS5a.
DR InterPro; IPR002166; HCV_RdRp.
DR InterPro; IPR004109; Peptidase_S29.

DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF01506; HCV_NS5a; 1.
DR Pfam; PF00998; Viral_RdRp; 1.
DR SMART; SM00487; DEAD; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
SQ SEQUENCE 2864 AA; 312702 MW; 5F5A7D8FAF0CDE81 CRC64;

Query Match 99.6%; Score 15317; DB 2; Length 2864;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2852; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MPVISTQTSVPAPRTRKKNKQTOASYPVSIKTSVERGQRAKRVQDARPRNYKIAGHD 60
Db 1 MPVISTQTSVPAPRTRKKNKQTOASYPVSIKTSVERGQRAKRVQDARPRNYKIAGHD 60
Qy 61 GLQTLAQAALPAHGWRGQDPRHKSRLGILLDPLGWIGDVTTHTPLVGLVAGAVRPV 120
Db 61 GLQTLAQAALPAHGWRGQDPRHKSRLGILLDPLGWIGDVTTHTPLVGLVAGAVRPV 120
Qy 121 CQIVRLLEDGWNWATGFWGHLFVCLLSLACPCSGARVTDPTNTTILNCCORNOVIY 180
Db 121 CQIVRLLEDGWNWATGFWGHLFVCLLSLACPCSGARVTDPTNTTILNCCORNOVIY 180
Qy 181 CSPSTCLHPEGCVTCACDECKVPANPYISHPSNNKTGDSFLADHIDFVWGALVTCDAIDG 240
Db 181 CSPSTCLHPEGCVTCACDECKVPANPYISHPSNNKTGDSFLADHIDFVWGALVTCDAIDG 240
Qy 241 ELGCACVLVGDWLVRLHILHIDNETGTCYLEVPTGIDPGFLGFGWAGKVEAVIFLTK 300
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Qy 361 AEFCSPLMIPCCHSYLSENVSEVICSPKWTPTLTLEYNNSISWYPTTIPGARGCWKF 420
Db 361 AEFCSPLMIPCCHSYLSENVSEVICSPKWTPTLTLEYNNSISWYPTTIPGARGCWKF 420
Qy 421 KNTTWGCCRIRNVPSTCTMGTDVNDTRNTYBACGVTPLWLTAAHNGSALKLAILQYPG 480
Db 421 KNTTWGCCRIRNVPSTCTMGTDVNDTRNTYBACGVTPLWLTAAHNGSALKLAILQYPG 480
Qy 481 SKMFKPHNMWSGHLYFEGSDTPIVYFDPVNSTLLDPPERWALPGTPPVVGRSMLQVPQ 540
Db 481 SKMFKPHNMWSGHLYFEGSDTPIVYFDPVNSTLLDPPERWALPGTPPVVGRSMLQVPQ 540
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Db 721 LTLHLVTPASADTEIIGGLTTPPVVVALVMSRFGFAHLPRCALVNSVLMORWENWF 780

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DB 781 WNVTLRPERFLLVLCVPGATYDILVTCVCHVALLCLTSSAASFFGTDSDRVRAHMLVR 840
QY 841 LGKCHAMVSHYVLKFFLLVFGENGFFYKHLHGDVLPNDPASKLPLQBPFFPFEGKARVY 900
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QY 961 MTGIDPRTWTGTIFRLGSLATS YMGFVCDNVLYTAHHGSKGRRLAHPTGSHIPTVDAAN 1020
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DB 1141 ILIAPTSGSKTKPLSLYMOEKYEVVLNPNVATTASMPKYMHA TYGVNPNICYFNKGKCTN 1200
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QY 1321 RKGITAVSYRGCDISKIPEGDCVVVATDALCTGYTGFDS VYDCSLMVEGTCHVDLDPT 1380
DB 1321 RKGITAVSYRGCDISKIPEGDCVVVATDALCTGYTGFDS VYDCSLMVEGTCHVDLDPT 1380
QY 1381 FTMGVRVCGVSAIVKQRRGRTGRAGIYIYVVDGSC TPGSMVPECNIVEAFDAKAWYG 1440
DB 1381 FTMGVRVCGVSAIVKQRRGRTGRAGIYIYVVDGSC TPGSMVPECNIVEAFDAKAWYG 1440
QY 1441 LSSTEAQIILDTYRQPLPAIGANLDEWADLFSMNWPEPSPVWTAKTADNYVLLTAAQ 1500
DB 1441 LSSTEAQIILDTYRQPLPAIGANLDEWADLFSMNWPEPSPVWTAKTADNYVLLTAAQ 1500
QY 1501 LQLCHOYGVAAPNDAPRWQGARLKKPCGVLRLOGADACPGPEPSEVTRYQMCFTVNT 1560
DB 1501 LQLCHOYGVAAPNDAPRWQGARLKKPCGVLRLOGADACPGPEPSEVTRYQMCFTVNT 1560
QY 1561 SGTAAALAVGVGVAMAYLAIDTFEGATCVRRCSITSVPTGATVAPVVDDEEIVEECASFIP 1620
DB 1561 SGTAAALAVGVGVAMAYLAIDTFEGATCVRRCSITSVPTGATVAPVVDDEEIVEECASFIP 1620
QY 1621 LEAMVAAIDKLKSTITTTSPFTLETALEKLNFTFLGPHAATILAIIEYCCGLVTLDPNPPA 1680
DB 1621 LEAMVAAIDKLKSTITTTSPFTLETALEKLNFTFLGPHAATILAIIEYCCGLVTLDPNPPA 1680
QY 1681 SCVPAFIAGITTPPLPHKIKNFLSLFGGALASKLTDPARGALAFMMAGAGTALGTWTSVGF 1740
DB 1681 SCVPAFIAGITTPPLPHKIKNFLSLFGGALASKLTDPARGALAFMMAGAGTALGTWTSVGF 1740
QY 1741 VFDMLGGVAAAASSTACLTFCILMGWPTMDQIAGLVYSAPNPAAGVGVYLSACAMFALT 1800
DB 1741 VFDMLGGVAAAASSTACLTFCILMGWPTMDQIAGLVYSAPNPAAGVGVYLSACAMFALT 1800
QY 1801 AGPDHWPNRLLTMLARSNTVCNEYFIATRDIRKILGILEASTPWSVISACIRWLHTTPE 1860
DB 1801 AGPDHWPNRLLTMLARSNTVCNEYFIATRDIRKILGILEASTPWSVISACIRWLHTTPE 1860

RESULT 4

Q8JKE4

ID Q8JKE4

AC Q8JKE4;

PRELIMINARY;

PRT; 1925 AA.

QY 1861 DDCLIAWGLEIMQYVCNFFVICFNVLKAGVQSMVNI PGCPFFYSCQKYGKGPWIGSMQLQ 1920
DB 1861 DDCLIAWGLEIMQYVCNFFVICFNVLKAGVQSMVNI PGCPFFYSCQKYGKGPWIGSMQLQ 1920
QY 1921 ARCPGCAELIFSVEENGFAKLYKGPRTCNSYWRGAVPVNARLCSARPDPTDWTSLVYNYG 1980
DB 1921 ARCPGCAELIFSVEENGFAKLYKGPRTCNSYWRGAVPVNARLCSARPDPTDWTSLVYNYG 1980
QY 1981 VRDYCKYEKMGDHI FVTAVSSPNVCFQVPPTLRAAAVADGVQVQCYLGPCKTPTWTTSAC 2040
DB 1981 VRDYCKYEKMGDHI FVTAVSSPNVCFQVPPTLRAAAVADGVQVQCYLGPCKTPTWTTSAC 2040
QY 2041 CYGPDGKGKTVKLPFRVDGHTPGVYRMQLNRDALETNDCNNTNTPSDEAAVSALVFKEQ 2100
DB 2041 CYGPDGKGKTVKLPFRVDGHTPGVYRMQLNRDALETNDCNNTNTPSDEAAVSALVFKEQ 2100
QY 2101 LRRTNQLLEIASAGVDTTKLPAPSI EEVVYRKQFRARTGSLTLPPPPRSVPGVSCPESL 2160
DB 2101 LRRTNQLLEIASAGVDTTKLPAPSI EEVVYRKQFRARTGSLTLPPPPRSVPGVSCPESL 2160
QY 2161 QRSPLGEGPSNLPPSPVLQOLAMPMLLGAGECNPFTAIGCAMTETGGDDDLPSYPKK 2220
DB 2161 QRSPLGEGPSNLPPSPVLQOLAMPMLLGAGECNPFTAIGCAMTETGGDDDLPSYPKK 2220
QY 2221 EVSEWSDSESWSTATTASSYVTGPPYKPIRGKDS TQSAPAKRPTKKLKGSEFSCMSYTW 2280
DB 2221 EVSEWSDSESWSTATTASSYVTGPPYKPIRGKDS TQSAPAKRPTKKLKGSEFSCMSYTW 2280
QY 2281 TDVLSFKTASKLSATRAITSGFLKQSLVYVTEPROABL KOKVTINRQPLFPSPVHKQ 2340
DB 2281 TDVLSFKTASKLSATRAITSGFLKQSLVYVTEPROABL KOKVTINRQPLFPSPVHKQ 2340
QY 2341 VRLAKEKASKVGVWMDYDEVAATHPSKASHITGLRGTDVRS GAARKAVLDLQKVEA 2400
DB 2341 VRLAKEKASKVGVWMDYDEVAATHPSKASHITGLRGTDVRS GAARKAVLDLQKVEA 2400
QY 2401 GEIPSHYRQTVIVPKEEVFKTPQKPTKPPRLISYPHLEMRCEYKMYGVQVAPDVVKAV 2460
DB 2401 GEIPSHYRQTVIVPKEEVFKTPQKPTKPPRLISYPHLEMRCEYKMYGVQVAPDVVKAV 2460
QY 2461 MGDAYGFVDRTRVKRLLSMWSPDAVGATCDTVC FDSITIPEDIMVETDIYSAAKLSDQH 2520
DB 2461 MGDAYGFVDRTRVKRLLSMWSPDAVGATCDTVC FDSITIPEDIMVETDIYSAAKLSDQH 2520
QY 2521 RAGIHTTARQLYAGCPMIAYDGREIGYRRCRSSGVYTTSSNSLTCWLKVNAAEQAGMK 2580
DB 2521 RAGIHTTARQLYAGCPMIAYDGREIGYRRCRSSGVYTTSSNSLTCWLKVNAAEQAGMK 2580
QY 2581 NPFLICGDDCTVIWKSAGADADKQAMRVFASMMKVMGAPQDCVPQPKYSLEELTSCSN 2640
DB 2581 NPFLICGDDCTVIWKSAGADADKQAMRVFASMMKVMGAPQDCVPQPKYSLEELTSCSN 2640
QY 2641 VTSGITSGKPYFLTRDPRIPLGRCSAEGLYNPSAAWIGYLIIHHYPCLWVSVLAVHF 2700
DB 2641 VTSGITSGKPYFLTRDPRIPLGRCSAEGLYNPSAAWIGYLIIHHYPCLWVSVLAVHF 2700
QY 2701 MEQMLFEDKLPETVTFDYGKNTVPVEDLPSII TAGVHGIEAFSVRYTNAEILRVOSL 2760
DB 2701 MEQMLFEDKLPETVTFDYGKNTVPVEDLPSII TAGVHGIEAFSVRYTNAEILRVOSL 2760
QY 2761 TDMTMPPLRAWKKARAVLASAKERGGAHAKLARFLMWHATSRPLDLDKTSVARYTTFN 2820
DB 2761 TDMTMPPLRAWKKARAVLASAKERGGAHAKLARFLMWHATSRPLDLDKTSVARYTTFN 2820
QY 2821 YCDVYSPBGDVFTTPQRLQKFLVKYLAIVFALGLI AVGLAIS 2864
DB 2821 YCDVYSPBGDVFTTPQRLQKFLVKYLAIVFALGLI AVGLAIS 2864

01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Non-structural polyprotein.
OS Hepatitis GB virus B.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
OX NCBI_taxid=39113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22092527; PubMed=12097587;
RX DOI=10.1128/JVI.76.15.7736-7746.2002;
RA De Tonassi A., Pizzuti M., Graziani R., Sbardellati A., Altamura S.,
RA Paonessa G., Traboni C.;
RT "Cell clones selected from the Huh7 human hepatoma cell line support
RT efficient replication of a subgenomic GB virus B replicon.";
RL J. Virol. 76:7736-7746(2002).
DR EMBL: AJ428955; CAD21957.1; -.
DR HSSP; P26664; 1HEI.
DR MEROPS; U39.001; -.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003958; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR000745; HCV NS4a.
DR InterPro; IPR001490; HCV NS4b.
DR InterPro; IPR002868; HCV NS5a.
DR InterPro; IPR002166; HCV_RdRP.
DR InterPro; IPR004109; Peptidase_S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF01506; HCV_NS5a; 1.
DR Pfam; PF00998; Viral_RdRP; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Polypeptidein.
SQ SEQUENCE 1925 AA; 208751 MW; 5B7D628413119C72 CRC64;
Query Match 66.6%; Score 10238; DB 2; Length 1925;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1922; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 941 APFTLQCLSERGTLISAMAVMTGIDPRWTGTITFRLGSLATSYMGFVCDNVLYTAHGSK 1000
Db 2 APFTLQCLSERGTLISAMAVMTGIDPRWTGTITFRLGSLATSYMGFVCDNVLYTAHGSK 61
Qy 1001 GRRLAHPTGSHIPTVDANDQDIYQPPCGAGSLTRCSCGETKGLVTRLGSLVEVNSK 1060
Db 62 GRRLAHPTGSHIPTVDANDQDIYQPPCGAGSLTRCSCGETKGLVTRLGSLVEVNSK 121
Qy 1061 DPYWCVCALPMVAKSGGAPILCSSHGHVIGMFTAAARNSGSVQIRVRPLVCAGYHPQ 1120
Db 122 DPYWCVCALPMVAKSGGAPILCSSHGHVIGMFTAAARNSGSVQIRVRPLVCAGYHPQ 181
Qy 1121 YTAHATLDTKFTVPNEYSVQILIAPTGSGKSTKLPLSYMQEYKLVNLPNSVATTASMPK 1180
Db 182 YTAHATLDTKFTVPNEYSVQILIAPTGSGKSTKLPLSYMQEYKLVNLPNSVATTASMPK 241
Qy 1181 YMHATYGVNPNYCNKCTNTGASLTSTYTYGMYLTGACSRNYDVIICDECHATTATTVLG 1240
Db 242 YMHATYGVNPNYCNKCTNTGASLTSTYTYGMYLTGACSRNYDVIICDECHATTATTVLG 301

Qy 1241 IGKVLTEAPSKNRLVVLATATATPPGVIPTPHANITEIQLTDEGTIPHGKKIKKENLKKG 1300
Db 302 IGKVLTEAPSKNRLVVLATATATPPGVIPTPHANITEIQLTDEGTIPHGKKIKKENLKKG 361
Qy 1301 RHLIFEATKKHCDLANELARKGITAVSYRGDISKIPEGDCVVVATDALCTGYTGD 1360
Db 362 RHLIFEATKKHCDLANELARKGITAVSYRGDISKIPEGDCVVVATDALCTGYTGD 421
Qy 1361 SVYDCSLMVEGTCVLDLDPFTTMGVRVCGVSALVKGORRGRTGRAGIYVYVDSGCTPS 1420
Db 422 SVYDCSLMVEGTCVLDLDPFTTMGVRVCGVSALVKGORRGRTGRAGIYVYVDSGCTPS 481
Qy 1421 GMVPECNIVAPDAKAWYGLSSTEATQITLDYRTQPLGAIGNLDEWADLFSVNPPEP 1480
Db 482 GMVPECNIVAPDAKAWYGLSSTEATQITLDYRTQPLGAIGNLDEWADLFSVNPPEP 541
Qy 1481 SFVNTAKRTADNVLLTAAQLQLCHQYGAAPNDAPRWQGRARLKGKPCGVLRWLDGADAC 1540
Db 542 SFVNTAKRTADNVLLTAAQLQLCHQYGAAPNDAPRWQGRARLKGKPCGVLRWLDGADAC 601
Qy 1541 PGPEPSEVTRYQMCFTTEVNTSGTAAALAVGVGVAMAYLAIDTFGATCVRRCWSITSVPTGA 1600
Db 602 PGPEPSEVTRYQMCFTTEVNTSGTAAALAVGVGVAMAYLAIDTFGATCVRRCWSITSVPTGA 661
Qy 1601 TVAPVDEEBIVBECASFIPLEAMVAAIDKLSITTTTSPFTLETKLNTFLGPHAAT 1660
Db 662 TVAPVDEEBIVBECASFIPLEAMVAAIDKLSITTTTSPFTLETKLNTFLGPHAAT 721
Qy 1661 ILAIIEYCCGLVLTLPDNPFCVCFATAGITTPHPKIKMFLSLFGGAIASKLTDARGAL 1720
Db 722 ILAIIEYCCGLVLTLPDNPFCVCFATAGITTPHPKIKMFLSLFGGAIASKLTDARGAL 781
Qy 1721 AFWMAGAAGTALGTWTSVGVFDMGLGGYAAASSTACLTFFKCLMGEMWTDQLAGLVTSF 1780
Db 782 AFWMAGAAGTALGTWTSVGVFDMGLGGYAAASSTACLTFFKCLMGEMWTDQLAGLVTSF 841
Qy 1781 NPAAGVGVLSACAMFALTATAGDPDHPNRLTLMARSNTVCNEYFIATRIDIRKILGILE 1840
Db 842 NPAAGVGVLSACAMFALTATAGDPDHPNRLTLMARSNTVCNEYFIATRIDIRKILGILE 901
Qy 1841 ASTPWSVISACIRWLHTPTEDDCGLIAWGLEIHWYVCNFFVICFNVLKAGVQSMVNLPGC 1900
Db 902 ASTPWSVISACIRWLHTPTEDDCGLIAWGLEIHWYVCNFFVICFNVLKAGVQSMVNLPGC 961
Qy 1901 PFYSCQKGYKGPWIGSMQARCPGCAELIFSVENGFAKLYKGPRTCNRYWAGVAVPNAR 1960
Db 962 PFYSCQKGYKGPWIGSMQARCPGCAELIFSVENGFAKLYKGPRTCNRYWAGVAVPNAR 1021
Qy 1961 LCGSARPDPTDWTSLVVNYGVDRDYCKYEKMGDHI FVTAVSSPNVCFPTQVPTLRAAVD 2020
Db 1022 LCGSARPDPTDWTSLVVNYGVDRDYCKYEKMGDHI FVTAVSSPNVCFPTQVPTLRAAVD 1081
Qy 2021 GVQVQCYLGPBKTWTTTACCYGDGKGTVKLPFRVDGHTPGVRMQLNLDALLETNDN 2080
Db 1082 GVQVQCYLGPBKTWTTTACCYGDGKGTVKLPFRVDGHTPGVRMQLNLDALLETNDN 1141
Qy 2081 STNTPSDEAAVSALVPKQLRNLLEAI SAGVDITTKLPAPSI EEEVVRKQFRARTG 2140
Db 1142 STNTPSDEAAVSALVPKQLRNLLEAI SAGVDITTKLPAPSI EEEVVRKQFRARTG 1201
Qy 2141 SLTLPPPRSPVPGVSCPESLQSDPLLEGPNLPPSPVQLQAMPMLLGAGECNPFTTAIG 2200
Db 1202 SLTLPPPRSPVPGVSCPESLQSDPLLEGPNLPPSPVQLQAMPMLLGAGECNPFTTAIG 1261
Qy 2201 CAMTETGGDDDLPSYPPKKEVSEWSDESSTATTASSYVTGPPYPKIRGKDSQTSAPAK 2260
Db 1262 CAMTETGGDDDLPSYPPKKEVSEWSDESSTATTASSYVTGPPYPKIRGKDSQTSAPAK 1321
Qy 2261 RPTKKLKGSEFSCMSYTWTDVISPKTASKVLSATRAITSGFLKQKSLVTVTPRAEL 2320
Db 1322 RPTKKLKGSEFSCMSYTWTDVISPKTASKVLSATRAITSGFLKQKSLVTVTPRAEL 1381
Qy 2321 RKQVTTINRQPLFPSPSYHKQVRLAKEKASKVGVWMDYDEVAHAHTPSKSAKSHITGLRG 2380

Db 525 GVPTYSHGENETDVLINSTRPRGAWFGCTWMNGTGFTKTCGAPPCRIRDRDNSTLDLL 584
Qy 439 MGTDAVNDTRNTYACGVTPWLT-----TAMHNGSALKLAILQ-----YPGSKEMFX 486
Db 585 CPTDCFRKHDPDTYIKGAGPWLTPCLIEYPRLMHYPCTVNTFIKVRMYVGVGE--- 641
Qy 487 PHNWSGHLYF-----EGSDTPIVYFDPVNSTLLPDRWARLPPTPPVVRGS 534
Db 642 --HRMSAACNFTRGDRCLRDRDQOQSLH-----ST-----TEWAVLPCS----- 682
Qy 535 WLQVPOGFYSVDKDLATGLITKDKAMKNQVLYSATGALSITGVTTKAVVLILLGLCSK 594
Db 683 -----FSDLPALSTGLMHLHQNIVDVQVLYGLSPAVTRYIVKWEVVVLLFLLADAR 734
Qy 595 YLILAYLCLSLCFGRASGYPLRPLPSQSLQAGWDVLSKAQVAPFALIFFICYLR 654
Db 735 --VCACLWMLI-----ILQBAEALEKLI----- 757
Qy 655 LRYAALLGFVPMAGLPLTFFVAAAQPDYDWWVRLLVAGLVLMAGNRGHRILLVGP 714
Db 758 -----LHSASAASANGPLWFFIFFTAA-----WYLGKRVVPVATYS-----VLGL 797
Qy 715 WPLVALLTLHLVTPASAFDEITIG--GLTIPPVVALVMSRFGFEAHLPRCALVNSYL 772
Db 798 WSP--LLLVLALPOQAYALDTAEQELGLVLILAIISITPLT--PAYKILSRSVWMLSYM 853
Qy 773 W-----QRW-----ENFW--NVTLRPERFFLV---LVCPPGATYDALVTFCVC 811
Db 854 LVLAEQIQQWVPLEARGGRDGIWAAILHPLRPLVEVTKWLLAILGSAY----- 904
Qy 812 HVALLCUTSSAASPFGTDSRVRAHRM-----LVRLGKCHAWSHYVUKFFLLVPE--NGV 865
Db 905 ---LLKASLARVPYF-----VRAHALLRVCTLVR-----HLAGAKYI-QMLLIITLGRWGT 951
Qy 866 FFYKHLHGDVLPNDFAKLPQ-----EP--PFPEEGKARVYRNGRELAC 909
Db 952 IYIDHLS-----PLSTWAAOGLRDLAVAVEPVVFPSPMEKKYIVNGAE--TVAC 997
Qy 910 GDTVDGLPVVARLDGLVAGLAMPD-----GWAITAPFTLQCLSERGTLISAMAVMTGI 964
Db 998 GDILHGLPVSNRGLKEVLLG---PADSVTSKGWKLAPITAYTQOTRGLLGAIVVSLTR 1054
Qy 965 DPRWTGTIFRLGLSATSYMGFVCDNVLYTAHHSKGRRLAHPTGSHPTVDAANDQDI 1024
Db 1055 DKNEQAGQVQLSSVTSFGLTSGVLWTVYHGAGNKTLAGPKGPVTQMYTSAEGLVG 1114
Qy 1025 YOPCGAGSLTRCSGETKGVLTRELGLSVEVNSKDDPYMCVCALPKAVAKSSGAPIL 1084
Db 1115 WPSPPGTKSLDPCCGAVDLVLTNRNADVIPVRKDRDRGALLSPRPLSTLKGSSGGPVL 1174
Qy 1085 CSSGHVIGMFTA---ARNSGSVSQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYSVQI 1141
Db 1175 CPRGHAVGLPRAACVARGVAKSIDFVPVESLAIATRTPSFSDNS--APPVPTQYQVY 1231
Qy 1142 LIAPTGSKSTKLPLSYMQEYKVLVNLNPSVATTASMPKYNHATYGVNPNCFYNGKCTNT 1201
Db 1232 LHAPTGSKSTKVPAAVASQYKVLVNLNPSVAATLFGAYMSKARHNPINRTGRTVTT 1291
Qy 1202 GASLTYSTYGMYL--TGACSRN--YDVIICDECHADTATVILGKVLTEAPSKNVLAVLA 1259
Db 1292 GDPITYSTYGFANGGCSAGAYDVIICDECHSDVATDTILGIVLDOAETAGARLVVLA 1351
Qy 1260 TATPPGVIPTPHANITBIQLTDEGTIPFHGKKIKEENLKKGRHLIFBATKKGCDLANEL 1319
Db 1352 TATPPGVTTPHNSINEVALGHEGEIIFYGKAIPLAIFRGRHLIFCHSKKCDLAAAL 1411
Qy 1320 ARKGITAVSYRGCDSKIP--EGDCVVVATDALCTGTGDFDSYVDCSLMWEGFCHVDLD 1378
Db 1412 RGMGNVAVYRGLDVSVIPQGDVVVVVATDALMTGVTGDFDSVIDCNVAVTQIVDFSLD 1471
Qy 1379 PTFMGVRCVSVIAIVGQRGRTRGRAGIYVYVDCSTPSGMVPECNIVEAFDAKAW 1438
Db 1472 PTFITTTQTVPDVAVSRQRGRTRGRGLGIYRYVSSGERPSGMFDSVILCECYDAGAAW 1531

Qy 1439 YGLSSTEAQITLDYTRTQPGLPALGANLNDWADLFS--MVNPEPSFVNTAKRTADNYVLLT 1497
Db 1532 YELTPAETTVLRLEYFNTPLGVCQHLEFWEAVFTGLTHIDAHFLSQTQGGSDNPAYLT 1591
Qy 1498 AAQOLQCHOVGYAAPNDAPRWQCARLGKPCGVLRWLDGADAC-----PGPEP----- 1545
Db 1592 AYQATVCAR-----AKAPPSWD-----VWKK-----CLTRUKPLTGTGTPLLYR 1631
Qy 1546 -----SEVTRY-----QMCFTEVNTSGTAALAAGVGVAMAYLAIDTFGATCVRRC 1590
Db 1632 LGAVTNEVTLTHPTKYIATCMQADLEIMTS--TWLAGGVLAAVAAYCLATGCVSIIIGRI 1690
Qy 1591 WSITSVPTGATVAPVDEBEI-----VEECASFPLP--EAMVAAIDKJKSTI-----TT 1637
Db 1691 HLNDQV-----WVAP--DKEVLYEAFDEMEBCSSKAALIEEQRIAEMLKSKIQLLOQAT 1744
Qy 1638 TSPFLETALE-----KLNTPLGPHAAATILAIIEVCCGLVTLTPNPPFASCVPFAITAGTTP 1693
Db 1745 RQAOIQPAIQSGWPVKLEQFWAKHMNFISGIQYLAGLSTLPGNPAVASMMAFSAALTSP 1804
Qy 1694 LPHKIKNFLSLFGAIAASKLTDARGALAFMMAGAAGTALGTWTSVG---FVFDMLGGYAA 1750
Db 1805 LPTSTILLNIMGWLASQIAPPAGATGFVVGSLVGAUG--SIGLGKILVDILAGYA 1861
Qy 1751 ASSTACLTFKCLMGWPTMDQLAGLVYAFNPAAGVVGVLSACAMFALTITAGPD--HWP 1808
Db 1862 GISGALVAPKIMSGEKPSVDVNNLLPAILSPGALVGVICAAILRRHRVGQEGAVQW 1921
Qy 1809 RLITMLARSNTVCNEFIATRIDRRKILGILEASTPWSVISACIRWLHTTDEDDCGLI-- 1866
Db 1922 RLIAFASRGNHVAPTHYVAESDASQRMVQLSLLT-----ITSLLRRLLHTWITDCPVPCS 1977
Qy 1867 -AWGLEIWOVCVNFVFCENVLKAGVQSMVNIPEGCPYSCQKGYKGPWISGMLQARCP 1925
Db 1978 GSWLRDWDWVCSILIDFKWLSS--KLLPKMGLPFIQCKGYRGVWAGTGVMTTRCPC 2035
Qy 1926 GABLIFSVENGFAKLYKGPRTCSNYRGVAPVNARLCSARP-DPTDWTSLVNVYGRDY 1984
Db 2036 GANISGHVRMGTMKI--TGPKTCLNLWQCTFPINCYTEGCPVKPPPNKYKTAIWRVAASEY 2094
Qy 1985 CKYEKMGDHFVTAVASPNVCFQVP---PTLRAAVADVGVQVQCYLGEPKTPWTSNACC 2041
Db 2095 VEYTOHGSFYSVGLTSDNL---KVCQVPAPEFFSWVDVQIHRFAPIP----- 2141
Qy 2042 YPGDGKGTVKLPRVDGHTPGVRMQLNRDALETNDCNNTNTPSD---EAAVSALVFK 2098
Db 2142 -GPFPRD---EVTFTVGLNSLVVGSQPCDPEDTEVLASMLTDPSSHITAEAAARLARG 2197
Qy 2099 QELRRTNQLLEAISA-----GVDTTKLPA----- 2122
Db 2198 SPFSQASSASQLSAPSLKATCTTHRMAYDCDMVDANLFGMGDVTRIESDKVIVLDSLD 2257
Qy 2123 -----PST--EEVVYRKQFRARTGSLTLPP--PPRSVPQVSCP--ESLQSRSDPLE 2167
Db 2258 TMTVEDDRPEPSVPSEYLVRKRF-----PPALPPWARPDYNPFVETWKR----- 2303
Qy 2168 GPNLPPS-----PPVLQAMPMLLIGACENPFTAIGCAMTE----- 2205
Db 2304 -PGYEPTVLGCALPPTPQTPVPPPPRRRAKVLTDQNVGEVILREMAKVLSPLODHNDSG 2362
Qy 2206 -----TGGPDDLPSPPKKEYSEMSDESWSATTASSYVTPGPPYPIRGK----- 2251
Db 2363 HSTGADTGG-----DSVQPSDE-----TAASEAGSSSSMPLEGEPCDPDLF 2406
Qy 2252 DSTQSPAPAKR-----PTKKLGKSEFSCSMSYTWTD--VISFKTASKVLSATR 2297
Db 2407 EPAESAPSEGECEVIDSDSKSWATVSDQEDSVICCSMSYSWTGALITPCGPEEKLPIN 2466
Qy 2298 AITSGFLKQSLVVTPEPRDAELRKOKVTINRQPLPPSPSYHKOVRLAKEKASKVGVWMD 2357
Db 2467 PLNSLMRPHNKVYITTSRSASLRKAKVTDFRVQVLDHAHVDVSLQDVRAASKVSARLLS 2526

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QY 2358 YDEVAHTPSKASHITGLRGTDVRSGAARKAVLDLQKCEAGEIPSHYR-QTIVIPKE 2416
D 2527 IEEACALTPPHSAKRY-GFGAKEVRS-LSRRVNHHSVWEDLLEDQHTPIDTVMKXN 2584
QY 2417 EVFVTKPKTKPPRLISYPHLENMRCVEKMYGQVADPVKAVMGDAYGF-VDPRTVK 2475
D 2585 EVFCVDPKAGGKPPARLIVYDPLGVRCVKMALYDIAQKLPKAIMGPSYGFQSPAEVD 2644
QY 2476 RLLSMW--SPDAVGATCTVCFDSTITPEDIMVEDDIYSAAKLSQHRAGHTIARQLYA 2533
D 2645 FLLKAWRSKKDPMGFSYDTRCFDSTVTERDINTESIIYQACSLPEARTVHSILTERLYV 2704
QY 2534 GGPMIAYDGRIGRYRCRSSGYTTSSNSLTCWLKVNAAAEQAGMKNPREFLICDDCTV 2593
D 2705 GGPWNSKQSGCYRRCRASGVFTTSMGNTWTCYIKALAAKCAAGIMPMWLCGDDLVV 2764
QY 2594 IWKAGADADQAMRVFASWKMVGAPQDQVQPKYSLEELTSCSNVTSITGSKGPKY 2653
D 2765 ISESQNEEDERNLRAFTTEAMTRYSAAPPDLPPEYDLELITSCSNVSVVALDSRGRRY 2824
QY 2654 FLTRDPRIPLGRCSAEGLYNPSAAWIGVLIHHYPCLVSRVLAVHFEQMLFEDKLPET 2713
D 2825 FLTRDPTTPTTAAWETVRRHSVNSWLGNIQYAPTIVRMVIMTHFFSILLAQDTLNQ 2884
QY 2714 VTFWYGNKYTVPVVEDLPSIIAGVHGIEAFSVRYTNAEILRVSOGLTDMTPPLRAWRK 2773
D 2885 LNFEMYGAVYSVNPDLPAIERLGLDAPSLHTSYSPHELSEVAATLKLGAAPPLRAWKS 2944
QY 2774 KARAVLASAKRGGGAHAKLAPLL-WHATSR-----PLPDLKTSVARVTRTNYCDVSPS 2828
D 2945 RARAVRASLIAQGGRAATCGRYLFENAVKTKLPLPEASRLDLSGNFT-----VGAGG 2999
QY 2829 GDVFTTPORRLQKFLKYLAVIVFALGLIANGLAI 2863
D 3000 GDYHSVSHARPRL-----LLCLLLSLVGVGI 3027

RESULT 6
Q77716 PRELIMINARY; PRT; 3033 AA.
ID Q77716
AC Q77716;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OC NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanabe Y., Nagayama K., Enomoto N., Izumi N., Tazawa J., Sato C.,
RA Watanabe M.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY232736; AAP55691.1; -.
DR HSSP; O8JYS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008036; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0006508; F:structural molecule activity; IEA.
DR GO; GO:0006350; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR002522; HCV_capsid.
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DR InterPro; IPR002521; HCV_core.
DR InterPro; IPR002519; HCV_env.
DR InterPro; IPR002531; HCV_NS1.
DR InterPro; IPR000745; HCV_NS4a.
DR InterPro; IPR001490; HCV_NS4b.
DR InterPro; IPR002868; HCV_NS5a.
DR InterPro; IPR002166; HCV_RdRP.
DR InterPro; IPR004109; Peptidase_S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_Core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF01506; HCV_NS5a; 1.
DR Pfam; PF00998; Viral_RdRP; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
SQ SEQUENCE 3033 AA; 239956 MW; D58C8C087216598C CRC64;

Query Match 21.5%; Score 3306.5; DB 2; Length 3033;
Best Local Similarity 30.3%; Pred.No.1.1e-205;
Matches 994; Conservative 428; Mismatches 1182; Indels 673; Gaps 110;

QY 8 TSPVPAPTRKTKQTQASYPVSIK-----TSVERGORAKKVKQDARPR 51
D 3 TNPQPKTKRNTNR---POQVFPGGQIVGVYLLPRRGRPLGRVARTKTSERSOPR 59
QY 52 NYKIAGHDGLQTLAQAALPAH-----GWGRODPRHKSRL 87
D 60 GRQPIPKDRSTGSKSGKFCYPWPLYNGECGWAGWLLSPRGSRPRTGPTDPRHRSNL 119
QY 88 GILLDPFLGIGDVTHTPLVGLVAGAVRVPVQIVRLLEDGVNWTG---WFGVHLFV 144
D 120 GKVIDTVCGFADLMGIVPVVGADV-GGVARALAHGVRLVDGYNATGNLPGCSFSIFL 178
QY 145 VCLLS-LACPCSGARVTDPTNTLTILNCCORNOVIYCSPTCLHEPCVCICADE----- 198
D 179 LALLSCVTVPVSAVEVRN-ISSYYATNDCSNNSITWQSGAVLHLPQGVPCENDNGTLR 237
QY 199 CWPANPYISHPSNWTGTSFLADHIDFVMGALVTCDALDIGELCGACVLVGDMLVRHWL 258
D 238 CWIQVTNVAVKYHGALTHN-LRTHVDMIVMAATVCSALYVDVCGAVMIVSQAFIISQ 296
QY 259 IHIDLNETGTCYLEVPTGIDPGFLGFGIMMAGKVEAVIFLTKLASQVPIYAIATWSSVHY 318
D 297 HH---NFTQECNCSIYQGRITGHRMAMDMMLNWSPTLTMLIAYAAARVPELALVFGGHW 353
QY 319 LAVGALLIYASRGKWKYQLLALMLYI-----EATSG-----NP 351
D 354 GVVFGLAYFSMQGAWAKVIAILLVAGVDADTYASGAQAGRVTSGFAPISFGPAKQINIL 413
QY 352 I-----RVPTGCS-----IAEF-----CSPLMIPC----- 371
D 414 IKTNGSWHINRTALNCNDSLNTGFIASLYVQHFNSSGCPERMSSRCGLDDFRIGWGTLE 473
QY 372 -----PCHSYSENV-SEVICYSPKWTPTITLEYNN-----SIS 404
D 474 YETNVTNDEDMRPYCMWHYPPKPCIGIVPARTVCGVPYCFPS---PVVVGTTDROGAPYS 530
QY 405 WYPTTIPGARGCMVKFKNNT-----WGC-----CRIR---NVPSYCT 438
D 531 W-----GENETDVLLNSTRPPRGAWFGCTWMNGTGFTKCGAPPKIRRDYNTSLDLL 584
QY 439 MGTDAVWMDTRNTYEACGVTPWLT-----TAMHNGSALKLAILQ---YPGSKEMFK 486
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Db 585 CPTDCPRKHDPATYIKCAGPWLTPRCLVDYPRYLWHYPCVTNPTIFKVRMYIGSVB--- 641
Qy 487 PHNMSGHLYF-----EGSDTPIVYFYDPVNSTLLPPERWARLPCTPPVVRGWS 535
Db 642 -HRSAAACNFRGRDRCLEDRDQOQSPLH-----ST-----TEWAVLPCS----- 682
Qy 536 LQVPGFYSDVKJATGLITKDKAMKNYQVLYSATGALSITGVTTKAVVILILGLGSKY 595
Db 683 -----FSDLPALSTGLLHLHQNIQVQVLYGLSPAVTRYIVKWEVWVLLFLLLADAR- 734
Qy 596 LILAYLYCLSLCFGRASGYPLRVPVPSQYLOAGWDVLSKAQVAPPALIFPICCYLRCL 655
Db 735 -ICACLMWLI-----ILQAEAALEKLI-----L 758
Qy 656 RYAALLGVPMAAGLPLTFFVAAAAOPVDVWVRLVAGLVWAGNRGRHRIALLVGPW 715
Db 759 HSAS-----ASANGL-LWFFIFFTAA-----WYLKGRVVPVATYS-----VLGLW 798
Qy 716 PLVALLTLHLVTPASAFDTEIIGGLTIPPVVALVMSRFGFFAHLPRCALVNSYLW-- 773
Db 799 SF--LLLVLALPQAYALNVAEQGELGLVWIVISIFTLTPAYKILLSRSVWMLSYMLVL 856
Qy 774 -----QRW-----ENWFN-NVTLRPRRFLV--LVCFPGATYDALVTECVCHA 814
Db 857 AEAQIOQWVPPLEARGGRDGIWVAVILHPRLVFEVTKWLLAILGSAY----- 904
Qy 815 LLLCTSSAASFFGTDSDRVRAHRM-----LVRLGKCHAWSHYLVKFFLVFGENGVFFYK 869
Db 905 LKASLLRVYF-----VRAHALLRVCTVLR-----HLAGAYIQMLITVGRWTGTIYD 955
Qy 870 HLHGDVLPNDPASKLPQ-----EP--FPPFEGKARVYRNEGRRLACGDV 913
Db 956 HLS-----PLSTAAOGLRDLAVAVPWFSPMEKKVIVNGAE--TVACGDIL 1001
Qy 914 DGLPVARLGLVFAGLAMPD-----GWAITAPFTLOCLSERGTLSAMAVMTGIDPRT 968
Db 1002 HGLFVSARLGRVLLG---PADSYTSKGWKLAPITAYAOQTGRLLSAIVVSLTRDKNE 1058
Qy 969 WTGTIFRLGSLATSYMGVPCDNVLYTAAHSGKGRRLAHTPSIHIPITVDAANDQDIQPP 1028
Db 1059 QAGQVQLSSVTQSLFGTISGVLTWYVHGAKNTLAGKPGVPTQMTYSAEGLVGPSP 1118
Qy 1029 CGAGSLTRCSCGETKGYLVTRGLSLVEYNKSDDPYWCVCAGPALPMAVARGSSGAPILCSSG 1088
Db 1119 PGTKSLDPTCTGAVDLVLTNRNADVIPURRKDRRGALLSPRLSTLKGSSGGPVLCPRG 1178
Qy 1089 HVIQMFYA---ARNSGVSQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYYSQILIA 1145
Db 1179 HAVGLFRAAVCARGVAKSIDIPVESLDIAARTPSFSDNS---TPPAVPTQYQVGYLHAP 1235
Qy 1146 TSGSKSTKLPLSYMOEKYEVILVLPNSVATTASMPKYMATYGVNPNCFYENGKCTNTGASL 1205
Db 1236 TSGSKSTKVPAAYSAGYKVLVLPNSVAATLFGAYMSKAGINPNTRTGVTVTGDPPI 1295
Qy 1206 TYSTYGMVLT-GAGSRN-YDVIIICECHATTATVLTGIGKVLTEAPSKNRLVVLATATP 1263
Db 1296 TYSTYKFLADGGCSAGAYDVIICECHSVDTTILGIGTGLVLDQAEATAGARLVVLATATP 1355
Qy 1264 PGVITPTPHANTITETQTDGTIPHGKKIKKEENIKKGRHLIPEATYKHCDBELANELARK 1323
Db 1356 PGTVTTPHNSINEEVALGHEGIPFYGKAIPLASIKGGRHLIFCHSKKKCDBELAAALRGMG 1415
Qy 1324 ITAVSYRGCDISKIP-EGDCVAVATDALCTGYTGDPSVVDVCSLMVEGTCHVDLDPDTFT 1382
Db 1416 VNAVAYHGLDVSVIPTGQDVVVVATDALMTGYTGDPSVDVDCNVAVTQVVDFSLDPTFT 1475
Qy 1383 MGVRCVGSALVKGQRGRGRTGRAGIYIYVYDGSCTPSGMVPECNIVAEAFDAKAWYGLS 1442
Db 1476 ITTQTVPODASVRSQRGRGTGRGLGIYIYVYSSGERPSGMDFSVVLCECYDAGAAMVELT 1535
Qy 1443 STEAQITLDTYRTOPLPAIGANLDEWADLFS-MVNPBPSFVNTAKRTADNVLLTAAQL 1501

Db 1536 PAETTVRLRAYFTNPGLPVCQDHLEFWEAVFTGLTHIDAHFLSQTKGGDNFAYLTAYQA 1595
Qy 1502 QLCHQCYAAPNDAPRMOQARLGKPCGVLRWLDGADAC-----PGPEP----- 1545
Db 1596 TVCAR-----AKAPPPSWD-----VMWK-----CLTRLKPTLTGPTLLYRLGAV 1635
Qy 1546 -----SEVTRY-----QMCFTVNTSGTAAALAVGVGVAMAYLAIDTFGATCVRRCWSIT 1594
Db 1636 TNEVTLTHPTKYIATCMQADLIMTS-TWVLAGGVLAAVAAYCLAT-----GCISII 1697
Qy 1595 S---VPTGATVAPVWDEEII-----VEECASFIPL-EMVAAIDKLKSTI-----TTT 1638
Db 1688 GRHLNDQVVAP--DKEVLYEAFDEMEECASKAALIEEGORMAEMLSKIQGLQLOATR 1745
Qy 1639 SPFTLEALE-----KLNTFLGPHAAATILAIIEYCCGLVTLDPNPFASCVPFAFIAGITPL 1694
Db 1746 QAQDIOAIPAIQSSWPKEQFWAKHMNFISIGIQYLAGLSTLPGNPAPAVASMAFSAALTSPL 1805
Qy 1695 PHIKMPLSLFGGAIASKLTDARGALAFMWAGAAGTALGTWTSVG-----FVPDMLGGYAAA 1751
Db 1806 PTSTTILLNIMGWLASQIAPPAGATGFVVSGLVGAAGV---SIGLGKILVDVLAGYGAG 1862
Qy 1752 SSTACTLFFKLMGEWPTMDOLAGLVTSARFPAAGVGVGLVSACAMFALTTAGPD--HWPNR 1809
Db 1863 ISGALVAFKIMSKEKSPSEVDVNNLLPAILSPGALVGVICAAILRRHVGOGEAVQVMNR 1922
Qy 1810 LLTMLARSNTVCNEYFIATDIRRKILGILEASTPMSVISACIRLWLTHTTDDCGLI--- 1866
Db 1923 LIAPASRGNHVAPHYVAESDASQRTQVLSLT-----ITSLRLRHAWITEDCPVPCSG 1978
Qy 1867 AWGLETHQVYCNFVICFNVLKAGVQSMVNI PCGPFYSCQKGYKGPWIGSMLOARCPG 1926
Db 1979 SWLQIDWMDVCSILADFPKWLSA--KLLPXMPGLPFISQKGYRGVWAGTGVMTTRPCG 2036
Qy 1927 AELIFSVEYENFVAVSSPNVCFQV---PTLRAAAVADVQVQVOCYLGEPKTPMTTSACCY 2042
Db 2096 EITQHSFSYVTLGTSNUL---KVPCQVPAPEFSSWVDGVQVHRFAPIP----- 2141
Qy 2043 GPQCKGKTVKLPFRVDGHTPGVRMLNRDALETNDCNSTNTPSD---EAAVSALVPKQ 2099
Db 2142 GPFFRD---EVTFTVGLNSFWVGQFPCDPEDTEVLASMLTDFSHITAEAAARLARGS 2198
Qy 2100 ELRRTNQLLEAIS-----GVDTTKLP----- 2122
Db 2199 PPSQASSASQLSAPLSLKATCTTKHTAYDCMDVDANLFMGDVTRIESDSKVIIVLSLDS 2258
Qy 2123 -----PSI-EEVVVRKQFRARTGSLTLP--PPRSVPGVSCP--ESLQSDPLEG 2168
Db 2259 MTEVEDDREPSIPEYLIRRRK-----PPALPPWARPDPNPPVIETWKR----- 2303
Qy 2169 PSNLPPS-----PPVLQOLAMP-----MPLLAGECNP 2195
Db 2304 PGVEPPTVLGALPPTLQAPVPPHRRRRRAKVLTDQNVVEGVLREMAKVFSPLOQNDSGH 2363
Qy 2196 FTAIGCANTGTGGPDDLPSYPPKKEVSEWSDESSTATTASSYVTGPPYKPKIGKDSQ 2255
Db 2364 STG-----AUTG---DSVQOPP-----DE--TAASEAGSLSSMPPLEGEGDPDLE 2405
Qy 2256 SAPAKRPTKKLKGSE-----FSCSMYSYTWTD-VISFKTASKVLSA 2295
Db 2406 FEPA-GPAPSEGECEVIDSDSKSWSTVSDOEDSVICCSMSYSWTGALITPCGPEEEKLP 2464
Qy 2296 TRAITSGFLKORSLYVYTEPRDAELRKQKVTINRQPLFPSPYHKQVRLAKEKSKYGVGM 2355
Db 2465 INPLNSLMRFHNKVVYTSRSASLRAKVTDFRVQLDAHYDVLQDVQKQAASKVSA 2524
Qy 2356 WDYDEVAHPTSKAKSHITGLRGTQDVRSKAARKAVLDLQCKVEAGEIPSHYR-QTVI 2414
Db 2525 LSVEEACALTPPHSAKSRY-GFGAKEVRS-LSRRRVNHRISVWEDLLEDQHTPDITDTTMA 2582

Db 2570 EDQHTPIDTTVMKNEVFCVDPKAGKGPAPRLIVVPDLGVRVCEKVALYDIAQKLPKAIM 2629
Qy 2462 GDAYGF-VDPTRVRKLLSMW--SPDAVGATCDTVCFDSTTIPEDIMVETDIYSAAKLSD 2518
Db 2630 GPSYGFQYSPAEVDFLJKAWSKKDPMGFSYDTRCFDSTVTERDIRTEESIYQACSUPE 2689
Qy 2519 QHRAGIHTIAQLYAGGPMIAYDGREIGYRRRCSSGVYTTSSNSLTCWLKVNAAEQAG 2578
Db 2690 EARTVTHSLTERLYVGGPMNTSKGSCGYRRCRASSGVTTSMGNTMTCYIKALAAACKAAG 2749
Qy 2579 MKNPRFLICGDDCTVIKWSAGADAKQAMRVFASMKWVGAPQDCVPQKYSLEBLTSCS 2638
Db 2750 IMPMMLVCGDVLVVISQNEEDERLRAFTTEAMTRYSAAPPGLPRPEYDLELITSCS 2809
Qy 2639 SNVTSGITKSGPYFLTRDRIPIGRCSAEGLYNPSAAMGYLIHHVPCLVWSRVLA 2698
Db 2810 SNVSVALDSRGRYFLTRDPTTPITRAWEVTRHSPVNSWLGNIQYAPTIVWRVIMT 2869
Qy 2699 HFMEQMLFEDKLPTVTFDWTGKNTVPVEDLPSIIAGVHGEAFSVVRYTNAEILRVSQ 2758
Db 2870 HFFSILLAQDTLNQNLFEMYGAVYSVNPDLDPALIERLHGLDAFSLHTYSPHELSRVAA 2929
Qy 2759 SLTDMTMTPLRAWRKARAVLASAKRGGAHAKLARFL-WhatsApp 2813
Db 2930 TLRLGAPPLRAWRKARAVRASLIAQGGRAICGRYLFNMAVTKLKLTLPLPEASRLDL 2989
Qy 2814 ARYTTFNVCVYSPGDFVITPQRLQKFLVKYLAVIVFALGLIAVGLAI 2863
Db 2990 SGWFT-----VGAGGDIYHVSVAHPRL-----LCLLLLSVGVG 3027

RESULT 8
Q77714 ID Q77714 PRELIMINARY; PRT; 3033 AA.
AC Q77714;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
ON NCBI_TaxID=11103;
RX Q8JYS1; 1CW.
RA Tanabe Y., Nagayama K., Enomoto N., Izumi N., Tazawa J., Sato C.,
RA Watanabe M.,
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY232738; AAP55693.1; -.
DR HSSP; Q8JYS1; 1CW.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:RNA-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV NS1.
DR InterPro; IPR000745; HCV NS4a.
DR InterPro; IPR001490; HCV NS4b.
DR InterPro; IPR002868; HCV NS5a.

InterPro; IPR002166; HCV RdRP.
InterPro; IPR004109; Peptidase S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR pfam; PF01543; HCV capsid; 1.
DR pfam; PF01542; HCV core; 1.
DR pfam; PF01539; HCV env; 1.
DR pfam; PF01568; HCV NS1; 1.
DR pfam; PF01538; HCV NS2; 1.
DR pfam; PF02907; HCV NS3; 1.
DR pfam; PF01006; HCV NS4a; 1.
DR pfam; PF01001; HCV NS4b; 1.
DR pfam; PF01506; HCV NS5a; 1.
DR pfam; PF00998; Viral_RdRP; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
SQ SEQUENCE 3033 AA; 329974 MW; 9448C41AFC5BB89E CRC64;
Query Match 21.5%; Score 3303.5; DB 2; Length 3033;
Best Local Similarity 30.2%; Pred.No.1.7e-205;
Matches 993; Conservative 434; Mismatches 1163; Indels 701; Gaps 110;
Qy 8 TSPVAPRTRKNKQTQASYPVSIK-----TSVERGORAKEKVQORDAPR 51
Db 3 TNPKPQRKTRKNTNR---PQDVKPGGGQIVGGVILLPRRPLGLVRATRKTRTSERSQPR 59
Qy 52 NYKIAGIHDGLQTLAQAALPAH-----GWGRODPRHKSRL 87
Db 60 GRQPIPKDRRSTCKSGKPCYPMPLYGNECGWAGWLLSPRGSRTWGPDPDRHRSNL 119
Qy 88 GILDYPLGIVGVTHTTLPVGLVAGVVRPVCQIVRLLEDGVNWTG---WFGVHLFV 144
Db 120 GRVIDTTTCGFADLMGIVPVVGAHV-GGVARALAHGVRLVEDGNYATGNLPGCSFISL 178
Qy 145 VCLAS-LACPCSGARVDPDNTTILNCCORNOVIYCSPTCLHPCGCVCICADE---- 198
Db 179 LALLSCVTVPVSAVEVRN-ISSSYATNDCSNNSITWQLANAVUHLPGCVPCENDNGTLR 237
Qy 199 CWPANPYIHPNSNWTGDSFLADHIDFVMGALVTCDALDIGELCGACVLVGDWL- 254
Db 238 CWIQVTENVAVKRGALTN-LRTHVDMVMAATVCSALYVDVCGAVMIVSQALIVSPE 296
Qy 255 RHWLIHDLNETGTCYLEVPTGIDPGLFGIWMAGKVEAVIFLTKLASQVPAIATWFS 314
Db 297 RH-----NFTQECNGSIYQGHITGHRMAWMDMLNWSPTLTWILAYAAARVPELVLEV 349
Qy 315 SVHYLAVGALTYVASRGKWKYQLLALMLY--IEAT----- 347
Db 350 GGHGTVVFGLAIFYSMQGAWAKVITAILLVAGVDATTYSTGAQAGRAASGIANLFTPGAK 409
Qy 348 -----SGNPRIYPT-----GC 358
Db 410 NIQLINTGSHWIRNTALNCNDSLOTGLASLFTYKSPNSSGCCPERSLSSCRGLDDFRIGW 469
Qy 359 SIABFCSP-----MIPCPCHSYLSENV-SEVICYSKPTRPTL----- 397
Db 470 GTLEYETKVTNDEDMRPYCHWHPKPGCVISAKTVCGPVYCFTPS---PIVVGTTDKQGV 526
Qy 398 -EYN-----NSI-----SWPYTTPGARGCWKPKNNWGC--CRIR---NVPS 435
Db 527 PTYNGNDETDFVLLNSTRPPQGAWFGCTWNGTGF-----TKTCGAPPCKIRRDFNSTL 581
Qy 436 YCTMGTDVAVMNDTRNTYEACGVTPFWLT-----TAWHNGSALKLAILQ---YPSKE 483
Db 582 DLLCPTDCFRKHDPDATYIKGAGPWLTPRCLIVEYPRYRLWHYVCTVNTFIPKVMYVGVE 641
Qy 484 MFKPHNWSGHLYP-----EGSDTPVIVFYDFPNVNSTLLPDRWARLPGTPPVV 531
Db 642 -----HRLSAACNFTGRDRCLEDRDRGQSQSPLLH-----ST-----TEWAVLPCS 682


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Db 2629 MGPSYGFQYSPAERVDLFLKAWGSKKDPMGFSYDTRCFDSTVTERDIRTHESIYQACSLP 2688
Qy 2518 DQHRAGIHTIARQLVAGGPMIAYDQREIGYRCRSGSVYVTTSSNSLTCMLKVNAAAQQA 2577
Db 2689 QEARTVTHSLTERLYVGGPMNTSKQSCGYRCRASGVFTTSMGNTWCYIKALAAKAA 2748
Qy 2578 QMKNPRLICGDDCTVIWKSAGADAKQAMRVFASMMKVMGAPQDQVCPQPKYSLEELTSC 2637
Db 2749 GIVDPVLMVCGDDLVIISQSGNEEDERNLRAFTTEAMTRYSGAPGDLRPRPEVDLELIISC 2808
Qy 2638 SSVNTSGITKSGKPYFLTRDRIPLRGCBSAGLGYNSAAWIGYLIIHHYPCLVWSRVLA 2697
Db 2809 SSVNSVALDSRGRRYFLTRDPTTPTITRAAWETVRHSPVNSWLGNIIOYAPTIVWRVMIM 2868
Qy 2698 VHFMEQMLFEDKLPETVTFDYGKNTYTPVEDLPSIIAGVHGIEAFSVRVYTNAREILRV 2757
Db 2869 THFSLIAQDTLQNLQNFEMWIGAVSYNPDLPAIIRLHGLEAFSLHTYSPELSRVA 2928
Qy 2758 QSLDTMTMPLPRAWKRAVLASAKRRGGAHAKLARELL-WHATSR---PLPDLDKTS 2812
Db 2929 ATLRLKGLAPPLAWKSRARAVRASLIQAQGRAAICGYLFENWAVTKLKLTPLEARELD 2988
Qy 2813 VARTTFNYCDVYSPGQVFTTPQRLQKFLVYKVLAVIFALGLIANGIAI 2863
Db 2989 LSGWFT----VGAGGGDIHFHVSHPARPLL-----LLCILLLSVGVGI 3027

RESULT 9
Q91ZAI PRELIMINARY; PRT; 3033 AA.
AC Q91ZAI;
ID 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Polypeptide.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RC STRAIN=MD2b-1;
RA Itakura J., Nagayama K., Enomoto N., Kurosaki M., Watanabe H.,
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF238486; AAF59945.1; -.
DR HSSP; Q8UYS1; 1CWX.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
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DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
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DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR000345; DEAD_heme_BS.
DR InterPro; IPR001410; DEAD_heme_BS.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV NS1.
DR InterPro; IPR000745; HCV NS4a.
DR InterPro; IPR001490; HCV NS4b.
DR InterPro; IPR002868; HCV NS5a.
DR InterPro; IPR002166; HCV RGRP.
DR InterPro; IPR004109; Peptidase_S29.
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DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF01506; HCV_NS5a; 1.
DR Pfam; PF00998; Viral_RGRP; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
SQ SEQUENCE 3033 AA; 330724 MW; FE04FEC7C385A13A CRC64;

Query Match 215%; Score 3303.5; DB 2; Length 3033;
Best Local Similarity 30.3%; Pred. No. 1.7e-205;
Matches 991; Conservative 447; Mismatches 1176; Indels 653; Gaps 112;

Qy 8 TSPVPAPRTRKXKQTOASYPVSIK-----TSVERGQRAKRVQDARPR 51
Db 3 TNPXP---QRKTRSTNRRPDQVFPGGGQIVGGVYLLPRGRPLGVRAATKTSERSQPR 59
Qy 52 NYKIAGIHDGLQTLAQALPAH-----GWGRDDPRHKSRL 87
Db 60 GRQPIPKDRRSTGSKGPKGYPWPLVYGNCGGWAGWLLSPGRSPRHGPTDPRHRSNL 119
Qy 88 GILDDYPLGWDGVTTHPLVGLVAGAVRVPVQIVRLLEDGVNWTG---WFGVHLFV 144
Db 120 GRVIDTTCGFADLMGVIPVVGAPV-GGVARALAHGVRLVEDGYNATGNLPGCSFSIFL 178
Qy 145 VCLLS-LACPCSGARVTPDPTNTLTILNCCORNVIYCSPTCLHEPGCVICABE----- 198
Db 179 LALLSCVTPVPSAVEVRN-ISSYYATNDCNSSITWLTNAVLHLPQVPCENDNGTLR 237
Qy 199 CWVPANPYIHPNSWTGTDSFLADHIDFVMGALVTCDAIDIGELCGACVLGDMLV----- 254
Db 238 CWIQVTENVAVKRGALTN-LRTHVDMIVMAATVCSALYVGDVCGAVMISQALIVSPE 296
Qy 255 RHMLIHIDLNETGTCYLEVPTGIDPGFLGFGIMWAGVEAVIFLTKLASQVPAIATWFS 314
Db 297 RH-----NFTQCNCISYQGHITGHRMAWMLNWSPTLTMLAYARVPELALEIVF 349
Qy 315 SVHYLAVGALIYYASRGKWYQLLALMLY--IEATSGNPIRVPTGCSIAEFCSP----- 367
Db 350 GGHGVAFLAYFSMQGAWAKVIAILLVAGVDAT-----YSTGAQVGTVSGFAGMFR 404
Qy 368 -----MTPCCHSYLSNVSEVICYSPKW-----RPI-- 395
Db 405 SGRSQNIQLINTGSHWINTALNCNDSLOTGFNASLIFYAKRPNSSGCGPERLSSCRLLD 464
Qy 396 -----TLEYNNIS- -WYPT- - - - - 409
Db 465 FRIGWGTLLEYETNTVNDMDMRPYCWHYPPKPGVSDKTVCGPFYCYTPSPVWVGTSDQ 524
Qy 410 -IP-----GARGCWVFKNNIT-----WGC-----CRIR-----NVPSY 436
Db 525 GVPTYSNGENETDVLINSTRPRGRDREGCTWMDGTGFTKTCGAPPCHIRRDYNSIDL 584
Qy 437 CTMGTDVAVNDTRNTYBACGVTPWLT-----TAWHNGSALKLALQ---YPGSKEM 484
Db 585 CP--TDCFRKHPGATYIKCGAGPWLTPRCVVVDYFYLWHYPCNVNFTIFKVRMYVGVGE- 641
Qy 485 FKPHNWMGSHLYF-----EGSDTPIVYFDVDPVNSTLLPPEWRWRLPGTTPVVR 532
Db 642 ----HRLTAACYFTRGDRCCLEDRDQGSPLLH-----ST-----TEWAVLPCT----- 682
Qy 533 GSWLQVPGQFYSDVKDLATGLITKDKAWKNYQVLYSATGALSATGLTGTVTTKAVVILLGLCG 592
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QY 2542 GREIGYRRCRSGVVTSSNSLTCMLKVNAAEQAGMKNPRFLICGDDCTVIWKSACD 2601
D 2713 GQSCGYRCRAGSVFTTSNGTWTCTYIICALACKAAGIMDPLMVLGDDLVVISESQNE 2772
QY 2602 ADQAMRVFASMMKVMGAPQDCVPQPKYSLBELTSCSSNVTSGITKSGKPYFLTRDPR 2661
D 2773 EDENLRVFEAMTRYSAAPPDLPPEYDLELITSCSSNVSVALDPGRRRYFLTRDPTT 2832
QY 2662 PLGRCSAELGYNESAAMIGYLIIHYPCLWVSRVLAVHFMQMLPEDKLPETVTFDWTGK 2721
D 2833 PITRAAWEVTRHSPVNSWLGNIQVAPTIWVRMVMIMTHFILLSAQDTLNQNLNPFMYGA 2892
QY 2722 NYTVPEVDEPLIIAGVHGIEAFSVVRYTNAETLRVSQSLTDMTWMPPLRAWRKKAVALAS 2781
D 2893 VYSVNPFLDPAIIEHLGDLAFSLHTYSPHELSRVAATLRKLGAPPLRAWRKKAVALAS 2952
QY 2782 AKRRGGAHAKLARPLL-WHATSR-----ELPDLKTSVARYTTTFNYCDVYSPGDFVITPQ 2836
D 2953 LIAQGGRAATCGRYLFNNVAVTKLKLTPLEASRLDLSGWFT-----VGAGGGDIFHSVS 3007
QY 2837 RRLQKFLVKYLAVIVFALGLIATVGLAI 2863
D 3008 HARPRLL-----LLCLLLLSVGVGI 3027

RESULT 10
Q777J1
AC Q777J1 PRELIMINARY; PRT; 3033 AA.
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; serNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
RN NCBI_TaxID=11103;
RX [1]
RP SEQUENCE FROM N.A.
RA Tanabe Y., Negayama K., Enomoto N., Izumi N., Tazawa J., Sato C.,
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY232731; AAP55686.1; -.
DR HSSP; Q8JYS1; 1CWX.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003958; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV NS1.
DR InterPro; IPR000745; HCV NS4a.
DR InterPro; IPR001490; HCV NS4b.
DR InterPro; IPR002868; HCV NS5a.
DR InterPro; IPR002166; HCV RdRp.
DR InterPro; IPR004109; Peptidase S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_PS.
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DR InterPro; IPR007094; RNA_pol_Psvir.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV Core; 1.
DR Pfam; PF01535; HCV env; 1.
DR Pfam; PF01560; HCV NS1; 1.
DR Pfam; PF01538; HCV NS2; 1.
DR Pfam; PF02907; HCV NS3; 1.
DR Pfam; PF01006; HCV NS4a; 1.
DR Pfam; PF01001; HCV NS4b; 1.
DR Pfam; PF01506; HCV NS5a; 1.
DR Pfam; PF00998; Viral_RdRp; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
SQ SEQUENCE 3033 AA; 330861 MW; C6673B5964AEC019 CRC64;

Query Match 21.5%; Score 3300.5; DB 2; Length 3033;
Best Local Similarity 29.8%; Pred. No. 2.6e-265;
Matches 982; Conservative 444; Mismatches 1163; Indels 703; Gaps 111;

QY 8 TSPVPAPRTRKNKQTOASYPVSIK-----TSVERGQRAKRVQORDARPR 51
D 3 TNPKPQRTKENTNRR---PDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPR 59
QY 52 NYKIAGIHDLGLTLAQAALPAH-----GWGRODPRKRSNRL 87
D 60 GRRQPIPKDRRSTGKSGKPGYPWPLYGNECGWAGWLLSPRSGRPHWPTDPRHSNRF 119
QY 88 GILDYPLGMIGDVTHTTPLVGLVAGAVRVPQIVRLLEDGVNWTG---WFGVHLFV 144
D 120 GKVIDTTTCGFDLGMGIVPVGAPV-GGVARALAHGVRLVEDGVNATGNLPGCSFSIFL 178
QY 145 VCLLS-LACPCSGARVTDPTNTILTNCCORNOVIYCSPTCLHEPGCVICABE----- 198
D 179 LALLSCVTVPVSAVEVRN-ISSSYATNDCSNNSITWOLENAVJLHLPQGVPCENDNGTLR 237
QY 199 CWVPANFVS--HPSNNWTGDSFLADHIDFVMGALVTCDALDIGELCGACVVLVDWLV-- 254
D 238 CWTQVTNVAVKRGALT--QHLRTHVDIVVAATVCSALYVDGVCAGVAMIAQALIVS 294
QY 255 --RHMLIHIDLNETGTCTYLEVPTGIDPGFLGFIGW--MAGKVEAVIFLTKLASQVPIA 310
D 295 PERH-----NFTQECNSIYQGRITGH--HMAWMDMLNWSPTITMILAYAAIRPELV 345
QY 311 TMFSSVHVLAVGALIIYASRGKWQLLLALMLY--IEA---TSGNPI----- 352
D 346 EVIFGGHWGMVFLAYFSMOGANSKVIVILLVAGVDARHHTTGLQVGKTLARVTSLSFI 405
QY 353 -----RVPTGCS-----IAEF-----CSPLMIPC----- 371
D 406 GPKQNIQLINTNGSWHINRTALNCNDSLOTGFIASLFVNNINSSGCPERMSSCRELDDF 465
QY 372 -----PCHSYLSENV-SEVICYSKPKWTRPTITLEVNN 401
D 466 RIGWGTLEYETNVTNDEDMRPYCWHPKPGCVIPARTVCQVPVYCFTPS---PIVVGTTD 522
QY 402 -----SISWYPYTIIPGARGCMVKFNNT-----WGC-----CRIR-- 431
D 523 KQGVETYSW-----GENETDVFLLNSTPRRPSGWSFGCTWNGTGFTKTCGAPPCRHRD 576
QY 432 -NVPSTYCTMGTDVAVNDTRNTYEACGVTPWLT-----TAWHNGSALKLAILQ---Y 478
D 577 YNSTLDLLCLPTDCFRKHPDITYLKCGSGPWLTPKCLVEYPYRLWHYPTVNTFTFKVRMY 636
QY 479 PGSKEMFKPHNMMSGHLYF-----EGSDTPIYFYDVPVNSTLLPPERWARLPGT 527
D 637 VGGVE---HRFSAACNFTGRDRCRLEDRCRQSQSPLLH-----ST-----TEWAVLPCS 682
QY 528 PPVVRGSLQVPGQFYSDVKDLATGLITKOKAWKNYOVLYSATGALSITGVTTRAVVLIL 587
D 683 -----FSDLPALSTGLLHLHQNTVDVQVLYGLSPATTRYIVKNEWVWLLF 727
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Dd 2688 PQEAKTVIHSALTERLYVGPGMTNSKQCGVRRRCRASGVFTTSMGNTWTCVIKALAAACKA 2747
Qy 2577 AGMKNPRLICDDCTVITWKSAGADADQAMRVFASWKKWGAPODCVPPQPKYSLEELTS 2636
Dd 2748 AGINDPTMLVCGDDLVVISEOGNEEDERNLRAFTTEAMTRYSAPEGDIPRPEYDLELITS 2807
Qy 2637 CSSNVTSGITKSGPKPYFLTRDPRIPLGRCSAEGILGYNPSAAWIGLYIHHPYCLMVSRVL 2696
Dd 2808 CSSNVSVVALDSRGRRRYFLTRDPTTPTITRAAWETVRHSPVNSLWNLIIQYAPTIVWRVNI 2867
Qy 2697 AVHFMQMLFEDKLPEVTTFWYGNKYVTPVEDLPSIIAGVHGIEAPSVVRYTNAEILRV 2756
Dd 2868 MTHFFSIILAOQTLNQNLFEMYGAVSYVNPDLPAIIRIHGLDAFSLHTYSPEHLSRV 2927
Qy 2757 SOSLDTMTMPPLARWKRARAVLASAKRRGGAHAKLARFLN-WHATSR- ----PLPDLDKT 2811
Dd 2928 AATLEKLGAPPLRAWKSARAVRASLIAGGGRALTCGRYLFNMAVVKLTPLPEASRL 2987
Qy 2812 SVARYTTFNYCDVSPGEGDVFITPQRRLOKFLVKYLAIVFALGLIAVGLAI 2863
Dd 2988 DLSGWFT- ----VGAGGGDIYHVSHPARPLL- ----LLCLLLLSVGVGI 3027

RESULT 11
Q9QAX1
ID Q9QAX1 PRELIMINARY; PRT: 3033 AA.
AC Q9QAX1
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2004 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=genotype 2; TISSUE=Serum;
RX MEDLINE=20328282; PubMed=10872881; DOI=10.1023/A:1008182901274;
RA Samokhvalov E.I., Hijiata M., Glyka R.I., Lvov D.K., Mishihiro S.;
RT "Full-genome nucleotide sequence of a hepatitis C virus variant
RT (arbitrarily 2k).";
RL Virus Genes 20:183-187(2000).
DR EMBL; AB031663; BAA88057.1; -.
DR HSSP; Q8JYJ1; 1CWX.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV NS1.
DR InterPro; IPR000745; HCV NS4a.
DR InterPro; IPR001490; HCV NS4b.
DR InterPro; IPR002868; HCV NS5a.
DR InterPro; IPR002166; HCV RdRP.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR004109; Peptidase_S29.
DR InterPro; IPR009003; Pept_Ser_Cys.

DR InterPro; IPR002518; Pept_U39 HCV NS2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSvir.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
DR Pfam; PF01539; HCV env; 1.
DR Pfam; PF01560; HCV NS1; 1.
DR Pfam; PF01538; HCV NS2; 1.
DR Pfam; PF02907; HCV NS3; 1.
DR Pfam; PF01006; HCV NS4a; 1.
DR Pfam; PF01001; HCV NS4b; 1.
DR Pfam; PF01506; HCV NS5a; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00998; Viral RdRP; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
FT CHAIN 734 1010 NS2 protein.
FT CHAIN 1011 1661 NS3 protein.
FT CHAIN 1662 1715 NS4A protein.
FT CHAIN 1 191 core protein.
FT CHAIN 1716 2017 NS4B protein.
FT CHAIN 2018 2442 NS5A protein.
FT CHAIN 2443 3033 NS5B protein.
FT CHAIN 192 383 E1 protein.
FT CHAIN 384 733 E2/NS1 protein.
SQ SEQUENCE 3033 AA; 329860 MW; 5245F9E0446A7E50 CRC64;

Query Match 21.4%; Score 3296.5; DB 2; Length 3033;
Best Local Similarity 30.4%; Pred. No. 4.8e-205;
Matches 985; Conservative 466; Mismatches 1191; Indels 597; Gaps 115;

Qy 8 TSPVAPRTRKN- ---KQTQASYP- ----VSIKTSVERGQAKRKVQR 46
Dd 3 TNPXPQRKTRKTRNRPRQDVKFGGQIVGGVYLLPRRGRPLGRVTRTKTSERSQPRGR 62
Qy 47 DARPNNYKIAGI- ----HGLQTLAQAALP- ----AHGWRQDDPRHKSRLGIL 90
Dd 63 QPIPKDRRSAGKSGRGYGPWPLYGNEGLWAGWLLSPRGRSPSWGPTDPRHRRNLGV 122
Qy 91 LDYPLGIGDVTTHPLVGLPAGAVVRVCQIVRLLEDGVNWTG- ----WFGVHLFVVCV 147
Dd 123 IDLTLCGFADLMGYIPVVGAPV-GGVARALAHGVRLVEDGINATGNLPGCSFIFLLAL 181
Qy 148 LS-LACPCSGARVTDPTNTT- ----ILTNCORNOVIYCSPTCLHEGCVIC- ----ADE 198
Dd 182 LSCMSVPVSAVEV- ----KNTSQIYMATNDCSNNSITWQLEGAVLHVPFCVCESTGNISR 237
Qy 199 CWVPANPYVISHPSNWTGTSFLADHIDFVMGALVTCDALDIGELCGACVLVGDMLV- --R 255
Dd 238 CWIPVTNVAVRERGALTGK-LRTHIDLIVVSATFCSALYIGDVCGAIMIAQAQITIS PQ 296
Qy 256 HWLHIHDLNETGTCYLEVPTGIDPGFL- -GFIGH- -MAGKVEAVIFLTKLASQVPIAAT 311
Dd 297 HHTFVQDCN- ----CSIVPGHVTGHRMAWDMNMNWSPATTMIMAYPMRVEVVD 346
Qy 312 MFSSVHYLAVGALIIYASRGKWQLLALML- ----TSGNPIRVPTGCSIAEF- 342
Dd 347 IITGAHGVNMFGLAYFSMOGAWAKVWVILLTAGVDAQTHITSGHAARTTHGLVSLFTPG 406
Qy 343 - ----VIEA- ----TSGNPIRVPTGCSIAEF- 363
Dd 407 SQNIQLVNTGSHWIRNTALNCNDSLKTGFIALFYSHKFNSSGCCQRMSSCSIEFR 466
Qy 364 - ----C- -SPLMIPCPCHSYLSEN-SEVICSPKWTPTITLEY 399
Dd 467 IGWGNLEVEENVTNDNMRPYCHYP- --PRPCGIVPAQVTCGPVYCFPTS- --PVVGT 520
Qy 400 NNSISWYPTIPGARGCMVFKNNT- ----WCC- ----CRIR- --NV 433
Dd 521 TDRRGVPTYTW-GENDDTVFLNLSNRPGRGWFCTWMNSTGTFTKTCGAPPCRIIRPDFNS 579


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Db 2564 VKOLLEDOQTPI---PTTIMAKNEVFCIDPTKGGKKAARLIVFDLGVVRCEKMAFYDI 2620
Qy 2453 APDVVYKVMGDAYGF-VDPRTVRKLLSNW--SPDAVGATCDTVCFDSTIIPEDIMVETD 2509
Db 2621 TOKLPQAVMGASYGQYSPAQRVDFLLRWKEKDPMGFSYDTRCFDSTVTERDIRTBES 2680
Qy 2510 IYSAAKLSDQHRAGHTHTARQLYAGCPMIAYDGREIGYRRRCSSGVYTTSSNSLTCWLK 2569
Db 2681 IYLACSLPEEARVAHSLTERLYVGGPMNWSKGSCGYRRCRASGVLTISMGNTITCYVK 2740
Qy 2570 VNAAEQAGMKNPRLICGDDCTVTJWSAGADADQAMRVFASMMKVMGAPDCVQPKPY 2629
Db 2741 ALAACKAAGIVAPTMVLCDDDLVWSESOGABEDERNLRFVTEAMTRYSAAPPDPPKDEY 2800
Qy 2630 SLEELTSCSSNVTSIGTSKRPYYELTRDPRPLGRCSAEGLYGNPSAAWGYLIHHYPC 2689
Db 2801 DLELITSCSSNVSVVALDOHGRMYLITRDPSTPLARAWEATARHSPVNSWLNIIQYAPT 2860
Qy 2690 LWSRVLAHFVMEQMLFEDKLPETVTTFDWYKNTVPVVEDLPSIIAGVHGIEAFSVRYT 2749
Db 2861 IWRVNLVMTHPFSLVMAQETLDDQLDNFEMYGNVYSVNPDLUPAIIERLHGLEAFSLHGS 2920
Qy 2750 NABILRVQSGLTDMTPPLRAWRKARAVLASAKRRGGAHAKLARFLI-WHATSR----P 2804
Db 2921 PTELTRVAALRKLGAPPLRAWRKARAVRASLISSQGRAATCGFYLFNVAVRTKRKLTP 2980
Qy 2805 LPDLDKTSVARTTNYCNDVSPEDGVFTTQRRLOKELVKYLAIVFALGLIAGLAI 2863
Db 2981 LPAARRLDLSGWFT-----VGAGGGDIYHSVSRARPFL-----LILCLLLSVGVGI 3027

RESULT 12
Q777J2
ID Q777J2 PRELIMINARY; PRT; 3033 AA.
AC Q777J2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]
RA Tanabe Y., Negayama K., Enomoto N., Izumi N., Tazawa J., Sato C.,
RA Watanabe M.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY232730; AAP55685.1; -.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008036; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0006508; P:structural molecule activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV NS1.
DR InterPro; IPR000745; HCV NS4a.
DR InterPro; IPR001490; HCV NS4b.
DR InterPro; IPR002868; HCV NS5a.
```

```
DR InterPro; IPR002166; HCV RdRP.
DR InterPro; IPR004109; Peptidase S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
DR Pfam; PF01539; HCV env; 1.
DR Pfam; PF01560; HCV NS1; 1.
DR Pfam; PF01538; HCV NS2; 1.
DR Pfam; PF02907; HCV NS3; 1.
DR Pfam; PF01006; HCV NS4a; 1.
DR Pfam; PF01001; HCV NS4b; 1.
DR Pfam; PF01506; HCV NS5a; 1.
DR Pfam; PF00998; Viral_RdRP; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
SQ SEQUENCE 3033 AA; 330641 MW; 593E6BD2358AF44E CRC64;

Query Match 21.4%; Score 3293.5; DB 2; Length 3033;
Best Local Similarity 30.1%; Pred. No. 7.5e-205;
Matches 984; Conservative 448; Mismatches 1176; Indels 665; Gaps 111;

Qy 8 TSPVPAERTRKNKQTQASYPVSIK-----TSVERGQRAKRVQORDARPR 51
Db 3 TNPQPKRTRKTRNR---PDVRFPGGQIVGVYLLPRRGPLRGVNRATKTSERSQPR 59
Qy 52 NYKIAGHDGLQTLAQALPAH-----GWGRQDPRHRSNRL 87
Db 60 GRQPIPKDRSTGKSGKGCYPMPLYGNECGWAGWLLSPRSPRHGPTDPRHSNRL 119
Qy 88 GILDYPLGWTGDTVTHPTPLVGLVAGAVRPVCOIVRLLEDGVNWTG---WFGVHLFV 144
Db 120 GKVIDTTTCGFADLMGVIPVIGAPV-GGVARALAHGVRLVDGVNYATGNLPGCSFSIFL 178
Qy 145 VCLLS-LACPCSGARVTDPTNTILTNCCORNOVIYCSPTCLHEPCVCVCADE----- 198
Db 179 LALLSCVTVPVSAVEVRN-ISSSYATNDCSNNSITWOLENAVHLHPCGVCPCENDNGTLR 237
Qy 199 CWPANPYISHPSNWTGDSFLADHIDFVMGALVTCDALDIGELCGACVLVGDMLV---- 254
Db 238 CWTQVTNVAVKRGALTON-LRTHVDVIVVAATVCSALYVDGCGAVMIASQALIVSPA 296
Qy 255 RHWLIHDLNETGTCYLEVPFGIDPGFLGFTGW--MAGKVEAVIFLTKLASQVPAIATM 312
Db 297 RH-----NFTQRCNCSIYQGRITGH--HMAWMDMLNWSPTITWILAYAAARIPELVLE 347
Qy 313 FSSVHYLAVGALIYYASRGKYYQLLLALMLY--IEA---TSGNPVRVPTGCSIAEFCSP 367
Db 348 IFGGHWGMFGLAYFSMOGAWAKVIVILLVAGVDARHHTTG---LQAGTKLARVTSLF 403
Qy 368 MIPC-----CHSYLS-----ENVSEVIC----- 386
Db 404 SIGAKNIQLINTNGSHINPTALNCDSLOTGFIASIFYNNINSSCCPERMSSCRELD 463
Qy 387 -YSPKWRTRPITLEYNNSIS-----W-YP-----YTIPGARGCM----- 417
Db 464 DFRIGWG---TLEYETNTNDEDMRPYKWHYPPKPGCIVPARTVCGPVYCTFSPPIVVG 520
Qy 418 -----VKPKNT-----WGC-----CRIR---NVP 434
Db 521 TDQGVFTYSWGENETDVFLLNSTRRPRGSGWFGCTWMNGTGTCTCGAPPCRIRRDYNST 580
Qy 435 SYCTMGTDVAVMNDTRNTYEACGVTPWLNT-----TAMHNGSALKLAILQ---YPSGSK 482
Db 581 LDLLCPTDCFRKHPDITYLKCGSGPWLTPKCLVEYPYRLWHYPCVTVNFTIFKVRMYGAV 640
Qy 483 EMFKPHNMMSGHLYF-----EGSDTPIVYFYDPVNVNLTLLPPERWARLPGTPPV 531
Db 641 E---HRFSAACNPTRGDRCLDRDRGQSQSPLLH-----ST-----TEWAVLPCS--- 682
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Db 2647 PKAMGSKDPMGFSYDTRCFDSTVTERDIRTEESIQACSLPQEAQTVIHSALTERLYVGG 2706
QY 2536 PMIAVDGEIGYRRCRSSGVYTTSSNSLTCHLKNVAAEQAGMKNPFLICGDDCTVIW 2595
Db 2707 PMTNSKSGCGYRRRCRSGVFTTSGNTWCYIKALAAKAGIMDPTMLVCGDDLNVIS 2766
QY 2596 KSAGADADQAMRVFASWVKWGAPODCVPQPKYSLEELTSCSSNVTSGITKSGKPYFL 2655
Db 2767 ESQNEEBERNLRAATEAMTRYSAPEGDIPREYDLELITSCSSNVVALDSRGRRTFL 2826
QY 2656 TRDPRIPGRCSAEGLYNPSAAWGYLIHYPCLWVSRLVLAHFMEQMLPDKLPETVT 2715
Db 2827 TRDPTTPTTRAAWETVRHSPVNSWLGNIQYAPTIVRWVIMTHFFSILLAQDTLNQNLN 2886
QY 2716 FDWGKNTVTPVEDLPSIIAGVHGIEARSVRYTNAEILRVQSOLTDMTPPLRAWRKA 2775
Db 2887 FEMYGANVSVNPLDLPALIERIHGLDAFSLHTYSPHELSRVAATLRKLGAPPLRAWKRA 2946
QY 2776 RAVLASAKRRGGAAKLARFL-WHATSR-PLPDLDKTSVARYTTFNYCDVYSPGD 2830
Db 2947 RAVRASLTAQGGRAICRYLENWAVTKLKLTPLEASRLDSGFT-----VGAGGD 3001
QY 2831 VFITPQRLOKPLVKYLAVIFALGLIAGLAI 2863
Db 3002 IVHSVSHARPLL-----LUCLLLSGVGVI 3027
RESULT 13
Q68801
AC Q68801 PRELIMINARY; PRT; 3019 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96226020; PubMed=8627233;
RA Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F.,
RA Lesmana L.A., Miyakawa Y., Mayumi M.;
RT "Hepatitis C virus variants from Jakarta, Indonesia classifiable into
RT novel genotypes in the second (2e and 2f), tenth (10a) and eleventh
RT (11a) genetic groups.";
RL J. Gen. Virol. 77:293-301(1996).
DR EMBL; D63821; BAA09890.1; -.
DR HSSP; O8JVS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003969; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005199; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR001917; AminoTrans II.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV env.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV NS1.
DR InterPro; IPR000745; HCV_NS4a.

DR InterPro; IPR001490; HCV_NS4b.
DR InterPro; IPR002868; HCV_NS5a.
DR InterPro; IPR002166; HCV_RGRP.
DR InterPro; IPR004109; Peptidase_S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF01506; HCV_NS5a; 1.
DR Pfam; PF00998; Viral_RGRP; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00599; AA TRANSFER CLASS 2; UNKNOWN_1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
SQ SEQUENCE 3019 AA; 328211 MW; AF7A6774BC6D95FA CRC64;
Query Match 21.4%; Score 3292.5; DB 2; Length 3019;
Best Local Similarity 30.6%; Pred. No. 8.6e-205;
Matches 985; Conservative 411; Mismatches 1188; Indels 637; Gaps 111;
QY 6 TQTSFVP-APTRKNKQTQASYPVSIKTSVRSRGQAKRKVQDARPRNYKIAGIHGLQT 64
Db 60 SRRQPIPRARRTEGRSQAQCPWPLYNGECGWAGWLLSPRGRP----- 105
QY 65 LAQAALPAHGWGRDPRHKSRLNLGILDYPLGWTGVDVTHPTLVGLVAGAVRPVCOIV 124
Db 106 -----SMGNPDRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPV-GGVARALAHGV 155
QY 125 RLLEDGYNWATG---WFGVHLFVVCLLS-LACPCSGARVTDPTNTTTLTNCQCORNOVIY 180
Db 156 RALEDGINFATGNLPGCSFIFLLALLSCLLTPTAGLEYRNASGLYIV-TNDCNGSIVY 214
QY 181 CSPSTCLHEPCVIC-----ADECWVPANP--YISHFSNMTGTDSFLADHIDFVMGALVT 233
Db 215 EAGDVILLHPCIFCVRLNNAASKWTPVSPVAVSRPGAATAS---LRTHVDMVMGAATL 271
QY 234 CDALDIDELCGACVLVG---DWLVR-HWLHIDLNETGTCVLEVTGIDPGFLG----- 283
Db 272 CSALYVGDLCGALFLVGQGSFWRHRQHWTVQ-DCN-----CSIYPGHLTGHRMAW 320
QY 284 --FIGWMAGKVEAVIFELTKLASQVPAIATMFSV--HYLAVGALIYYASRGKWKYQLLL 338
Db 321 DMMNWSPA-----MTLIVSQVLRLPQTMFDLIVGAHWGMAGVAYYSQGNWAKVFL 373
QY 339 ALMLYI-----EATSG-----NPIRV----- 354
Db 374 VLCLFSGVDASTTITGGVAASGATITSLFTGAKQPLHLVNTGNSWHINRTALNCNDSL 433
QY 355 -----PTGC-SIAEFCSP-----MLPC 371
Db 434 NTGFIAGLLYYHKFNSSGCVVERMSACSPDLRFAQGWGFLGPANISGFSSEKPYCWHYAPR 493
QY 372 PCHSVLSENV-SEVICYSPKWTTRPITILEYNNISIMWYPT-----IPGAR----- 414
Db 494 PCDTPAQSVCGPVYCFTPS---PVVGATDKRGAPYTWGENESDVLLESARPTPEPW 550
QY 415 -GCMVKFKNNTW-----GCCIRNVPSYCTMG-----TDVAVNDTRNTYEACG 456
Db 551 FGC-----TWMNGSVVKTGCGAPPCHYIYGGREGSKSNLSVCPDTCRKHDPDATYNRCG 603
QY 457 VTPWLT-----TAWHNGSALKLAILQ-----YPGSKEMFKPH-NWMSG-HLYFEGSD 501
Db 604 AGPWLTTPRCLVDYPRYLMHYPTVNYTIFKVRMVFVGGLEHFRNAAACNWTGRERCNLEDRD 663


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Db 2619 YGFQYSPKQRYVEYLLKMWNSKKTPLGFSYDTRCFDSTVTVEQDIRVEESIYQACDLKDEAR 2678
QY 2522 AGIHTIARQLYAGGPMIAYDREIGYRCRCRSGVTTSSNSLTWLKVNAAAEAGMKV 2581
Db 2679 RVITSLTERLYCGGPMFNKGQHCYRCRASGLVPTSGNTVTCYLKAKAATKAAGIKD 2738
QY 2592 PRFLICGDDCTIVKISAGADADKQAMRVFASMMKVMGAPQDCVPOPKYSLEELTSCSSNV 2641
Db 2739 PSFLVCGDULVIAESAGIDEDKSALRAFTENATRYSAAPPDPPOPTDYDELEITSCSSNV 2798
QY 2642 TSGITKSKPKYFFLTRDPRIPILGRCSAGLGNYPNSAAMWIGYLIIHHYPCLMVSRVLAVHFM 2701
Db 2799 SVAHDGAGKRYVYLTRDPETPLARAWEETARHTPVNSWMLGNIIMYAPTIVRWVIMTHFF 2858
QY 2702 EQMLFEDKLPETVTDYCKNYTPVEDLPSIIAGVHGIEAFSVRYTNAELIRVSQSLT 2761
Db 2859 SILQAQEQLEKALDFEMYGAVYSVTPLDLPALIERLHGLSAPLSHSYSPVELNRVAGALR 2918
QY 2762 DWTMPPLRAWRKARAVLASAKRRGGAHAKLARFLLMH-----ATSRPLPLDLDKTSVAR 2815
Db 2919 KLGIPLRAWRHRAVARAKLISQGG-KAKICGLYLFNWAVRTKAKLTPLPQAGLLDLSR 2977
QY 2816 YTFNYCDVYSPGDFVITPQRRLOKFLVKYLAVIVFALGL 2856
Db 2978 WFT-----VGAGGNDIYHSVRSRARSRHLLGLLLTVGVGI 3013

RESULT 14
ID Q7T7H7 PRELIMINARY; PRT; 3033 AA.
AC Q7T7H7;
DC 01-OCT-2003 (TremBrel. 25, Created)
DT 01-OCT-2003 (TremBrel. 25, Last sequence update)
DT 01-MAR-2004 (TremBrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
ON NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanabe Y., Nagayama K., Enomoto N., Izumi N., Tazawa J., Sato C.,
RA Watanabe M.,
RL Submitted (FEB-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY232745; AAP55700.1; -.
DR HSPF; Q8JY61; 1CW4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR0019087; P:viral transformation; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV NS1.
DR InterPro; IPR000745; HCV NS4a.
DR InterPro; IPR001490; HCV NS4b.
DR InterPro; IPR002868; HCV NS5a.
DR InterPro; IPR002166; HCV RdRp.
DR InterPro; IPR004109; Peptidase S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
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InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_PSVir.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_env; 1.
Pfam; PF01560; HCV_NS1; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF02907; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00998; Viral_RdRp; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
KW Coat protein, Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
SQ SEQUENCE 3033 AA; 330477 MW; 3616B01905C3143E CRC64;

Query Match 21.4%; Score 3289.5; DB 2; Length 3033;
Best Local Similarity 29.9%; Pred. No. 1.4e-204;
Matches 985; Conservative 444; Mismatches 1155; Indels 713; Gaps 110;

QY 8 TSPVPAPRTRKKNQOTQASYPVSIK-----TSVERGORAKKVVORDAPR 51
Db 3 TNPXPQRKTKRNTNR---PDVXFGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPR 59

QY 52 NYKIAGIHGDLQTLQA-----ALPAHG-----WGQDPRHKSRN 86
Db 60 GRR-QPIPKRRRSVSKSMGKPGYPWPLYGNEGCGMTGWLISPPRSRPTMGTDPRHRSR 118

QY 87 LGILLDYPLGWIGDVTHTPLVGLVAGVVRVPCQIVRLLEDGVNWTG---WFGVHLF 143
Db 119 LKVIDIITCGFADLMGIYPVVGAPV-GGVARALAHGVRLVEDGINATGLPCGSFIF 177

QY 144 VVCLLS-LACPCSGARVTPDNTTILTNCCQRNOVIYCSPTCLHBPFGCVICADE---- 198
Db 178 LLALLSCVTPVSAVEVRN-ISSSYATNDCSNNSITWQLSNVAVLHLPGCVPCENDNGTL 236

QY 199 -CWVPANPYISHPNSWTGTSFLADHIDFVMGALVTCDAIDIGELCGACVLGVMLV--- 254
Db 237 RCWITQVTFNVAVGRGALTNH-LRTHYDMIVMAATVCSALYVGVDCGAVMTVSQALIVSP 295

QY 255 -RHWLIHIDLNETGTCYLEVPTGIDPGFLGFIQGNMAGKVEAVIFLTKLASOVPAIATMF 313
Db 296 ERH-----NFTQECNSIYQGHVTQORMANDMNLNWSPLTLMILAYAAVPEVMLEII 348

QY 314 SSVHYLAVGALIYYASRGWYQLLLALMLY--IBAT----- 347
Db 349 FGHWGVVFGLAYFSMOGAWAKAVIAILLVAGVDATTYSSGAQVGRALGGLTGIFSPGAK 408

QY 348 -----SGNPRIVPTGCSIAEF--- 363
Db 409 QNIQLINTNGSHWIRNTALNCNDSLOTGFIASLPYTHRFNSSGCGPERLSSCRGLDDFRIG 468

QY 364 -----C-SPLMIPCCHSVLSENV-SEVICYSPKWRTPITLEYNN 401
Db 469 WGTLEYETNVNDEDMRPYCHYP---PKPCGIVSAKTVCGPVVCFTPS---PVVVGTTD 522

QY 402 -----SISWPEYTIIPGARGCMVKFNNT-----WGC-----CRIR-- 431
Db 523 RQGVPTYSW-----GENETDVFLLNSTRPPQGAWFGCTWMNGTGFTKCGAPPCRIIRD 576

QY 432 -NPESYCTMGTDVAVNDTRNTYEAAGVTPLT-----TAWNGSALKLAIQ---Y 478
Db 577 YNSTDLLCPTDCFRKHPDATYLCKGAGPMLTPRCLVEYPYRLWHYPCTVNTFTFKVRMY 636

QY 479 PGKEMFKPHNWSGHLYF-----EGSDTPIVYFDVPNVSTLLPPERWARLP 526
Db 637 VGVVE-----HRLSAACNFTRGDRCLDRDRGQOSPLH-----ST-----TEWAVLPC 681

QY 527 TPVVRGSLQVPOGFYSVDVKDLATGITKDKAWKNYQVLYSATGALSGLTGTTKAVVLI 586
Db 682 S-----FSDLPALSTGLLHLHQNIQVLDVQYLYGLSPALTRYIVKMEWVLL 726
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Db 2693 QACSLPQEARTVIHSLTRLYVGGPMNTSKGQSCYRRCRASGVTTSMGNTMTCYIKAL 2742
QY 2572 AAEEQAGKMNPRFLICGDDCTVIWISAGADADKQAMRVFASWMKVMGAPQDCVPOPKYSL 2631
Db 2743 AACKAAGVDPIMLVCGDDLVVISESQGNEEDERNLRAFTTEAMTRYSPAGDLPPEYDL 2802
QY 2632 EELTSCSNVTSIGIKSGKPYVFLTRDRIPIGRCSAEGLVNPSAAMIGVLIHHYPCW 2691
Db 2803 ELITSCSNVSVLDPGRRRYFLTRDPTTITRAAWETVRHSPVNSWLNIIQVAPIW 2862
QY 2692 VSRVLAVHMEQMLPEDKLPETVTFDYGKNTYVPVEDLPSIIAGVHGIEAFSVVRYTNA 2751
Db 2863 VRVIMTTHFFSILLAQDTLQNQLNFEMYGAVSVNPLDLPAIERLHGLDAFSLHTYS 2922
QY 2752 EILRVQSLSLTDMTDPLRAWRKARAVLASAKVRGGAHAKLARFLL-WHATSR-----PLP 2806
Db 2923 ELSRVNATRLKLGAPPLRAWKSRAVARASLTAQGGRAAICGRYLFNVAVKTLKLTLP 2982
QY 2807 DLDKTSVARYTTFNYCDVYSPGDFVITPQRRLQKFLVKYLAVIVFALGLIAVGLAI 2863
Db 2993 EASRLDLSGWTF-----VGAGGDFHFSVSRARPRLL-----LLCILLISVGVI 3027

RESULT 15
Q7717 PRELIMINARY; PRT; 3033 AA.
AC Q7717,
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanabe Y., Nagayama K., Enomoto N., Izumi N., Tazawa J., Sato C.,
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY232735; AAP55690.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR0019087; P:viral transformation; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001410; DEAD/DEAH_N.
DR InterPro; IPR001545; DEAD/DEAH_N.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV NS1.
DR InterPro; IPR000745; HCV NS4a.
DR InterPro; IPR001490; HCV NS4b.
DR InterPro; IPR002868; HCV NS5a.
DR InterPro; IPR002166; HCV RdRp.
DR InterPro; IPR004109; Peptidase S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_BS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF01543; HCV_capsid; 1.
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DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF00998; Viral_RdRp; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
DR Coar protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
SQ SEQUENCE 3033 AA; 330352 MW; A8349279059172C0 CRC64;

Query Match 21.4%; Score 3289.5; DB 2; Length 3033;
Best Local Similarity 30.2%; Pred. No. 1.4e-204;
Matches 985; Conservative 446; Mismatches 1189; Indels 641; Gaps 109;

QY 8 TSPVPAPRTRKNKQTOASYPVSIK-----TSVERGQRAKEKVKQDARPR 51
Db 3 TNPKPQRTKXNTNR---PODVFPGGQIVGGVYLLPRGPRLGVRATRTKTSERSQPR 59
QY 52 NYKIAGHDGLQTLAQAALPAH-----GWGRQDPRHKSRL 87
Db 60 GRRQPIPKDRRSTGKSGKPGYWPPLYGNEGCGWAGWLLSPRGSRPWTGPTDPRHRSRL 119
QY 88 GILLDDPLGWDGVTHTPLVGLVAGAVRVCQIVRLLEDGVNWTG---WFGVHLFV 144
Db 120 GKVIDTITCGFADLMGVIPVIGAPV-GGVARALAHGVRLVEDGVNATGNLPGCSFSIFL 178
QY 145 VCLLS-LACPCSGARVTPDNTTILTNCCORNQVIYCSPTCLHEPGCVI CADE----- 198
Db 179 LALLSCVTVPVSAVEIRN-ISSYYATNDCNSNITWLTNAVHLPGCVPCENDNTLR 237
QY 199 CWPANPYISHPSNWTGDSFLADHIDFVMGALVTCDAIDIGELCGACVVLGDMLV----- 254
Db 238 CWIQVTNPVAVKRGALTN-LRTHVDMIVMAATVCSALYVGDVCGAVMIVSQALIVSPQ 296
QY 255 RHWLHIDLNETGTCTYLEVPTGIDPGLFGFGWAGKVEAVIFLTKLASQVPAIATWFS 314
Db 297 RH-----NFTQCNCISYQGHITGHRMAWMDMLNWSPTLITMILAYAAARPELALELVF 349
QY 315 SVHYLVGALYYASRGKWYOLLALMLYIATSGNPIRVPTGCSIAEF---CSPLMIPC 371
Db 350 GGHGVVFLAYFSQGNWAK-VIAILLVAGVDAN--TYSYGAQAGHTISGLSGLFAPG 406
QY 372 P-----CHSYLSENVSEVICSPKWT-----RPI----- 395
Db 407 PRQRIHLINTNGSHINRTALNCDSLKTGFIASLYFTNNFNSGCPERLSSCALDDFR 466
QY 396 ---TLEYNNSIS-----W-YP-----YTIPGARGCM----- 417
Db 467 IGWGTLEYETNVTNDEDMRPMYHPPKPGCIVSARTVCGPVYCFTPSPVVVGTTRDQGV 526
QY 418 -----VKFKNNT-----WGC-----CRIR---NVPSYCTMG 440
Db 527 PTYSNGENETDVFLLNSTRPPQGAWFGCTWNGTGFTKTCGAPPCRIRRDYNSTLDDLCP 586
QY 441 TDVVMNDTRNTYEACGVTPWLT-----TAMHNGSALKLAILQ---YPSGKEMFKPH 488
Db 587 TDCPRKHGTTYIKCGAGPWLTPKCLVEYPYRLWHYPCTVNFTIFKVRMYVGGVE----- 641
QY 489 NWSGHLYP-----EGSDTPIVYVDPVNSTLLPPEWRARLPGTPPVVRSWL 536
Db 642 HRLSAACNFTRGDRCLDRDQGOOSPLLH-----ST-----TEWAVLPQS----- 682
QY 537 QVPGQFSDVKDLATGLITKDKAWNKYQVLSATGALSILTGVTKAVVLIILLGLCGSKYL 596
Db 683 -----FSDLPALSTGLLHLHQNIVDVQYLYGLSPAVTRYIVKWEVVLFLALLADAR-- 734
QY 597 ILAVLCYLSLFCGRASGYLPRVLPSOSYLOAGWDVLSKAQVAPFALIFCICCYLRCLR 656
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Db 735 VCACLMMLI-----ILGOABAALEKLIU----- 757
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Db 758 ---LHSAASAANGPLAFFIFTAA-----WYLGKRVVPAATYS-----VLGLMS 799
Qy 717 LVALLTLHLVTPASAPDETEIIGLTLTPVVALVVMRPGF---FAHLLPRCALVNSYLM 773
Db 800 F---LLLVLALPQOAYALDAAEQGBLGL---VILVLSIFTLTPAYKILLSRVWMLSYML 854
Qy 774 ---QRW-----ENWFW-NVTLRPERFELV---LVCFCGATDALVTFVCVCH 812
Db 855 VLBAQIQOQVPPLEARGGRDGIILVILHPRLVFETKWLAILGSAV----- 904
Qy 813 VALICLTSSAASFEGTDSRVRAHRM-----LVRLGKCHAMYSHYVLVFLVLFVGENGVFF 867
Db 905 --LLKASILRIPYF-----VRAHALLRVCTLVR---HLAGARYIOMLLITIGRWTGYI 953
Qy 868 YKHLHGVDLNDPASKULPQ-----EP---FPFEGKARVYRNEGRRACGD 911
Db 954 YDHLSS-----PLSTWAAQGLRDLAVAVEPVVFSPMERKVIWGAEE--TVACGD 999
Qy 912 TVDGLPVVARGDLVAFGLAMPD-----GWAITAPETLOCLSERGTLSAMAVVMGTGDP 966
Db 1000 ILHGLPVSAKRGREVLG---PADSYTSGMKWLLAPITAYTQOTRGLLGAIVVSLTGRDK 1056
Qy 967 RTWTGTIFRLGSLATSYMGFVCDNVLTAKHSGKGRRLAHPGTSIHPITVDAANDQDIYQ 1026
Db 1057 NEQAGOVQLSSVTQSFLGTSISGLVTVVHGAGKTLAGKPGATQMTYSAGEDLVGMP 1116
Qy 1027 PPCAGSLTRCSCGETKGYLVTRGLSVLVNKSDDPYVCVCGALPMAVAKSGSAPILCS 1086
Db 1117 SPPGKSLDPCGAVDLVTRNADVIPVRKDDRRGALLSPRLSTLKGSSGCPVLCP 1176
Qy 1087 SGHVGHTAARNSGG---SVSQIRVRPLVCAGVHPQYTAHATLDTKYTPVNEYSVQILI 1143
Db 1177 RGHAGLFRAAVCSRGVAKSIDFIPVESLDIARTPFSFDSNS---TPPAVPSQVQVGYLH 1233
Qy 1144 APTGSGKSTKLPLSYMOBEKVELVLPNSVATTASMPKMYATYGVNPNVFNCGKCTWGA 1203
Db 1234 APTGSGHSTKVPAAVYASQGYKVLVNSVATLGFAGYMSKMGHINIRTVRTVTG 1293
Qy 1204 SLTVSTYGMWLT-GACSRN-YDVIICDECHADATTVLIGIKVLTEAPSKNVRVLVLATA 1261
Db 1294 SITYSTYKFLADGCCAGAYDIIICDECHSVDATILGIGTVLDOAETAGVRLVLATA 1353
Qy 1262 TPGVITPHANITEIOLTBEGTTPFHGKKIKEENLKKGRHLIFEATKXCKDELANELAR 1321
Db 1354 TPGTIVTPHNSIBEVALGHEGEIPFYGKAIPLAFIKGRHILIFCHSKCKDELANAALRG 1413
Qy 1322 KGITAVSYRGCDISKIP-EGDCVVVATDALCTGYTGDQFDSVYDCSLMVEGTCHEVDLDP 1380
Db 1414 MGNVAVAYRGLDVSLVPTQGDVVVVVATDALMTGYTGDQFDSVIDCNVAVTQIVDFSLDPT 1473
Qy 1381 FTMGVRVCGVSIAIKGQRRGRTGRAGIYIYVYDGSCTPSGMWPECNIVEAFDAKAWYG 1440
Db 1474 FTITQTVPQDAVSRSQRRGRTGRGLTRYVYSSGERPSGMFDSVVLCECYDAGAAWYE 1533
Qy 1441 LSSTEAQTILDTYRTQGLPAIGANLEWADLFS-MYNPEPSFVNTAKRTADNVLLTAA 1499
Db 1534 LTPAETVRLRAYFNTPLPCVQDHLFEAFVFTGLTHIDAHFLSQTQKGENFAYLTAY 1593
Qy 1500 QLOLCHOYGYAAPNDAPRWQCARLGK---PCGVLRDLGADACPGPESEVTRY---- 1551
Db 1594 QATVCARAKAPPSSWDVTKCLTRKLTGLTGLPTLLYRL-GAVTNEVTLTHPVTKYIATC 1652
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Qy 1609 BEIVBECASFIPL-EAMVAIDKUKSTI-----TTTSPPTLETALE-----KLTNLFGLPH 1657
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Db 1769 MNPFISGIOYLAGLSTLPGNPAVASMAFSAALTPLSTSTILLNMGWLASQIAPPA 1828
Qy 1718 GALAFMWAGAGTALGTWTSVG---FVFDMLGCGYAAAASSTACLTFFKCLMGEMPTMDQLAG 1774
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Qy 1775 LVTSAFNPAAGVGVVLSACAMPALTTAGPD---HWPNRLLTMLARSNTVTCNEYFIATDIR 1832
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Qy 1833 RKILGILEASTPNSVISACIRWLHTPTEDDCGLI---AWGLEIWWYVCNPFVCFNVLKA 1889
Db 1946 QRWQVQLSSLT---ITSLRLRLHTWITEDCPVPCSGSWLRDIWDMVCSLITDFKNWLS 2001
Qy 1890 GVOSMNIIPCCPFYSCOKGYKGMWISGMLOARPCGCAELIFSVENGFAKLYKGPRTCSN 1949
Db 2002 --KLLPKMPLGLPFLSCQGYRGVWAGTGMVMTTRPCGANISGHVRMGTMKI-TGPKTCLN 2058
Qy 1950 YMRGAVPVNARLCSARPDPDT-DWTSLVVNYGVDRDYCKYBKMGDHIFVTAVSSPNVCFTQ 2008
Db 2059 LMQGTPIHCYTEGCPVKPESPNYKTAIRWAASEYVEVTQKGSFSYVGTGLTSDNL---K 2115
Qy 2009 VP---PTLRAAAVAVDGVQVQCYLGEPKTPMTTTSACCYGP---DGKGTVKL-PFRVDGHT 2061
Db 2116 VPCQVPAPEFESVMDGVQIHRPAPIP-----GPFPRDEVTFVGLNSPVVSGHL 2164
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Db 2165 PWDPEPTEVLASLTDPSHITAEAAARRLAARGSPFSQASSQSLSAPSLKATCTTHKM 2224
Qy 2105 ---NQLLEA-ISAGVDTTKLPA-----PSI-EEVVVRKQFRAR 2138
Db 2225 AYCDMDVAMLFMGGDVTRIESDKVILDSLSMTEVEDREDPSPVSEVLIIRRKFP--- 2281
Qy 2139 TGSULTUPP---PPRSVPGVSCP---ESLQRSPLLEGPS-----NLPPSPVVLQALMP- 2184
Db 2282 ---PPALPPWARPDPYNPPVLETWKRPD-YEPPTVLGALPPTP---QTPVPVPPRRR 2331
Qy 2185 -----MPLLGAGECNPPTAIGCA-----MTGTG----- 2207
Db 2332 AKVLTQDNVBLREMAWKVLSPLQDHNDHSGHSTGVDTGDSVQQPSDETPASETGLSS 2391
Qy 2208 -----GQPD---DLPSYPPKK---EVSSESDSWSTATTASSVYVTPPYPKIRGKD 2252
Db 2392 MPLEGEPPGDDLEFEPAGSAPPSEGECEIVDSDSKSWSTVSDQED----- 2437
Qy 2253 STQSAPAKRPTKKLKGKSEFSCSMSTYTTD-VISPKTASKVLSATRAITSGLKQKRSLVY 2311
Db 2438 -----SVICCSMSYSMTGALLITPCGPBEEKLPINPLNSLMRPHNKVY 2480
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Db 2481 STTSRSATLRAKVTDFRVQVLDHAHYDVSIVDKRAASKSARLLSIEEACALTPPHSAK 2540
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Db 2541 SRY-GFGAKEVRS-LSRRVNHIRSVWEDLLEDOHTPIDITTIMAKNEVFCLDPTKGGKCP 2598
Qy 2431 PRLISYPHLEMCRCVEKNYQGVAPDVVVKAVMGDAYGF-VDPRTVRVRLLSNMW---SPDAVG 2487
Db 2599 ARLIVPDLGVRVCEKMAVLDIAKLPKAVMGFSQGFQYSPAERVDVFLKAWGSKDKPMG 2658
Qy 2488 ATCDTFCDFSTIIPEDIMVETDIYSAKLSQDHRAGIHTIARQLYAGGPMIAYDGRIGY 2547
Db 2659 PSYDTRCFDSTVTERDIRTEESIYLA CSLPQEKATATHSLTERLYVGGPMTNSKGQCGY 2718
Qy 2548 RRCRSSGVYTTSSNSLTCWLKYNAAEQAKMKNPRFLICGDDCTVIWKSGADADQAM 2607
Db 2719 RRCRASGVFTTSMGNTWTCYIKALAAKAAAGIVDPIMLVCGDDLLVISEQGNSEBERNL 2778

Qy	2608	RVFASMMKMGAPQCVQPKYSLBELTSCSSNVTSGITKSGKPYFLTRDPRIPLGRCS	2667
Db	2779	RAFTAMTRYSGPPGDLRPEYDLELITSCSSNVSVALDSRGRRYYLTROPTTITRAA	2838
Qy	2668	AEGLYNPSAAWIGYLIHHYPCLWVRVLAVHFMQMLFEDKLPETVTFDYGKQYTPV	2727
Db	2839	WETVRHSPVNSWLGNIIOYAPTITWVRVIMTHFFAILLAQDTLNQNLNFEMYGAVYSNP	2898
Qy	2728	EDLPSIIAGVHGIEAFSVVRVTNAEILRVSOQLTDMTPPLRAWRKKARAVLASAKREGG	2787
Db	2899	LDLPAILERLHGLEAFSLHTYSPHELSRVAATLRKLGAPPLRAWKSRARAVRASLIAQGG	2958
Qy	2788	AHAKLARELL-WHATSR----PLPDLDKTSVARYTTFNYCDVYSPGSDVFITPQRRLOKF	2842
Db	2959	RAATCGRYLENWAVRTKLKLTPLPEASRLDLSGWFT-----VGAGGGDIFHSVSHARPRL	3013
Qy	2843	LVKYLAVIVFALGLIANGLAI	2863
Db	3014	L-----LCLLLLSVGVI	3027

Search completed: October 27, 2005, 15:46:51
Job time : 354 secs

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OM protein - protein search, using sw model

Run on: October 27, 2005, 15:32:46 ; Search time 64 Seconds
(without alignments)
3340.546 Million cell updates/sec

Title: US-10-009-002-2

Perfect score: 15376

Sequence: 1 MPVISTQTPVPAPRTRNK.....KYLAVIVFALGLIANGLAIS 2864

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15317	99.6	2864	US-08-469-260A-394	Sequence 394, App
2	15317	99.6	2864	US-08-488-446-394	Sequence 394, App
3	15317	99.6	2864	US-08-467-344A-394	Sequence 394, App
4	15317	99.6	2864	US-08-424-550B-394	Sequence 394, App
5	7380	48.0	1422	US-08-469-260A-83	Sequence 83, Appl
6	7380	48.0	1422	US-08-488-446-83	Sequence 83, Appl
7	7380	48.0	1422	US-08-467-344A-83	Sequence 83, Appl
8	7380	48.0	1422	US-08-424-550B-83	Sequence 83, Appl
9	3274.5	21.3	3033	US-07-925-695-8	Sequence 8, Appl
10	3269	21.3	3033	US-07-925-695-5	Sequence 5, Appl
11	3262	21.2	3010	US-09-539-601-3	Sequence 3, Appl
12	3261	21.2	3010	US-09-539-601-33	Sequence 33, Appl
13	3255	21.2	3010	US-09-539-601-27	Sequence 27, Appl
14	3252	21.1	3010	US-09-539-601-21	Sequence 21, Appl
15	3247	21.1	3010	US-09-014-416-3	Sequence 3, Appl
16	3230.5	21.0	3033	US-07-925-695-9	Sequence 9, Appl
17	3218	20.9	3010	US-08-324-977-2	Sequence 2, Appl
18	3218	20.9	3010	US-08-324-977-14	Sequence 14, Appl
19	3218	20.9	3010	US-08-384-616-2	Sequence 2, Appl
20	3218	20.9	3010	US-08-384-616-14	Sequence 14, Appl
21	3218	20.9	3010	US-08-904-686A-2	Sequence 2, Appl
22	3218	20.9	3010	US-08-904-686A-14	Sequence 14, Appl
23	3218	20.9	3010	US-09-315-850-2	Sequence 2, Appl
24	3218	20.9	3010	US-09-315-850-14	Sequence 14, Appl
25	3215.5	20.9	3011	US-08-850-328-1	Sequence 1, Appl
26	3214.5	20.9	3011	US-09-014-416-1	Sequence 1, Appl
27	3214.5	20.9	3011	US-09-952-572-9	Sequence 9, Appl

28	3209.5	20.9	3011	1	US-08-188-281B-1	Sequence 1, Appl
29	3209.5	20.9	3011	1	US-08-453-552-1	Sequence 1, Appl
30	3209.5	20.9	3011	2	US-08-710-637-1	Sequence 1, Appl
31	3209.5	20.9	3011	5	PCT-US93-00907-1	Sequence 1, Appl
32	3209.5	20.9	3011	5	PCT-US94-07280-1	Sequence 1, Appl
33	3209.5	20.9	3011	5	PCT-US95-01087-1	Sequence 1, Appl
34	3208.5	20.9	3012	3	US-08-811-566-2	Sequence 2, Appl
35	3208.5	20.9	3012	3	US-09-034-756-2	Sequence 2, Appl
36	3204.5	20.8	3011	1	US-08-440-103-36	Sequence 36, Appl
37	3204.5	20.8	3011	1	US-08-440-542-36	Sequence 36, Appl
38	3204.5	20.8	3011	1	US-07-910-760-10	Sequence 10, Appl
39	3204.5	20.8	3011	1	US-08-440-519-10	Sequence 10, Appl
40	3204.5	20.8	3011	1	US-08-231-368-36	Sequence 36, Appl
41	3204.5	20.8	3011	1	US-08-440-210-36	Sequence 36, Appl
42	3204.5	20.8	3011	3	US-09-388-874-2	Sequence 2, Appl
43	3204.5	20.8	3011	3	US-09-046-604-36	Sequence 36, Appl
44	3204.5	20.8	3011	3	US-08-440-549-10	Sequence 10, Appl
45	3204.5	20.8	3011	4	US-09-916-359-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-469-260A-394
; Sequence 394, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 394:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-469-260A-394

Query Match 99.6%; Score 15317; DB 4; Length 2864; Best Local Similarity 99.6%; Pred. No. 0; Matches 2852; Conservative 4; Mismatches 8; Indels 0; Gaps 0;									
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Db	61	GLQTLAQAALPAHNGRODPRHKSRLGLLDYPLGWDVTHTPPLVPLVAGAVRPV	120						
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Qy	1021	DQDIYQPPCGAGSLTRCSCGETKGYLVTRLGSLVEVNKSDDPYWCVCGALPMAVAKGSSG	1080						
Db	1021	DQDIYQPPCGAGSLTRCSCGETKGYLVTRLGSLVEVNKSDDPYWCVCGALPMAVAKGSSG	1080						
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Db	1141	ILIIAPTSGSKTKLPLSYMQEKYEVLNPSVAITATSMPKYMHATYGVNPNCFNGKCTN	1200						
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Db	1261	ATPFGVPTPHANITEIQLTDEGTIPFHGKKIKEENLKKGRHLIPEATKKGHCDELANELA	1320						
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Qy	1381	FTMGVVRVCGVSAIVKGORRGRTGRAGIYVYVDSCTPSCWVPECNIVEAFDAKAWYG	1440						
Db	1381	FTMGVVRVCGVSAIVKGORRGRTGRAGIYVYVDSCTPSCWVPECNIVEAFDAKAWYG	1440						
Qy	1441	LSSTEAQTLTYRTQPLGPAIGANLDEWADLFSVMNPEPFSVNTAKRTADNYVLLTAAQ	1500						
Db	1441	LSSTEAQTLTYRTQPLGPAIGANLDEWADLFSVMNPEPFSVNTAKRTADNYVLLTAAQ	1500						
Qy	1501	LQLCHOYGAAPNDAPRWQGARLCKKPCGVLRWLDGADACPGPEPSEVTRVQMCETEYNT	1560						
Db	1501	LQLCHOYGAAPNDAPRWQGARLCKKPCGVLRWLDGADACPGPEPSEVTRVQMCETEYNT	1560						
Qy	1561	SGTAALAVGVGVAMAYLAIDTFGATCVRRCSWITSVPTGATVAPVWDEEEIVEECASIP	1620						
Db	1561	SGTAALAVGVGVAMAYLAIDTFGATCVRRCSWITSVPTGATVAPVWDEEEIVEECASIP	1620						
Qy	1621	LEAMVAADKLKSTITTTSPFTLEALKNTFLGPHAATILAIIEYCCGLVTLDPNPPA	1680						
Db	1621	LEAMVAADKLKSTITTTSPFTLEALKNTFLGPHAATILAIIEYCCGLVTLDPNPPA	1680						
Qy	1681	SCVFAFTAGITTPPHKIKMFLSLFGGAIASKLTDARGALAFMAGAGTAGTWTWSVGF	1740						
Db	1681	SCVFAFTAGITTPPHKIKMFLSLFGGAIASKLTDARGALAFMAGAGTAGTWTWSVGF	1740						
Qy	1741	VFDMLGGVAAAASSTACLTFFKLMGEWPTMDQLAGLVSAFNPAAAGVGVLSACAMFALT	1800						
Db	1741	VFDMLGGVAAAASSTACLTFFKLMGEWPTMDQLAGLVSAFNPAAAGVGVLSACAMFALT	1800						
Qy	1801	AGPDHWPNRLLTMLARSNTVCNEYFIATRDIRRKILGILEASTPMSVISACIRWLHTPTE	1860						
Db	1801	AGPDHWPNRLLTMLARSNTVCNEYFIATRDIRRKILGILEASTPMSVISACIRWLHTPTE	1860						
Qy	1861	DDCGLIANGLEBIWQVVCNFFVFCFNVLKAGVQSMWNIPGCCPFYSCQKYGKPGWISGMLQ	1920						
Db	1861	DDCGLIANGLEBIWQVVCNFFVFCFNVLKAGVQSMWNIPGCCPFYSCQKYGKPGWISGMLQ	1920						
Qy	1921	ARPCGAEILIESVNGFAKLYKGPRTCNSYWRGAPVNVNARLCSGARPDPTDWTSLVVNYG	1980						
Db	1921	ARPCGAEILIESVNGFAKLYKGPRTCNSYWRGAPVNVNARLCSGARPDPTDWTSLVVNYG	1980						
Qy	1981	VRDYCKYKMGDHI FVTAVSSPNVCFTQVPPTLRAAAVADGVQVQCYLGEPKTPMTTSAC	2040						
Db	1981	VRDYCKYKMGDHI FVTAVSSPNVCFTQVPPTLRAAAVADGVQVQCYLGEPKTPMTTSAC	2040						
Qy	2041	CYGPDKGKTKVLPFRVDGHTPGVRMQLNLRDALETNDCSNNTNTPSPDEAAVSALVFQOE	2100						
Db	2041	CYGPDKGKTKVLPFRVDGHTPGVRMQLNLRDALETNDCSNNTNTPSPDEAAVSALVFQOE	2100						

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Qy 2101 LRRTNOLLEAISAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLPBPPRSVPGVSCPESL 2160
Db 2101 LRRTNOLLEAISAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLPBPPRSVPGVSCPESL 2160
Qy 2161 QRSPLLEGPSNLPSPVQLQAMPVLLGAGECNPFTAGCAMTETGGGDDLPSPYPPK 2220
Db 2161 QRSPLLEGPSNLPSPVQLQAMPVLLGAGECNPFTAGCAMTETGGGDDLPSPYPPK 2220
Qy 2221 EVSEWSDESMTATTASSYVTPPYKPIRGKDSQSAKAPKPTKKGLGKSEFSCSMSTY 2280
Db 2221 EVSEWSDESGWSTTTTASSYVTPPYKPIRGKDSQSAKAPKPTKKGLGKSEFSCSMSTY 2280
Qy 2281 TDVLSFKTASKVLSATRAITSGLFKQSLVYVTEPRDAELKQKVTINRQPLFPSPYHK 2340
Db 2281 TDVLSFKTASKVLSATRAITSGLFKQSLVYVTEPRDAELKQKVTINRQPLFPSPYHK 2340
Qy 2341 VRLAKEKASKVGVWMDYDEVAANTPKSAKSHITGLRGTDVRSQAARKAVLDLQKVEA 2400
Db 2341 VRLAKEKASKVGVWMDYDEVAANTPKSAKSHITGLRGTDVRSQAARKAVLDLQKVEA 2400
Qy 2401 GEIPSHYRQTVIVPKKEEVFKTPKPTKKPRLISYPHLEMRCEKMYGQVAPDVVKAV 2460
Db 2401 GEIPSHYRQTVIVPKKEEVFKTPKPTKKPRLISYPHLEMRCEKMYGQVAPDVVKAV 2460
Qy 2461 MGDAYGFVDPRTVRKRLLSMNSPDAVGATCTVCFDSTITPEDIMVETDIYSAAKLSDQH 2520
Db 2461 MGDAYGFVDPRTVRKRLLSMNSPDAVGATCTVCFDSTITPEDIMVETDIYSAAKLSDQH 2520
Qy 2521 RAGIHTTARQLYAGPMIAYDGRIGYRRCRSSGYVTTSSNSLTCWLKVNAAAEQAGMK 2580
Db 2521 RAGIHTTARQLYAGPMIAYDGRIGYRRCRSSGYVTTSSNSLTCWLKVNAAAEQAGMK 2580
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Db 2581 NPRELICGDDCTVIWKSAGADADQAMRVFASMMKVMGAPQDCVPQPKYSLEELTSCSSN 2640
Qy 2641 VTSGITSGKPYFLTRDPRIPLRGSAEGLGYNPSAAWIGYLIIHHYPCLMWSRVLAHF 2700
Db 2641 VTSGITSGKPYFLTRDPRIPLRGSAEGLGYNPSAAWIGYLIIHHYPCLMWSRVLAHF 2700
Qy 2701 MEQMLFBDKLPETVTFDYGKNTVPVEDLPSIITAGVHGIEAFSVRYTNAEILRVQSOL 2760
Db 2701 MEQMLFBDKLPETVTFDYGKNTVPVEDLPSIITAGVHGIEAFSVRYTNAEILRVQSOL 2760
Qy 2761 TDMTMPPLRAWRKARAVLASAKRGGAHAKLARFLMWHATSRLPLDLDKTSVARYTTFN 2820
Db 2761 TDMTMPPLRAWRKARAVLASAKRGGAHAKLARFLMWHATSRLPLDLDKTSVARYTTFN 2820
Qy 2821 YCDVYSPGSDVFTIPQRRLOKFLVKYLAVIVFALGLIAVGLAIS 2864
Db 2821 YCDVYSPGSDVFTIPQRRLOKFLVKYLAVIVFALGLIAVGLAIS 2864
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RESULT 2

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US-08-488-446-394
; Sequence 394, Application US/08488446
; Patent No. 6558998
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATTIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
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; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 394:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-446-394
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Query Match 99.6%; Score 15317; DB 4; Length 2864;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2852; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MPVISTQTSVPAPRTTRKNQTOASYPVSIKTSVERQORAKRVQDARPRNYKIAGIHD 60
Db 1 MPVISTQTSVPAPRTTRKNQTOASYPVSIKTSVERQORAKRVQDARPRNYKIAGIHD 60
Qy 61 GLOTLAAALPAHGWGRQDPRHKSRLGILLDYPGLWIGDVTTHPLVGLVAGAVRVP 120
Db 61 GLOTLAAALPAHGWGRQDPRHKSRLGILLDYPGLWIGDVTTHPLVGLVAGAVRVP 120
Qy 121 CQIVRLLEDGVNMTAGVGHVLFVCLLSLACPCSGARVTDPTNTTILTNCCORNOVIY 180
Db 121 CQIVRLLEDGVNMTAGVGHVLFVCLLSLACPCSGARVTDPTNTTILTNCCORNOVIY 180
Qy 181 CSPSTCLHEPGCVICADECWPNANPYISHPSNWTGDSFLADHIDFVNGALVTCOALD 240
Db 181 CSPSTCLHEPGCVICADECWPNANPYISHPSNWTGDSFLADHIDFVNGALVTCOALD 240
Qy 241 ELGCACVLVGDMLVRHWHLIHIDLNETGTCYLEVPTGIDRGLFGIWMAGKVEAVIFLTK 300
Db 241 ELGCACVLVGDMLVRHWHLIHIDLNETGTCYLEVPTGIDRGLFGIWMAGKVEAVIFLTK 300
Qy 301 LASQVPAIATMFSSVHYLAVGALIIYASRGKWQLLLALMLYIETATSGNPIRVPTGCSI 360
Db 301 LASQVPAIATMFSSVHYLAVGALIIYASRGKWQLLLALMLYIETATSGNPIRVPTGCSI 360
Qy 361 ABFCSPLMIPCPCHSYLSENVSEVICSPKWRTPITLEYNNISISWYPTTIPGARGCMVKP 420
Db 361 ABFCSPLMIPCPCHSYLSENVSEVICSPKWRTPITLEYNNISISWYPTTIPGARGCMVKP 420
Qy 421 KNTWGCCTIRNVPSYCTMGTDVWMDTRNTYEACGVTPLTTAHHNGSALKLAILQVPG 480
Db 421 KNTWGCCTIRNVPSYCTMGTDVWMDTRNTYEACGVTPLTTAHHNGSALKLAILQVPG 480
Qy 481 SKEMFKPHNWSGHLYFEGSDTPIVYFDPVNSLTLLPPERWARLPPTPVVGRGSLQVPG 540
Db 481 SKEMFKPHNWSGHLYFEGSDTPIVYFDPVNSLTLLPPERWARLPPTPVVGRGSLQVPG 540
Qy 541 GFVSDVKDLATGLITTKDKAMKNYQVLSATGALSGLTGVTTKAVVLLILLGLCGSKYLILAY 600
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Qy 2761 TDMTPPLRAWRKKARAVLASAKRRGGAHAKLARFLLWHATSRLPDLDKTSVARYTTFN 2820
Db 2761 TDMTPPLRAWRKKARAVLASAKRRGGAHAKLARFLLWHATSRLPDLDKTSVARYTTFN 2820
Qy 2821 YCDVYSPGSDVFTPQRLQKFLVKYLAIVFALGLIAVGLAIS 2864
Db 2821 YCDVYSPGSDVFTPQRLQKFLVKYLAIVFALGLIAVGLAIS 2864

RESULT 3
US-08-467-344A-394
; Sequence 394, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATTIAS
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUERHOFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 394:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 394:
US-08-467-344A-394

Query Match 99.6%; Score 15317; DB 4; Length 2864;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2852; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPVISTQTSPPAPRTRKNKQTQASYPVSIKTSVERGORAKRKVQORDARPNYKIAGIHD 60
Db 1 MPVISTQTSPPAPRTRKNKQTQASYPVSIKTSVERGORAKRKVQORDARPNYKIAGIHD 60
Qy 61 GLOTLAQAALPAHGWGRQDPRHKSRNIGILLDYLPLGWIGDVTTHTPLVGLVAGAVRVP 120

Db 61 GLOTLAQAALPAHGWGRQDPRHKSRNIGILLDYLPLGWIGDVTTHTPLVGLVAGAVRVP 120
Qy 121 CQIVRLLEDGVNNAWTFMGVHFLFVVCLLSLACPCSGARVTDPTNTTILTNCCORNQVIY 180
Db 121 CQIVRLLEDGVNNAWTFMGVHFLFVVCLLSLACPCSGARVTDPTNTTILTNCCORNQVIY 180
Qy 181 CSPSTCLHBPCCVICADECWVPANPYISHPSNWTGDSFLADHIDFVNGALVTCOALDIDG 240
Db 181 CSPSTCLHBPCCVICADECWVPANPYISHPSNWTGDSFLADHIDFVNGALVTCOALDIDG 240
Qy 241 ELGCACVLVGDMLVRHMLIHI DLNETGTCYLEVPTGIDPGFLGPIGMAGKVEAVIFLTK 300
Db 241 ELGCACVLVGDMLVRHMLIHI DLNETGTCYLEVPTGIDPGFLGPIGMAGKVEAVIFLTK 300
Qy 301 LASQVPYAIATMFSSVHYLAVGALIIYYASRGKMYQLLALMLYIEATSGNPRIRPTGCSI 360
Db 301 LASQVPYAIATMFSSVHYLAVGALIIYYASRGKMYQLLALMLYIEATSGNPRIRPTGCSI 360
Qy 361 AEFCSPLMI PCPCHSYLSENVSEVICYSYSPKWTPTLEYNNSISWYPTTIPGARGCMVKF 420
Db 361 AEFCSPLMI PCPCHSYLSENVSEVICYSYSPKWTPTLEYNNSISWYPTTIPGARGCMVKF 420
Qy 421 KNTWGCCRIRNVPSYCTMGTDVMDNTRNTYBACGVTPLMTTAWHNGSALKLAILOVPG 480
Db 421 KNTWGCCRIRNVPSYCTMGTDVMDNTRNTYBACGVTPLMTTAWHNGSALKLAILOVPG 480
Qy 481 SKEMFKPHNMWSGHLYPEGSDTPIVIFYDPVNSTLLPPERWARLPGTPPVVRGSLVQVP 540
Db 481 SKEMFKPHNMWSGHLYPEGSDTPIVIFYDPVNSTLLPPERWARLPGTPPVVRGSLVQVP 540
Qy 541 GFYSVDKDLATGLITKDKAWNKYQVLSATGALSLTGVTTKAVVLIILLGCGSKYLILAY 600
Db 541 GFYSVDKDLATGLITKDKAWNKYQVLSATGALSLTGVTTKAVVLIILLGCGSKYLILAY 600
Qy 601 LCYLSLCFGRASGYPLRPVLPQSQYLAQNDVLSKAQVAPFALFFCCYLCRCLRVAAL 660
Db 601 LCYLSLCFGRASGYPLRPVLPQSQYLAQNDVLSKAQVAPFALFFCCYLCRCLRVAAL 660
Qy 661 LGFVPMAGLPLTFVFAAAAAQPDYDWMVRLLVAGLVWAGRNRRHRIALLVGPWPLVAL 720
Db 661 LGFVPMAGLPLTFVFAAAAAQPDYDWMVRLLVAGLVWAGRDGRPRIALLVGPWPLVAL 720
Qy 721 LTLHLVTPASAFDTEIIIGGLTTPPVVALVVMRSGFPAHLPCALVNSYLWGRWENWF 780
Db 721 LTLHLVTPASAFDTEIIIGGLTTPPVVALVVMRSGFPAHLPCALVNSYLWGRWENWF 780
Qy 781 WNTVLRPERFVLVCPGATYDALVTFVCHVALLCLTSSAASFFGTSRVRHMLVR 840
Db 781 WNTVLRPERFVLVCPGATYDALVTFVCHVALLCLTSSAASFFGTSRVRHMLVR 840
Qy 841 LGKCHAWYSHYVLKFFLLVFGENGVPFYKHLHGDVLPNDPASKLPQEPFPFEGKARVY 900
Db 841 LGKCHAWYSHYVLKFFLLVFGENGVPFYKHLHGDVLPNDPASKLPQEPFPFEGKARVY 900
Qy 901 RNEGRRLACGDTVDGLPVVARLGDVLPAGLAMPDGWAIITAPFTLQCLSERGTLSAMAV 960
Db 901 RNEGRRLACGDTVDGLPVVARLGDVLPAGLAMPDGWAIITAPFTLQCLSERGTLSAMAV 960
Qy 961 MTGIDPRPTWTGTIFRLGSLATSYMGFVCDNVLYTAHHGSKRRLAHPTGSIHPITVDAAN 1020
Db 961 MTGIDPRPTWTGTIFRLGSLATSYMGFVCDNVLYTAHHGSKRRLAHPTGSIHPITVDAAN 1020
Qy 1021 DQDIYQPPCGAGSLTRCSCGETKGYLVTRLGSLVENVKSDDPYWCVCALPMAVAKGSSG 1080
Db 1021 DQDIYQPPCGAGSLTRCSCGETKGYLVTRLGSLVENVKSDDPYWCVCALPMAVAKGSSG 1080
Qy 1081 APILCSSHGHVGMFTAAARNSGGVSQIRVRPLVCAGYHPQYTAHATLDTKPTVNEYSVQ 1140
Db 1081 APILCSSHGHVGMFTAAARNSGGVSQIRVRPLVCAGYHPQYTAHATLDTKPTVNEYSVQ 1140
Qy 1141 ILIAPTSGSGSTKLPLSYMQEKEYVLNPSVATTASMPKYMHTATYGVNPNCEYNGKCTN 1200
Db 1141 ILIAPTSGSGSTKLPLSYMQEKEYVLNPSVATTASMPKYMHTATYGVNPNCEYNGKCTN 1200

QY 1201 TGAISLYTYGMYLTGACSRNYDVIIICDECHADATTVLGIGKVLTEAPSKNRLVVLAT 1260
DB 1201 TGAISLYTYGMYLTGACSRNYDVIIICDECHADATTVLGIGKVLTEAPSKNRLVVLAT 1260
QY 1261 ATPPGVIPTPHANITEIQLTDEGTTIPFHGKKIKEENLKKGRHLIPEATYKHCDELANELA 1320
DB 1261 ATPPGVIPTPHANITEIQLTDEGTTIPFHGKKIKEENLKKGRHLIPEATYKHCDELANELA 1320
QY 1321 RKGITAVSYRGCDISKIPGDCVVVATDALTCTGYTGFDSVYDCSLMVEGTCVLDLPT 1380
DB 1321 RKGITAVSYRGCDISKIPGDCVVVATDALTCTGYTGFDSVYDCSLMVEGTCVLDLPT 1380
QY 1381 FTMGVRVCGSAIVKQGRGRTGRAGIYYVVDGSCCTPSGMVPECNIVEAFDAKAWYG 1440
DB 1381 FTMGVRVCGSAIVKQGRGRTGRAGIYYVVDGSCCTPSGMVPECNIVEAFDAKAWYG 1440
QY 1441 LSSTEAQTILDTYRTPQGLPAIGANLDEWADLFMSVNPPEPFPVNTAKRTADNYLLTAAQ 1500
DB 1441 LSSTEAQTILDTYRTPQGLPAIGANLDEWADLFMSVNPPEPFPVNTAKRTADNYLLTAAQ 1500
QY 1501 LQLOCHOYGAAPNDAPRQOGLKPKCGVLWRLDGADACPGPESEVTRYQMCETEYNT 1560
DB 1501 LQLOCHOYGAAPNDAPRQOGLKPKCGVLWRLDGADACPGPESEVTRYQMCETEYNT 1560
QY 1561 SGTAAALAVGVGAMAYLAIDTFGATCVRRCSITSVPPTGATVAPVVDSEEVIEECASFP 1620
DB 1561 SGTAAALAVGVGAMAYLAIDTFGATCVRRCSITSVPPTGATVAPVVDSEEVIEECASFP 1620
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DB 1621 LEAMVAADKUKSTITTTSPFTLETALEKJNTFLGPHAATILAIIEYCCGLVTLDPNPPA 1680
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DB 1681 SCVFAFIAGITTPLEPHKIMFSLFPGGAISKLTDAARGALAFMMAAGATLGTWTSVGF 1740
QY 1741 VFDMLGGYAAASSTACLTFFKCLMGWPTMDQLAGLVYSAFNPAAGVGVLSACAMFALT 1800
DB 1741 VFDMLGGYAAASSTACLTFFKCLMGWPTMDQLAGLVYSAFNPAAGVGVLSACAMFALT 1800
QY 1801 AGPDHWPNRLLTMLARSNTVCNEYFIATRDTRRKILGLEASTPMSVISACIRWLHTPTE 1860
DB 1801 AGPDHWPNRLLTMLARSNTVCNEYFIATRDTRRKILGLEASTPMSVISACIRWLHTPTE 1860
QY 1861 DDCGLIANGLEIWOVQCNFFVTCFNVLKAGVQSMWNIIPGCPYSCQYKGPWIGSMLO 1920
DB 1861 DDCGLIANGLEIWOVQCNFFVTCFNVLKAGVQSMWNIIPGCPYSCQYKGPWIGSMLO 1920
QY 1921 ARCPGABELIFSVENGFAKLYKGPRTCSNYRGAVPVNARLCSARPDPDWTSLVNVYG 1980
DB 1921 ARCPGABELIFSVENGFAKLYKGPRTCSNYRGAVPVNARLCSARPDPDWTSLVNVYG 1980
QY 1981 VRDYCKYKEMGDHIFVTAVSSPNVCFQVPTPLRAAVADVQVQCYLGEKPTWTTTAC 2040
DB 1981 VRDYCKYKEMGDHIFVTAVSSPNVCFQVPTPLRAAVADVQVQCYLGEKPTWTTTAC 2040
QY 2041 CYGPDGKGTWKLPRFVNGHTPGVWQNLDALETNDCNSINNTFSPDEAAVSALVFKQE 2100
DB 2041 CYGPDGKGTWKLPRFVNGHTPGVWQNLDALETNDCNSINNTFSPDEAAVSALVFKQE 2100
QY 2101 LRRTNQLLEAISAGVDDTKLPAPSIIEVVVRKQFRARTGSLTLPPLPPRSPGVSCPESL 2160
DB 2101 LRRTNQLLEAISAGVDDTKLPAPSIIEVVVRKQFRARTGSLTLPPLPPRSPGVSCPESL 2160
QY 2161 QRSDPLEGNSLPPRSPVQLAMPPLLAGECNPFITAICAMTETGGDDPLSPYPPKK 2220
DB 2161 QRSDPLEGNSLPPRSPVQLAMPPLLAGECNPFITAICAMTETGGDDPLSPYPPKK 2220
QY 2221 EVSEWSDESWSATTASSVVTGPPYKIRGKDSQTOSAPAKRPTKKLKGSEFSCMSYTW 2280
DB 2221 EVSEWSDESWSATTASSVVTGPPYKIRGKDSQTOSAPAKRPTKKLKGSEFSCMSYTW 2280

QY 2281 TDVISFKTASKVLASATRAITSGFLKQRLSVLVYTEPRDAELRQKQVTINRQPLFPSPSYHKQ 2340
DB 2281 TDVISFKTASKVLASATRAITSGFLKQRLSVLVYTEPRDAELRQKQVTINRQPLFPSPSYHKQ 2340
QY 2341 VRLAKEKASKVGVWMDYDEVAHAHTPSKSAKSHITGLRGTDVRSGAARKAVLDLQKVEA 2400
DB 2341 VRLAKEKASKVGVWMDYDEVAHAHTPSKSAKSHITGLRGTDVRSGAARKAVLDLQKVEA 2400
QY 2401 GEIPSHYRQTVIVPKEEVFKTPKPKPPRLISYPHLEMRCEVKMYGQVADPVVKAV 2460
DB 2401 GEIPSHYRQTVIVPKEEVFKTPKPKPPRLISYPHLEMRCEVKMYGQVADPVVKAV 2460
QY 2461 MGDYGFVDPRTVRKRLLSMWSPDVAGATCDTVCDFSTITTPEDIMVETDIYSAAKLSQDQ 2520
DB 2461 MGDYGFVDPRTVRKRLLSMWSPDVAGATCDTVCDFSTITTPEDIMVETDIYSAAKLSQDQ 2520
QY 2521 RAGIHTIARQLYAGPPIAYDGREIGYRRCRSSGVYTTSSNSLTCWLKVNAAAEOAGMK 2580
DB 2521 RAGIHTIARQLYAGPPIAYDGREIGYRRCRSSGVYTTSSNSLTCWLKVNAAAEOAGMK 2580
QY 2581 NPRLICGDDCTVIWKSGADADQAMRVFASWMMKMGAPQDCVPQPKYSLEELTSCSSN 2640
DB 2581 NPRLICGDDCTVIWKSGADADQAMRVFASWMMKMGAPQDCVPQPKYSLEELTSCSSN 2640
QY 2641 VTSGITKSGPYFLTRDPRIPRLGRCSAEGLYNPSAAWIGYLIHHYPCLWVSRVLAHF 2700
DB 2641 VTSGITKSGPYFLTRDPRIPRLGRCSAEGLYNPSAAWIGYLIHHYPCLWVSRVLAHF 2700
QY 2701 MEQMLFEDKLPETVTFWYKKNYTPVEDLPSIITAGVHGIEAFSVRYTNAEILRVSQL 2760
DB 2701 MEQMLFEDKLPETVTFWYKKNYTPVEDLPSIITAGVHGIEAFSVRYTNAEILRVSQL 2760
QY 2761 TDMTPPLRAWRKKARAVLASAKRRGGAHAKLARFLLWHATSRLPDLDKTSVARYTTFN 2820
DB 2761 TDMTPPLRAWRKKARAVLASAKRRGGAHAKLARFLLWHATSRLPDLDKTSVARYTTFN 2820
QY 2821 YCDVYSPGDFVITPQRLQKFLVKYLAVIVFALGLIAVGLAIS 2864
DB 2821 YCDVYSPGDFVITPQRLQKFLVKYLAVIVFALGLIAVGLAIS 2864
RESULT 4
US-08-424-550B-394
; Sequence 394, Application US/08424550B
; Patent No. 6720166
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATTIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HSPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B

Db 1861 DDCGLIANGLEIWOVCNFFVICFNVLRAGVQSWNIIPGCPFYSCQKYGKPGWISGMLQ 1920
Qy 1921 ARCPGAEILISVENGFPAKLYKGPRCTCSNYRGAVPVNARLCSARPDPDTWTSLVVNG 1980
Db 1921 ARCPGAEILISVENGFPAKLYKGPRCTCSNYRGAVPVNARLCSARPDPDTWTSLVVNG 1980
Qy 1981 VRDYCKYKMGDHIIEVTAIVSSPNVCFVQVPTLRAAVALDVGVQVQCYLGEKPTWTTISAC 2040
Db 1981 VRDYCKYKMGDHIIEVTAIVSSPNVCFVQVPTLRAAVALDVGVQVQCYLGEKPTWTTISAC 2040
Qy 2041 CYGPDGKGTVKLPFRVDGHTGPGVMQNLNRDALETNDCNSTNTPSDEAAVSALVFQOE 2100
Db 2041 CYGPDGKGTVKLPFRVDGHTGPGVMQNLNRDALETNDCNSTNTPSDEAAVSALVFQOE 2100
Qy 2101 LRRTNOLLEAISAGVDTTKLPAPSEEVVVRKQFRARTGSLTLPPRSVPGVSCPESL 2160
Db 2101 LRRTNOLLEAISAGVDTTKLPAPSEEVVVRKQFRARTGSLTLPPRSVPGVSCPESL 2160
Qy 2161 QRSDPLEGPSNLPPSPVQLAMPPLLGAGECNFTAIGCAMTETGGPDDLPSPYPPK 2220
Db 2161 QRSDPLEGPSNLPPSPVQLAMPPLLGAGECNFTAIGCAMTETGGPDDLPSPYPPK 2220
Qy 2221 EVSEWSDSWSTATTASSYVTGPPYKIRGKDSQSPAKRPTKKLKGKSFSCSMSTW 2280
Db 2221 EVSEWSDSWSTATTASSYVTGPPYKIRGKDSQSPAKRPTKKLKGKSFSCSMSTW 2280
Qy 2281 TDVISFKTASVLSATRAITSGFLKORSIVVYTEPRDAELRKQVTINRQPLFPSPSYHQ 2340
Db 2281 TDVISFKTASVLSATRAITSGFLKORSIVVYTEPRDAELRKQVTINRQPLFPSPSYHQ 2340
Qy 2341 VRLAKEKASKVGVNWDYDEVAHHTPSKSAKSHITGLRGTDVRSAGAAKAVLDLQKVEA 2400
Db 2341 VRLAKEKASKVGVNWDYDEVAHHTPSKSAKSHITGLRGTDVRSAGAAKAVLDLQKVEA 2400
Qy 2401 GEIPSHYQTVIVPKEEVFVKTPQKPTKPPRLISYPHLEMRCEVKMYGVQVAPDVXAV 2460
Db 2401 GEIPSHYQTVIVPKEEVFVKTPQKPTKPPRLISYPHLEMRCEVKMYGVQVAPDVXAV 2460
Qy 2461 MGDAGYFVDPTRVRLKLSMSPDAGATCDVCFDSTITPEDINMETDIYSAAKLSQH 2520
Db 2461 MGDAGYFVDPTRVRLKLSMSPDAGATCDVCFDSTITPEDINMETDIYSAAKLSQH 2520
Qy 2521 RAGIHTIARQLYAGGPMIAYDGREIGYRCRSSGVYTTSSNSLTCWLKVNAAAQAGWK 2580
Db 2521 RAGIHTIARQLYAGGPMIAYDGREIGYRCRSSGVYTTSSNSLTCWLKVNAAAQAGWK 2580
Qy 2581 NPFRLICGDDCTVIWKSAGADAKQAMRVFASWKMVGAPQDCVPQPKYSLEELTSCSN 2640
Db 2581 NPFRLICGDDCTVIWKSAGADAKQAMRVFASWKMVGAPQDCVPQPKYSLEELTSCSN 2640
Qy 2641 VTSGITKSGKPYFLTRDPRPLGRCSAEGLYNPSAAWIGYLIHHYBCLWVSRVLAVHF 2700
Db 2641 VTSGITKSGKPYFLTRDPRPLGRCSAEGLYNPSAAWIGYLIHHYBCLWVSRVLAVHF 2700
Qy 2701 MEQMLFEDKLPETVTFDYGKNTYVPVEDLPSIIAGVHGIEAFSVVRYTNABILRVQS 2760
Db 2701 MEQMLFEDKLPETVTFDYGKNTYVPVEDLPSIIAGVHGIEAFSVVRYTNABILRVQS 2760
Qy 2761 TDMTWPPLRAWKKARAVLASAKRRGGAAHAKLARFLWHATSRLPDLDKTSVARYTTFN 2820
Db 2761 TDMTWPPLRAWKKARAVLASAKRRGGAAHAKLARFLWHATSRLPDLDKTSVARYTTFN 2820
Qy 2821 YCDVYSPEGDVFIPTQRLQKFLVKYLAIVIVFALGLIAVGLAIS 2864
Db 2821 YCDVYSPEGDVFIPTQRLQKFLVKYLAIVIVFALGLIAVGLAIS 2864

RESULT 5
US-08-469-260A-83
; Sequence 83, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSAHWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 1422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-260A-83

Query Match 48.0%; Score 7380; DB 4; Length 1422;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1392; Conservative 2; Mismatches 27; Indels 10; Gaps 2;
Qy 1005 AHPTGSIHPITVDAANDQDIYQPPCGAGSLTRCSCGETKGLVTRLGLSLVEVNSKDDPYW 1064
Db 1 AHPTGSIHPITVDAANDQDIYQPPCGAGSLTRCSCGETKGLVTRLGLSLVEVNSKDDPYW 60
Qy 1065 CVCCALPMAVAKGSGAPILCSSGHVIGMFTAAARNSGVSQIRVRLVCAGYHPQYTAH 1124
Db 61 CVCCALPMAVAKGSGAPILCSSGHVIGMFTAAARNSGVSQIRVRLVCAGYHPQYTAH 120
Qy 1125 ATLDTKPTVPNEYSVQILIAPTGSGKSTKGLPLSYMQEKEYVLVNLNPSVATTASMPKYMHA 1184
Db 121 ATLDTKPTVPNEYSVQILIAPTGSGKSTKGLPLSYMQKXKEVLVNLNPSVATTASMPKYMHA 180
Qy 1185 TYGVNPNICYFNGKCTNTGASLTYSYGMVLTGACSRNVDVILICDECHATDATTVLGIGKV 1244
Db 181 TYGVNPNICYFNGKCTNTGASLTYSYGMVLTGACSRNVDVILICDECHATDATTVLGIGKV 240
Qy 1245 LTEAPSKNRLVVLATATPPGVIPTPHANITEIOLTDSEGTIPFHGKKIKENLKKGRHLI 1304
Db 241 LTEAPSKNRLVVLATATPPGVIPTPHANITEIOLTDSEGTIPFHGKKIKENLKKGRHLI 300
Qy 1305 FEATKKCHCELANELARKGITAVSYRGCDSIKIPEGDCVVVATDALCTGYTGDPSVDY 1364

Db 301 |||||FEATKGCDELANLARKG|TAVSYRGCDISKMPGDCVVAATDALCTGYTGDFDSVYD 360
Qy 1365 CSLMVEGTCHVDLDP|TTMGVVRVCGVSAI|VKQRRGRTGRAGI|YVYVDSGCTPSPGWP 1424
Db 361 CSLMVEGTCHVDLDP|TTMGVVRVCGVSAI|VKQRRGRTGRAGI|YVYVDSGCTPSPGWP 420
Qy 1425 ECNIVEAFDAKAWY|GLSSTEAQ|ILDTYRTQGLPAIGAN|LDDEWADLFMSVNPSPFVN 1484
Db 421 ECNIVEAFDAKAWY|GLSSTEAQ|ILDTYRTQGLPAIGAN|LDDEWADLFMSVNPSPFVN 480
Qy 1485 TAKETADNYVLLTAA|OLCHOYGYAAPNDAPR|QOARLKKPCGVLRDLGDACDGPPE 1544
Db 481 TAKETADNYVLLTAA|OLCHOYGYAAPNDAPR|QOARLKKPCGVLRDLGDACDGPPE 540
Qy 1545 PSEVTRYQMCFTENV|TSGTALAAGVGVAMAY|LAIDTFGATCVRRCWSITSVPTGATVAP 1604
Db 541 PSEVTRYQMCFTENV|TSGTALAAGVGVAMAY|LAIDTFGATCVRRCWSITSVPTGATVAP 600
Qy 1605 VVDEEEIVEECASPI|PLEAMVAADK|LSTITTTSPFTLETALEK|NTFLGPHAATILAI 1664
Db 601 VVDEEEIVEECASPI|PLEAMVAADK|LSTITTTSPFTLETALEK|NTFLGPHAATILAI 660
Qy 1665 IEYCCGLVTLDPN|PASCVPFAFIAGIT|TPLPHKIKMFLS|LPGGAIASKLTDARGALAFMM 1724
Db 661 IEYCCGLVTLDPN|PASCVPFAFIAGIT|TPLPHKIKMFLS|LPGGAIASKLTDARGALAFMM 720
Qy 1725 AGAAGTALGTWTS|VGFVMDLGGVAAAS|STAFLTKCLMG|SWPTMDOLAGLVSAFNPAA 1784
Db 721 AGAAGTALGTWTS|VGFVMDLGGVAGAS|STAFLTKCLMG|EWXTMDQAGLVSAFNPAA 780
Qy 1785 GVGVLSACAMFALT|TAGDPHWPNRLL|TMLARSN|TVCNFPIATRD|IRRKILGILEASTP 1844
Db 781 GVGVLSACAMFALT|TAGDPHWPNRLL|TMLARSN|TVCNFPIATRD|IRRKILGILEASTP 840
Qy 1845 WSVLSACIRMLHT|PTEDDCGLIANG|LIWQVVCN|FPVICFNVLKAGVQSWNIPGCPFPYS 1904
Db 841 WSVLSACIRMLHT|PTEDDCGLIANG|LIWQVVCN|FPVICFNVLKAGVQSWNIPGCPFPYS 900
Qy 1905 CQKYGKGPWISGM|QWLRQPCGAB|LIFS|VENGPAKLYG|PRTCSNYWRGAVPVNARLCGS 1964
Db 901 CQKYGKGPWISGM|QWLRQPCGAB|LIFS|VENGPAKLYG|PRTCSNYWRGAVPVNARLCGS 960
Qy 1965 ARPDPTDWTSLV|NNGYVDYCKY|EKMGDHI|FVTAV|SSPNVCF|TQVPTLRAAAVADGVQV 2024
Db 961 ARPDPTDWTSLV|NNGYVDYCKY|EKMGDHI|FVTAV|SSPNVCF|TQVPTLRAAAVADGVQV 1020
Qy 2025 QCYLGEKPTWTT|SACCYGPDKG|KTKVL|PPRV|DGHTPGV|RMQNLN|DLALETNDCSINN 2084
Db 1021 QCYLGEKPTWTT|SACCYGPDKG|KTKVL|PPRV|DGHTPGV|RMQNLN|DLALETNDCSINN 1080
Qy 2085 TPSDEAAVSALV|FKQELRRNTN|LLEAIS|AGVDTTKL|PAPS-|IEBVVVRKQFRARTGSLT 2143
Db 1081 TPSDEAAVSALV|FKQELRRNTN|LLEAIS|AGVDTTKL|PAPS|QIEBVVVRKQFRARTGSLT 1140
Qy 2144 LPPPPRSVPGV|SCPSLQSD|PLEGPNL|PSPV|LQAMP|PLL|GAGCN|PFTTAIGCAM 2203
Db 1141 LPPPPRSVPGV|SCPSLQSD|PLEGPNL|PSPV|LQAMP|PLL|GAGCN|PFTTAIGCAM 1200
Qy 2204 TETGGGDDDLPS|YPPPKKEV|SWSDES|WSTATT|ASSY|TGGPY|PKIRK|DSTQSA|PAKRPT 2263
Db 1201 TETGXEPXLLPS|YPPPKKEV|SWSDES|WSTATT|ASSY|TGGPY|PKIRK|DSTQSA|PAKRPT 1260
Qy 2264 KKLKGSEFSCMS|YTTWDTV|ISFTASKV|SATRAIT|SGFL|KORS|LVVY|TTEPRDAELRKQ 2323
Db 1261 KKLKGSEFSCMS|YTTWDTV|ISFTASKV|SATRAIT|SGFL|KORS|LVVY|TTEPRDAELRKQ 1320
Qy 2324 KVTINRQPLFP|PPSYHKQV|RLAKEK|ASKV|GVMW|DYDEVA|AHTPSK|SAKSHIT|GLRGTDVR 2383
Db 1321 KVTINRQPLFP|PPSYHKQV|RLAKEK|ASKV|GVMW|DYDEVA|AHTPSK|SAKSHIT|GLRGTD-- 1378
Qy 2384 SGAARKAVDLQ|KCVEAGE|IPSHYRQTV|IVPKBEV|FVKTPQK|TKKPPRLI 2434
|||||

Db 1379 -----VLDLQKCVEAGE|IPSHYRQTV|IVPKBEV|FVKTPQK|TKKPPRLI 1422
RESULT 6
US-08-488-446-83
; Sequence 83, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BULJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1422 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-446-83
Query Match 48.0%; Score 7380; DB 4; Length 1422;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1392; Conservative 2; Mismatches 27; Indels 10; Gaps 2;
Qy 1005 AHPTGSHPTVDAANDQDIYQPPCGAGSLTRCSCGETKGYLVTRLGSLVEVNSDDPYW 1064
Db 1 AHPTGSHPTVDAANDQDIYQPPCGAGSLTRCSCGETKGYLVTRLGSLVEVNSDDPYW 60
Qy 1065 CVCGLPMAVAKSSGAPILCSSHVIGMETAAARNSGSVSOIRVRPLVCAGYHPQYTAH 1124
Db 61 CVCGLPMAVAKSSGAPILCSSHVIGMETAAARNSGSVSOIRVRPLVCAGYHPQYTAH 120
Qy 1125 ATLDTKFTVNEYSVQILIAPTSGSGSKLPLSYMQEKYEVNLNPSVATTASMPKYMHA 1184
Db 121 ATLDTKFTVNEYSVQILIAPTSGSGSKLPLSYMQEKYEVNLNPSVATTASMPKYMHA 180
Qy 1185 TYGVNPNCFNGKCTNTGASLTYSTYGMVLTGACSRNYDVIICDECHATDATTVLGIGKV 1244

Db 181 TYGVNPNCFYNGKCTNTGASLTYSYGMKLTGRCSRNVDIICDECHATDRTTVLIGKV 240
QY 1245 LTEAPSKNVLVLVATATPPGVIPPHANIITEIQLTDEGTTIPFHGKKIKEENLKKGRHLI 1304
Db 241 LTEAPSKNVLVLVATATPPGVIPPHANIITEIQLTDEGTTIPFHGKKIKEENLKKGRHLI 300
QY 1305 FEATKKHCDLANELARKGITAVSYRGCDSKIPEGDCVVVATDALCTGYTGDFDSYVD 1364
Db 301 FEATKKHCDLANELARKGITAVSYRGCDSKIPEGDCVVVATDALCTGYTGDFDSYVD 360
QY 1365 CSLMVEGCHVDLDPFTFMGVRVVCVSAIVKQRRGRTGRGRAGIYVYVDSCTPSGMVP 1424
Db 361 CSLMVEGCHVDLDPFTFMGVRVVCVSAIVKQRRGRTGRGRAGIYVYVDSCTPSGMVP 420
QY 1425 ECNIVEAERDAKAWYGLSSTEAQTILDTYRTPGLPAIGANLDEWADLFPMVNPESFVN 1484
Db 421 ECNIVEAERDAKAWYGLSSTEAQTILDTYRTPGLPAIGANLDEWADLFPMVNPESFVN 480
QY 1485 TAKRTADNVLLTAAQLQCHQYGYAAPNDAPRWQCARLKKPCGVLRWLDGACACGPE 1544
Db 481 TAKRTADNVLLTAAQLQCHQYGYAAPNDAPRWQCARLKKPCGVLRWLDGACACGPE 540
QY 1545 PSEVTRYQMCFTVNTSGTAAALAVGVGVAMAYLAIDTFGATCVRRCWSITSVPTGATVAP 1604
Db 541 PSEVTRYQMCFTVNTSGTAAALAVGVGVAMAYLAIDTFGATCVRRCWSITSVPTGATVAP 600
QY 1605 VVDEEEIVEECASFIPLEAMVAAIDKLKSTITTSPTFTALEKLNFTFLGPHAATILAI 1664
Db 601 VVDEEEIVEECASFIPLEAMVAAIDKLKSTITTSPTFTALEKLNFTFLGPHAATILAI 660
QY 1665 IEYCCGLVLPDNPFPASCVPFAFIAGITTPHKKIKNFLSLFGGATASKLTDARGALAFWM 1724
Db 661 IEYCCGLVLPDNPFPASCVPFAFIAGITTPHKKIKNFLSLFGGATASKLTDARGALAFWM 720
QY 1725 AGAAGTALGTWTSVGFVDMGLGGYAAASSTAACLTFKCLMGEMPTMDQLAGLVYSAPNAA 1784
Db 721 AGAAGTALGTWTSVGFVDMGLGGYAAASSTAACLTFKCLMGEMXTMDQLAGLVYSAPNAA 780
QY 1785 GWVGLSACAMFALTAGDPHWPBNLLTMLARSNTVCNEYFIATRDIRKILGILLEASTP 1844
Db 781 GWVGLSACAMFALTAGDPHWPBNLLTMLARSNTVCXEYFTATRDIRKILGILEASTP 840
QY 1845 WSVISACIRWLHTPTEDDCGLIANGLEIWQYVCNEFVFCFNVLKAGVQSMVNIQCPFPYS 1904
Db 841 WSVISACIRWLHTPTEDDCGLIANGLEIWQYVCNEFVFCFNVLKAGVQSMVNIQCPFPYS 900
QY 1905 CQKGYKGPWIGSGLMQLQARCPGCAELIFSVENGFAKLYKGPRTCSNYWRGAVPVNARLCS 1964
Db 901 CQKGYKGPWIGSGLMQLQARCPGCAELIFSVENGFAKLYKGPRTCSNYWRGAVPVNARLCS 960
QY 1965 ARPDPTDWTSLVNVYGVDRDYCKYKMGDHIIFVTAVSSPNVCFQVPTLRAAVAVDGVQV 2024
Db 961 ARPDPTDWTSLVNVYGVDRDYCKYKMGDHIIFVTAVSSPNVCFQVPTLRAAVAVDGVQV 1020
QY 2025 QCYLGEKPTPWTTSACCGPDGKGTVKLPPRVGDHTPGVLMQLNRDALENDNCNNTN 2084
Db 1021 QCYLGEKPTPWTTSACCGPDGKGTVKLPPRVGDHTPGVLMQLNRDALENDNCNNTN 1080
QY 2085 TPSDEAAVSALVFKQLRRTNQLLEBAISAGVDTTKLPAPS-IEEVVVRKQPRARTGSLT 2143
Db 1081 TPSDEAAVSALVFKQLRRTNQLLEBAISAGVDTTKLPAPSQIEEVVVRKQPRARTGSLT 1140
QY 2144 LPPPPRSVPVGCPSLORSPLGSPNLPSPVVLQAMPNPLLGAGECNPFTIAGCAM 2203
Db 1141 LPPPPRSVPVGCPSLORSPLGSPNLPSPVVLQAMPNPLLGAGECNPFTIAGCAM 1200
QY 2204 TETGGGDDLPSPYPPKGVSEWSDESWSATTASSVVTGPPYKPIRGKDSQTOSAPAKRPT 2263
Db 1201 TETGXCPXXLPSPYPPKGVSEWSDESWSATTASSVVTGPPYKPIRGKDSQTOSAKRPT 1260
QY 2264 KKKLGKSEFSCMSYTTWTDVTSFKTASKVLSATRAITSGFLKQSLVYVTEPRDAELRQ 2323

Db 1261 KKKLGKSEFSCMSYTTWTDVTSFKTASKVLSATRAITSGFLKQSLVYVTEPRDAELRQ 1320
QY 2324 KVTINRQPLFPSPYHVKVRLAKERASKVGVWMDYDEVAHAHTPSKSAKSHITGLRGTDVR 2383
Db 1321 KVTINRQPLFPSPYHVKVRLAKERASKVGVWMDYDEVAHAHTPSKSAKSHITGLRGTD-- 1378
QY 2384 SGAARKAVLDLQKCEAGEIPSHYRQTVIVPKKEVFVKTPQKTKKPPRLI 2434
Db 1379 -----VLDLQKCEAGEIPSHYRQTVIVPKKEVFVKTPQKTKKPPRLI 1422

RESULT 7
US-08-467-344A-83
; Sequence 83, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATTIAS
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUERHOFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESS: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-Jun-1995
; APPLICATION NUMBER: US/08/467,344A
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1422 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-08-467-344A-83

Query Match 48.0%; Score 7380; DB 4; Length 1422;
Best Local Similarity 97.3%; Pred. NO. 0;
Matches 1392; Conservative 2; Mismatches 27; Indels 10; Gaps 2;
QY 1005 AHPTGSHPTIVDAANDODIYQPPCGAGSLTRCSGCTKGYLVTRGLSLVNVKSDDPVW 1064
Db 1 AHPTGSHPTIVDAANDODIYQPPCGAGSLTRCSGCTKGYLVTRGLSLVNVKSDDPVW 60

QY 1065 CVCALPMAVAKGSGAPILCSSGHVIGMFTAARNSGSVSIQIRVRLVCAGYHPQYTAH 1124
DB 61 CVCALPMAVAKGSGAPILCSSGHVIGMFTAARNSGSVGIQIRVRLVCAGYHPQYTAH 120
QY 1125 ATLDTKPTVNPNEYVQVLIILAPTGSGKSTKLPLSYMQEKYEVVLNPSVATTASMPKYMHA 1184
DB 121 ATLDTKPTVNPNEYVQVLIILAPTGSGKSTKLPLSYMQEKYEVVLNPSVATTASMPKYMHA 180
QY 1185 TYGVNPNCYFNGKCTNTGASLTYSYTGMYLTGACSRNYDVIICDECHATTATTVLIGIKV 1244
DB 181 TYGVNPNCYFNGKCTNTGASLTYSYTGMYLTGACSRNYDVIICDECHATTATTVLIGIKV 240
QY 1245 LTEAPSKNRLVWLATATPGVITPHANITEIQLTDEGTIPFGKKIKEENLKKGRHLI 1304
DB 241 LTEAPSKNRLVWLATATPGVITPHANITEIQLTDEGTIPFGKKIKEENLKKGRHLI 300
QY 1305 FEATKKHCDLANELARKGITAVSYRGCDISKIPEGDCVVAATDALCTGVTGDFDSVYD 1364
DB 301 FEATKKHCDLANELARKGITAVSYRGCDISKIPEGDCVVAATDALCTGVTGDFDSVYD 360
QY 1365 CSLMVEGTCHVDLDPFTFMGVYRVCVSAIVKQRRGRTRGRAGIYVYVDSCTPSGMVP 1424
DB 361 CSLMVEGTCHVDLDPFTFMGVYRVCVSAIVKQRRGRTRGRAGIYVYVDSCTPSGMVP 420
QY 1425 ECNIVEAFDAKAWYGLSSTEAQIILDTYRTQPLPAIGANLDEWADLFMSVNPPEPSFVN 1484
DB 421 ECNIVEAFDAKAWYGLSSTEAQIILDTYRTQPLPAIGANLDEWADLFMSVNPPEPSFVN 480
QY 1485 TAKTADNYVLLTAQOLCHOYGYAAPNDAPRQGARLGKPCGVLRWLDGADACPGPE 1544
DB 481 TAKTADNYVLLTAQOLCHOYGYAAPNDAPRQGARLGKPCGVLRWLDGADACPGPE 540
QY 1545 PSEVTRYQMCFTVNTSGTAAALAVGVGMAYLAIDTFGATCVRRCWSITSVPTGATVAP 1604
DB 541 PSEVTRYQMCFTVNTSGTAAALAVGVGMAYLAIDTFGATCVRRCWSITSVPTGATVAP 600
QY 1605 VDBEEIVEECASPIPLEAMVAADKLSITTTSPFTLETALSKLNTFLGPHAATILAI 1664
DB 601 VDBEEIVEECASPIPLEAMVAADKLSITTTSPFTLETALSKLNTFLGPHAATILAI 660
QY 1665 IEYCCGLVTLDPNPFASCVAFIAGITTPHKLKMFSLFGGAIASKLTDARALAFMM 1724
DB 661 IEYCCGLVTLDPNPFASCVAFIAGITTPHKLKMFSLFGGAIASKLTDARALAFMM 720
QY 1725 AGAAGTALGTWTSVGFVDFMLGGYAAASSTACLTFFKCLMGSEWPTMDQLAGLVYSAFNPA 1784
DB 721 AGAAGTALGTWTSVGFVDFMLGGYAGASSSTACLTFFKCLMGSEWPTMDQLAGLVYSAFNPA 780
QY 1785 GVGVLSACAMPALTATAGPDHWPNRLLTMLARSNTVCNEYPIATRDTRRKLILGLEASTP 1844
DB 781 GVGVLSACAMPALTATAGPDHWPNRLLTMLARSNTVCNEYPIATRDTRRKLILGLEASTP 840
QY 1845 WSVISACIRWLHTPTEDDCGLIANGLEIWOVCNFFVICENVLKAGVQSMVNIPEGPFYS 1904
DB 841 WSVISACIRWLHTPTEDDCGLIANGLEIWOVCNFFVICENVLKAGVQSMVNIPEGPFYS 900
QY 1905 CQKYGKGPWIGSMGLQARCPGABELISFVENGFAKLYKGPRTCNSYWRGAVPVNARLCGS 1964
DB 901 CQKYGKGPWIGSMGLQARCPGABELISFVENGFAKLYKGPRTCNSYWRGAVPVNARLCGS 960
QY 1965 ARPDPTDWTSLVNVYGVYDYCKYERMGDHI FVTAVSSPNVCFPTQVPTPLRAAVADVQV 2024
DB 961 ARPDPTDWTSLVNVYGVYDYCKYERMGDHI FVTAVSSPNVCFPTQVPTPLRAAVADVQV 1020
QY 2025 OCYLGEKPTPMTTACCYPGDKCTVKLPPRVDPGHTPGVPMQNLNDALETNDCNSTNN 2084
DB 1021 OCYLGEKPTPMTTACCYPGDKCTVKLPPRVDPGHTPGVPMQNLNDALETNDCNSTNN 1080
QY 2085 TPSDEAAVSALVFKQELRRNTNQLLEAISAGVDTTKLPAPS-IEEYVVKRQFRARTGSLT 2143
DB 1081 TPSDEAAVSALVFKQELRRNTNQLLEAISAGVDTTKLPAPS-IEEYVVKRQFRARTGSLT 1140
QY 2144 LPPPPRSVPGVSCPESLQSRDPLEGPNLPPSPVQLAMPMPLLGAGECNPFPTAIGCAM 2203

DB 1141 LPPPPRSVPGVSCPESLQSRDPLEGPNLPPSPVQLAMPMPLLGAGECNPFPTAIGCAM 1200
QY 2204 TETGGGDDDDPSYPPPKKEVSEWSDSTATTASSYVTGPPYKIRGKOSTQSAPAKRPT 2263
DB 1201 TETGXPPXLLPSYPPPKKEVSEWSDSTATTASSYVTGPPYKIRGKOSTQSAPAKRPT 1260
QY 2264 KKKLGKSEFSCSWSYTTWDVTSFKTASKVL SATRAITSGFLKQBSLVYVTEPRDAELRKQ 2323
DB 1261 KKKLGKSEFSCSWSYTTWDVTSFKTASKVL SATRAITSGFLKQBSLVYVTEPRDAELRKQ 1320
QY 2324 KVTINRQPLPPPSYHKQVRLAKKASKVGVGMWDYDEVAHAHTPSKSAKSHITGLRGTDVR 2383
DB 1321 KVTINRQPLPPPSYHKQVRLAKKASKVGVGMWDYDEVAHAHTPSKSAKSHITGLRGTD-- 1378
QY 2384 SGAARKAVLDLQKCVKEAGEIPSHYRQTVIIVPKBEVFKTKPKTKPPRLI 2434
DB 1379 -----VLDLQKCVKEAGEIPSHYRQTVIIVPKBEVFKTKPKTKPPRLI 1422

RESULT 8

US-08-424-550B-83
; Sequence 83, Application US/08424550B
; Patent No. 6720166
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/APED
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1422 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-424-550B-83

Query Match 48.08; Score 7380; DB 4; Length 1422;
Best Local Similarity 97.34; Pred. No. 0;
Matches 1392; Conservative 2; Mismatches 27; Indels 10; Gaps 2;

QY 1005 AHPTGSIHPITVDAANDODIYQPPCAGSLTRCSCGETKGYLVTRLGLSLVEVWKSDDPYW 1064
Db 1 AHPTGSIHPITVDAANDODIYQPPCAGSLTRCSCGETKGYLVTRLGLSLVEVWKSDDPYW 60
QY 1065 CVCALPMAVAKGSSGAPILCSSGHVIGMFTAAARNSGGSVQIRVRPLVCAHYHPQYTAH 1124
Db 61 CVCALPMAVAKGSSGAPILCSSGHVIGMFTAAARNSGGSVQIRVRPLVCAHYHPQYTAH 120
QY 1125 ATLDTKPTVPNEYSVQIILAIATGSGSKTKLPLSYMOEKEYEVLVLPNSVATTASMPKYNHA 1184
Db 121 ATLDTKPTVPNEYSVQIILAIATGSGSKTKLPLSYMOEKEYEVLVLPNSVATTASMPKYNHA 180
QY 1185 TYGVNPNCFNGKCTNTCASLITYSYGMYLGTACSRNYDVIIICDCHATDATTVLIGICKV 1244
Db 181 TYGVNPNCFNGKCTNTCASLITYSYGMYLGTACSRNYDVIIICDCHATDTRTVLIGICKV 240
QY 1245 LTEAPSKNVLVVLATATPPGVIPTPHANITEIQLTDEGTIPFHGKKIKEENLKKGRHLI 1304
Db 241 LTEAPSKNVLVVLATATPPGVIPTPHANITEIQLTDEGTIPFHGKKIKEENLKKGRHLI 300
QY 1305 FEATKKHCDLANELARKIGITAVSYRGCDISKIPBGDCVVVATDALTCTGVTGDFDSYVD 1364
Db 301 FEATKKHCDLANELARKIGITAVSYRGCDISKIPBGDCVVVATDALTCTGVTGDFDSYVD 360
QY 1365 CSLMVEGTCVVDLDPFTFMGVRCVSAIVKQRRGRTGRGRAGIYVYVVGSCPTSGMVP 1424
Db 361 CSLMVEGTCVVDLDPFTFMGVRCVSAIVKQRRGRTGRGRAGIYVYVVGSCPTSGMVP 420
QY 1425 ECNIVEAFDAAKAWYGLSSTEAQTILDTYRTQPLPAIGANLDEWADLFMSVNPSPSVN 1484
Db 421 ECNIVEAFDAAKAWYGLSSTEAQTILDTYRTQPLPAIGANLDEWADLFMSVNPSPSVN 480
QY 1485 TAKRTADNYVLLTAQLOLCHOYGVAAPNDAPRWQCARLKKPCGVLRLOGDACPCPE 1544
Db 481 TAKRTADNYVLLTAQLOLCHOYGVAAPNDAPRWQCARLKKPCGVLRLOGDACPCPE 540
QY 1545 PSEVTRYQMCFTVNTSGTALAUGVGVAMVLAJDTFGATCVRRCWSITSVPTGATVAP 1604
Db 541 PSEVTRYQMCFTVNTSGTALAUGVGVAMVLAJDTFGATCVRRCWSITSVPTGATVAP 600
QY 1605 VVDEEIVEECASFIPLEAMVAADKLKSTITTTSPFTLETALEKLNFTFLGPHAATILAI 1664
Db 601 VVDEEIVEECASFIPLEAMVAADKLKSTITTTSPFTLETALEKLNFTFLGPHAATILAI 660
QY 1665 IEYCCGLVTLDPNPASCVPFAFIAGITTPHKKIKNFLSLFGGATASKLTDARGALAFPM 1724
Db 661 IEYCCGLVTLDPNPASCVPFAFIAGITTPHKKIKNFLSLFGGATASKLTDARGALAFPM 720
QY 1725 AGAAGTALGTWTSVGFVFDMLGGYAAASSTACLTFFKCLMGWPTMDQLAGLVYSAPNAA 1784
Db 721 AGAAGTALGTWTSVGFVFDMLGGYAAASSTACLTFFKCLMGWPTMDQLAGLVYSAPNAA 780
QY 1785 GVGVLSACAMPALTTAGDPHWPNNLLTMLARSNTVCNEYFIATRIDRKKILGILEASTP 1844
Db 781 GVGVLSACAMPALTTAGDPHWPNNLLTMLARSNTVCNEYFIATRIDRKKILGILEASTP 840
QY 1845 WSVISACIRWLHTPTEDDCGLIANGLEIWOYVCNFFVICPNVLKAGVQSWNIPCCPPYS 1904
Db 841 WSVISACIRWLHTPTEDDCGLIANGLEIWOYVCNFFVICPNVLKAGVQSWNIPCCPPYS 900
QY 1905 CQKYGKGPWIGMGLQARCPCCAGELI FSVENGFAKLYKGPRTCSNWRGAVPVNARLCGS 1964
Db 901 CQKYGKGPWIGMGLQARCPCCAGELI FSVENGFAKLYKGPRTCSNWRGAVPVNARLCGS 960
QY 1965 ARPDPTDWTSLVNVYGVDRDYCKYERKMGDHI FVTAVSSPNVCFTQVPPTLRAAVADGVQV 2024
Db 961 ARPDPTDWTSLVNVYGVDRDYCKYERKMGDHI FVTAVSSPNVCFTQVPPTLRAAVADGVQV 1020
QY 2025 QCYLGEPTKPTWTTSAACCGPDGKGTVKLPFRVDGHTPGVRMQLNRLDALENDNCSTNN 2084
Db 1021 QCYLGEPTKPTWTTSAACCGPDGKGTVKLPFRVDGHTPGVRMQLNRLDALENDNCSTNN 1080

QY 2085 TPSDEAAVSALVFKQELRRTNQLLEAISAGVDTTTLKPAPS-IEEVVVRKQFRARTGSLT 2143
Db 1081 TPSDEAAVSALVFKQELRRTNQLLEAISAGVDTTTLKPAPSQIEEVVVRKQFRARTGSLT 1140
QY 2144 LPPPPRSVPGVSCPESLQSDPLEGPNLPPSPVQLAMPMLLGGAGECNPFTAIGCAM 2203
Db 1141 LPPPPRSVPGVSCPESLQSDPLEGPNLPPSPVQLAMPMLLGGAGECNPFTAIGCAM 1200
QY 2204 TETCGGDDLPSPYPPKKEVSEWSDESSTATTASSYVTGPPYPKIRGKDSQTSAPAKRPT 2263
Db 1201 TETGXFPXLPSPYPPKKEVSEWSDESSTATTASSYVTGPPYPKIRGKDSQTSAPAKRPT 1260
QY 2264 KKLKLGSEFSCSMSTYTTDVISFRTASKVLSATRAITSGFLKQSLVYVVTBPRDAELRQ 2323
Db 1261 KKLKLGSEFSCSMSTYTTDVISFRTASKVLSATRAITSGFLKQSLVYVVTBPRDAELRQ 1320
QY 2324 KVTINRQPLPPSPVHVKVRLAKEKASKVGVWMDYDEVAHAHTPSKSAKSHITGLRGTDVR 2383
Db 1321 KVTINRQPLPPSPVHVKVRLAKEKASKVGVWMDYDEVAHAHTPSKSAKSHITGLRGTD - 1378
QY 2384 SGAARKAVLDLQKVEAGEIPSHYRQTVIVPKBEVFVKTPKPKPPRLI 2434
Db 1379 -----VLDLQKVEAGEIPSHYRQTVIVPKBEVFVKTPKPKPPRLI 1422

RESULT 9
US-07-925-695-8
; Sequence 8, Application US/07925695
; Patent No. 5428145
; GENERAL INFORMATION:
; APPLICANT: NAKAMOTO, Hiroaki
; APPLICANT: NAKAMURA, Tetsuo
; TITLE OF INVENTION: NON-A. NON-B HEPATITIS VIRUS GENOME.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBODY AND
; TITLE OF INVENTION: DETECTION SYSTEMS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young
; STREET: 1850 M Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: US
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/925,695
; FILING DATE: 19920807
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 287402/91
; FILING DATE: 09-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 360441/91
; FILING DATE: 05-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Weilacher, Robert G.
; REGISTRATION NUMBER: 20,531
; REFERENCE/DOCKET NUMBER: 06/87-48009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2811
; TELEFAX: (202) 659-1462
; TELEX: WUI 64470
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
US-07-925-695-8

Query Match	21.3%;	Score 3274.5;	DB 1;	Length 3033;
Best Local Similarity	29.9%;	Pred. No. 1.9e-272;		
Matches 980;	Conservative 437;	Mismatches 1181;	Indels 685;	Gaps 107;
Qy	8	TSPVAPRTRKNKQTQASYPVSIK-----TSVERGQBARAKVORDARPR	51	
Db	3	TNPQQRKTGNTNR---PODVKPPGGQIVGGVYLLPRRGRPLGVRATKRTKTSERSQPR	59	
Qy	52	NYKLAGHDGJQTLQAALPAH-----GWGRODPRHKGSRNL	87	
Db	60	GRRQPIKDRSTGKSMGKPGYPWPLYNECGWAGWLLSPRGSRPTWGTDPDRHRSNL	119	
Qy	88	GILLDYPGLWGTDTHTTPLVGLPVAGAVRPVCOIVRLLEDGVNWTG---WFGVHLFV	144	
Db	120	GRVIDTTTCGFADLMGVIPIVVGAPV-GGVARALAHGVRLVDGYNATNLPGCSFISFL	178	
Qy	145	VCLLS-LACPCSGARVTPDNTTILNCCORQIVICSPSTCHEBGCVCICADE-----	198	
Db	179	LALLSCVTPVPSAVEVRN-ISSSYATNDCSNNSITWQLTDAVLHLPGCPVCENDGTLLH	237	
Qy	199	CWPEANPVISHPSNWTGDSFLADHIDFVMGALVTCDAIDIGELCGACVLVGDMLV---	254	
Db	238	CHIQTWNVAVKRGALTRS-LRTHDMIVMAATACSAIYVGDVCGAVMILSQAFMWSPQ	296	
Qy	255	RHMLIHIDLNETHGTCYLEVPTGIDPGFLGFTGMAGVVEAVIFLTKLASQVPIAIATMFS	314	
Db	297	RH-----NFTQBCNCSIYQGHITGHRMAWMLWSPTLTMILAYAAARPVELVLEIIP	349	
Qy	315	SVHYLAVGALIYYASRGKWYQLLALMLY--IEAT---SGNPIRVPTGCSIAEFCSPIMI	369	
Db	350	GGHVGWVFLAYFSMQGAWAKVIAIALLVAGVDATYSSGQ---EAGRTVAGFAGLETT	405	
Qy	370	PCP-----CHSYLSENVSVCVSPKWT-----RPT---	395	
Db	406	GAKQNLVILNTGSHWIRNLTALNCNDSLOTGFLASLFTYHKFNSSGCGPERLSSRCGLDDP	465	
Qy	396	-----TLEYNNIS-----W-YP-----YTIPGARGCM-----	417	
Db	466	RIGWGTLEYETNVTNDGDMRPHYCHYPRPGCIVPARTVCVPGVYCTPSPVWGTDTKQG	525	
Qy	418	-----VQPKNT-----WGC-----CRIR-----NVFSYC	437	
Db	526	VPTYTNGENETDVFLLNSTRPGRGAWFGCTWMNGTGTCTCGAPPCKIRKDYNSTIDLLC	585	
Qy	438	TMGDAVMDNTRNTYEAGVTPMLT-----TAWHNGSALKALILQ---YPSKEMF	485	
Db	586	P--TDCFRKHPDAILYKCGAGFWLTPRCLVDYPRYLWHYPCTVNTTIFKARMYVGGVE--	641	
Qy	486	KPHNMSGHLYF-----BGSDTPIVYFYDPVNSTLLPPERWARLPFTPPVVRGS	534	
Db	642	--HRFSAACNFTRGDRCLDRDRGQSQPLAH-----ST-----TENAVLPCS-----	682	
Qy	535	WLQVPGQFYSVDKOLATGLITKDAWKYQVLYSATGALSUTGTTTAAVULILGLCGSK	594	
Db	683	-----FSDLPALSTGLLHLQHONVDVQVLYGLSPALTRYIVKWEWVILLFLLADAR	734	
Qy	595	YLILAYLCLSLCFGRASGYPLRPVLPQSQYLOAGWDVLSKAQVAPFALIFFICCYLRCR	654	
Db	735	--ICACLWMLI-----ILGQEAALSKLII-----	757	
Qy	655	LYRAALLGFVPMAGLPLTFFVAAAAAQPDYDMWVRLLVAGLVWAGNRGHRITALLVGP	714	
Db	758	-----LHSASAASANGPLWFFIFTAA-----WYLKGRVVPVATYS-----VLGL	797	
Qy	715	WPLVALLTLHLVTPASAFDTEITGGTIPPVVALVWMSRGFFFAHLLPRCALVNSYLM-	773	
Db	798	WSF--LLVLALPOQVADALDAEQLGLLAILIISIFTLTPAYKILLRSRVSVMVLSMLV	855	
Qy	774	-----ORW-----ENWFV-NVTLRPERFLV---LVCPFGATYDALVTFCHV	813	
Db	856	LAEAQIQQWPPLEVRGRDGIHWAVILHRLVFEVTKMLLAILGPAY-----	904	
Qy	814	ALLCLTSSAASFFGTDSRVRAHRML---VRLGKCHAWYSHVYLKFFLLVFGENGFFVFKHL	871	
Db	905	LLKASLLRIPYP-----VRAHALLRVCTLVK-HLAGARIQMLLITIGRTGTGYIDHL	957	
Qy	872	HGDVLPNDPASKPLQ-----EP--FPPEKGARVYRNEGRRLACGDTVDG	915	
Db	958	S-----PLSTWAAQGLRDLAIAVEPVVFSPEKKVIVMGAE--TVACGDILHG	1003	
Qy	916	LPVVARLGDVLFAGLAMPD-----GWAITAPETLQCLSERGTLSANMAVMTGIDPRWT	970	
Db	1004	LPVSARLGREVLLG---PADGYTSKGWKLAPITAYTQOTRGLLGAIVLSLGRDKNEQA	1060	
Qy	971	GTIFRGLSLATSYMGVCDNVLVYTAHHGSGKRRLAHTGSIHPITVDAANDODIYQPPCG	1030	
Db	1061	GOVQLSSVTQTFLGTSISGVLMTVTHGAGNKTLAGPKGPVTQMYTSAEGDLVGPSPPG	1120	
Qy	1031	AGSLTRCSCGETGYLVRGLSILEVENKSDDPYWCVCALPMAVAKSSGAPILCSSHV	1090	
Db	1121	TKSLDPCCTCGVDLYLVTRNADVIPRRKODRRGALLSPRLSTLKGSSGGPVLCSRGHA	1180	
Qy	1091	IGMFTA---ARNSGGSVSQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYSVQILAPTG	1147	
Db	1181	VGLFRAAVCARGVAKSIDFIPVESLDVATRTPSFDNS---TPPAVPSQYQVGYLHAPTQ	1237	
Qy	1148	SGSKTLPPLSYMOKYEVVLNPSVATTASMPKYMHATYGVNPNCYENGKCTNTGASLTY	1207	
Db	1238	SGSKTKVPAAYASQYKVLNPSVAATLFGAYMSKAHGINPIRTGVRTVTTGDSITY	1297	
Qy	1208	STYGMWLT-CACSRN-YDVLIICDECHATDATVILGICKVLTEAPSKKVLVVLATATPPG	1265	
Db	1298	STYKGFADGGCAAGAYDIIICDECHSVDATIILGIGTVLDOAETAGVRLVVLATATPPG	1357	
Qy	1266	VITPHANITEIQLTDEGTIPFHGKKIKBNLKKGRHLIFEATKKHCELANELARKGIT	1325	
Db	1358	TVTTPSHNIEVALGHEGEPFYGKAIPLAFIKGRHLIFCHSKKCDLAAALRGHVN	1417	
Qy	1326	AVSYRGCDISKIP-EGDCVWVATDALCTGYTGDVDSVDCSLMVEGTCHVDLPTPTFMG	1384	
Db	1418	AVAYRGLDVSIVPTQGDVVVVATDALMTGYTGDVDSVIDCNVAVSQIVDFSLDPTETIT	1477	
Qy	1385	VRVCGVSAIVKGORRGTRGRAGIYVYVDSGCTPSCMVPECNIVEAFDAKAVYGLST	1444	
Db	1478	TQTPQDAVRSQRGRTRGRIGRVYVSSGRPSGMSFVSLCECYDAGAAWYELTPA	1537	
Qy	1445	EAOTILDYRTQGLPAIGANLDEWADLFS-MVNPSPSVNTAKRTADNVTLLTAQAOLQ	1503	
Db	1538	ETTIVRLRAYFNTGLPVCQDHLSEWAEVFTGLTHIDAHFLSQTKQGENFAYLTAYQATV	1597	
Qy	1504	CHOYGAAPNDAPRWQGARIGKXPCGVLRDLGDAC-----PGPEP-----	1545	
Db	1598	CAR-----AKAPPSPWD-----VWVK-----CLTRLKPLTGTPTLLYRLGAVTN	1637	
Qy	1546	-----SEVTRY-----QMCFTVNTSGTAAALAVGVVAVLAIDTFCGTCVRRCMSITS-	1595	
Db	1638	EVLTHPVTYIATCMQADLEIMTS-SWVLAGGVLAAVAAYCLAT-----GCISIIGR	1689	
Qy	1596	--VPTGATVAPVDEE-----BIVERCASFIPL-EAMVAADIKLKSTI-----TTTSP	1640	
Db	1690	LHLNDRVVVAP--DKEILYEAFDMECECAKALIEBQRMALMKSKIQGLLOQATROA	1747	
Qy	1641	FTLETALE----KLNTFLGPHAATILAIIBYCCGLVTLDPNPFASCVAFIAGTITPLPH	1696	
Db	1748	QDIQAIQSSWPVKLEQFWAKHWNFIISGQYLAGLSTLPGNPVAVSMWAFSAALTSPLT	1807	
Qy	1697	KIWMFLSFGATASKLTDARGALAFMMAGAGTALGTWTSVG---FVFDMLGVAAS	1753	
Db	1808	STTILLNIMGWLASQIAPPAGATGFVVSGLVGAAGV---SIGLGTKLVDVLGYAGIS	1864	
Qy	1754	TACLTFCKLAGEPTMDOLAGLVYSAFNPAAGVVGVLSACAMFALTITAGPD--HWPNRLL	1811	
Db	1865	GALVAFKIMSGEKTVEDVNLPLPAILSPGALVGVICAILLRHRHVGQEGEGAVOMNRLLI	1924	
Qy	1812	TMLARSNTVCNEVFIATRDIRRKILGLEASTPMSVTSACIRWLHTPTEDDCGLI---AW	1868	

Qy	2104	T-----NQLEA-ISAGVDTTKLPAPSI BEVVVRKKQFRARTGSLTLPPPPRSVPG	2153
Db	2218	TCTTHGRAYDVMVDANLFGMGDVTRIESES--KVYV-----	2252
Qy	2154	VSCPESLQSRDPL-EGPSNLPSS-----PPVLQL-AMP--MPLLGA---GEC	2193
Db	2253	-----LDSJDPMVVEERSDLEPSIPSYMLPKRFPFALPAWARPDPNPLVBSWKRPDY	2306
Qy	2194	NPFTAICAMTETGGGDDLPSPYPKKE-----VSEWS-----DBS	2229
Db	2307	QPATVACCALPP---PKKTPTPPPRRRTVGLSESSIALQOLAISFGQPPPSGDSG	2362
Qy	2230	WST-ATTASSYVTGPP-----YPKIRGKDSTOSAPAKRPTKKKL-----	2267
Db	2363	LSTGADAADSGSRTPPDELALSETGSISSMPPLEGEFGD---PDLEPEQVELQPPQGGV	2419
Qy	2268	-----GKSEFS-----CSMSVTWTD-VTSPKTSKVLKSATRAITSGFLKQRSIV	2310
Db	2420	VTGSGSGSWTSCSEEDSVCCSSYSWTGALITPCSPEEKUPINPLNSLURVHNKV	2479
Qy	2311	YVTEPRDAELRKOKVTINRQFLPPSYHHQVRLAKAKASKVGMVDYDVAHAHTPSKSA	2370
Db	2480	YCTTSKSASLRKVKVTPDRMQALDAHYSVLKDILKAAASKVTARLLTLEACQLTPHSA	2539
Qy	2371	KSHITGLRGTDVR--SGAARKAUDDLOK-CVEAGETPSHVYRQTVIVPKBEVFKVTKOPT	2427
Db	2540	RSKY-GFGAKEVRSLSGRAVNHISKVMKOLLEDTQTPI---PTTIMAKNEVFCVDPDTKGG	2595
Qy	2428	KKPRLISYPHLEMRCEVKVYGOVAPDVVKVNGDAYGF-VDPRTVRKLLSMWS--PD	2484
Db	2596	KKAARLLYVDPDLGVRCRKNALYDITQKLFQAVNGASYGQYSPAQRVFELLKAWAEKD	2655
Qy	2485	AVGATCDVCFDSTITPEDIMVETDIYSAAKLSDQHRAGIHTIARQLYAGGPMIAYDGRE	2544
Db	2656	PMGFSYDTRCFDSTVTERDIRTEESIVYRCSLPEEAHTA IHSLTERLYVCGPMFNSKGQT	2715
Qy	2545	IGYRCRSSGVYTTSSNSITCMUKVNAABEQAKMKNPRELIGDDCTVIWKSGADADAK	2604
Db	2716	CGYRRCRASGLVTTSMGNTITCYKALAAACAAGIIAPTMLVCGDDLDLVSESQGTGEDE	2775
Qy	2605	QAMRVASPMKVMGAPDCVQPPKYSLEELTSCSSNVTSGITKSGPKPYFLTRDPRIPLG	2664
Db	2776	RNLRAFTEMTRYSAPGCDPRPEYDLELITSCSSNVSVALGQGRRRYLYLTRDPTPIA	2835
Qy	2665	RCSAEGLYNPSAAWIGYLIIHHYPCLVWVSRLAVHFMEQMLFEDKLPETVTFDMYGNKYT	2724
Db	2836	RAAWETVRHSPVNSWLNIIOYAPTIWARVMVLMTHFFPSILMAQDTLDONLNFEMYGAVYS	2895
Qy	2725	VPVEDLPSIIAGVHGIAFVSRYVRYTNAEIIIRVSQSLTDMTMPLRAWRKARAVLASAKR	2784
Db	2896	VSPDLPLPAIIERLHGLDAFSLHTYTPHELTRVASALRKLGAAPPLRAWKSRARAVRASLIS	2955
Qy	2785	RGGAHAKLARFLL-WHATSR----PLPDLDKTSVARVYTTFNICYDVSPEGDVITTPORRL	2839
Db	2956	RGGRAAVCGRYLFNWAVKTKLTPLEARLLDLSWFT-----VGAGGGDIYHSVSRAR	3010
Qy	2840	QKFLVKYLAIVIVFALG	2856
Db	3011	PRLLIGLALLFVGVL	3027

RESULT 11
US-09-539-601-3
; Sequence 3, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY

[illegible]

Db 2115 QVPAPEFTEVDGVRLLHRYAPACKPLUREEVTFLVGLNQYLVGSQLPC---EPE----- 2165
Qy 2039 ACCYGPDPKGTVKL--PFRVDGHTPGVRLMQLNRDALETND-----CNSNN 2084
Db 2166 -----PDVAVLTSMITDSHITAETAKRLARGSPPLASSASQLSAPSLKATCTTRHD 2220
Qy 2085 TPSDEAAVSALVFKQEL-----RRTNOLL-----EASAGVTTTKLPAPSIEVVVRK 2132
Db 2221 SPDADLEIANLLWRQEMGNITRVESENKVVILDSFEPLQAEEREVSVPAA--EILRRS 2278
Qy 2133 QFRARTGSLTLPPLRRSPGVSCP-----ESLQSRD-----PLEGPNLPPSP 2176
Db 2279 RKF-----PRAMPWAPDPVNPPLLESWKOPDYVPPVHVHCPLP-PAKAPPIP 2325
Qy 2177 P-----VLQAMPMLLGGAGCNPF-----TAIGCAMTETGGGPDPLP 2214
Db 2326 PSRRKRTVLSESTVSSALAEAL--TETFGSSESAVDSGTATASPDQSDGDAGSDVE 2383
Qy 2215 SY-----PP---KKEVSEWDSWSTATTASSVTPGPPYKPKINGKOSTOSAPAKRPTKKKLK 2268
Db 2384 SYSSMPPLEGPGPDPLSDGWSVSEAS----- 2413
Qy 2269 KSEFSCMSYTWTD-VLSFKTASVLSATRAITSGFLKQRLSVVYTPRDAELRKKQVTI 2327
Db 2414 EDVVCCSMTYWTGALITPCAAEETKLPINALSNLLRHHLNVYATTSSASLRKKQKVT 2473
Qy 2328 NRQPLFPSPYHKQVRLAKEKASKVGVNMWDYDEVAATHPSKASHITGLRGTDVRGAA 2387
Db 2474 DRLQVLDHYEDVLKEMKAKASTVKAKLLSVEACKLTPPHISARSKP-GYKAKDVNR-LS 2531
Qy 2388 RKAVIDLOK-----CWEAGEIPSHYRQTVIVPKEEVVTKPKTKPPRLISYPLEHWRK 2443
Db 2532 SKAVNHIRSVNKKOLLEDTETPI---DITIMAKNEVFCVQPEKGRKPARLIVFPDLGVV 2588
Qy 2444 VEKMYVQGVADPVVYKAVMGDAYGF-VDPRTVRKLLSMWSPD--AVGATCTVCFDSTIT 2500
Db 2589 CERKALVDVSTLTPQAVNGSSYGFQYSPQKRVBFVFNWAKKACPMGFAYDTRCFDSTV 2648
Qy 2501 PEDIWVETDIYSAAKLSQHRAGHTHTARQLYAGGPMIAYDGRIGYRRRCSSGYVTTSS 2560
Db 2649 ENDIRVEESIYQCCDLAPEARQAIRSLTERLIYIGPLTNSKGQNGYRRCBASGLVTTSC 2708
Qy 2561 SNSITCMLKVNAAABQGMKNPRFLICGDDCTVTIWKSGADADAKQMRVPFASMMKVNAP 2620
Db 2709 GNTLTCYLKAAACRAAKLOCDTMLVCGDDLVIWICESAGTQDEASLRAPTEAMTRYSA 2768
Qy 2621 QDCVPOPKYSLELTSCSNVTSGITKSGKPYFLTRDPRIPLGRCAEGLYNPSAAWI 2680
Db 2769 PGDPKPEYDLELITSCSNVSVADHAGSKRVYVLTTRDPTTPLARAAMETARHTPPVNSWL 2828
Qy 2681 GYLTHHPCLVWSRVLAHFMEOMLFEDKLPETVTFDYGKNTVVPVEDLPSIIAGVHGI 2740
Db 2829 GNIITWYAPTLWARMILMTHFFSIIAAGOLEKALDCQIYGACYIEPLDLPQILQRLHGL 2888
Qy 2741 BAFSVRYTNAIILRVQSGLTDMTPPLRAWRKARAVLASAKRGGGAHAKLARFLI-WH 2799
Db 2889 SAFSLHSYSPCEINRVASCLKGLGVPPLRVWRHARSVRARLLSQGGRAATCGKYLEFWA 2948
Qy 2800 ATSR-----PLP-----DLDKTSVARYTTFNVCYDVSPEGDFVITPQRLQKFLVKYLA 2850
Db 2949 VRTKLKUTPIPAASQOLDSSWFVAGYS-----GGDIYHLSLRARPR-----F 2991
Qy 2851 VFALGLIAVGLAI 2863
Db 2992 MWCLLLLSVGVI 3004

RESULT 14

US-09-539-601-21
; Sequence 21, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW

; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; EARLIER FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 3010
; TYPE: PR1
; ORGANISM: Hepatitis C virus
; US-09-539-601-21

Query Match 21.1%; Score 3252; DB 4; Length 3010;
Best Local Similarity 29.9%; Pred. No. 1.7e-270;
Matches 968; Conservative 453; Mismatches 1197; Indels 622; Gaps 115;
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Db 3 TNPKPQRTKRTNRR---PDVKFPGGGQIVGGVYLLPRRPRGLGVRAKTRKTSERSQPR 59
Qy 52 NYKIAGIHGLOTLAQALP-----AHGWRQD 79
Db 60 GRR-----QPIPKARQPEGRAMAQPGYWPVLYGNEGLGWALLSPGSRSPSMGPTD 111
Qy 80 PRKSRNLGILLYPLGVLGIGDVTHTTPLVGLVAGAVVRVQCIVRLLEDCGVNMTG--- 136
Db 112 PRRSRLNGKVIDTLTCGFADLWGYIPLVGAFLGGA-ARALAHGVRVLEDGVNATGNLP 170
Qy 137 WFGVHLFVVCLLS-LAPCPSGARVTDPTNTTILTNCCQNRQVITYCSPTCLHBPQVC 195
Db 171 GCSFSEFLALLSLCTIPASAYERNV-SGVYHVYTNDCSNASIVYEADIMHTPGCVPC 229
Qy 196 ADE-----CWVPANPYTSHSPNMTGDSFLADHIDFVWGLVTCDDALDLCGACVLVG 250
Db 230 VRENNSRRCWALTPTLA-ARNASVPTTIRRHVDLLVGAALCSAMVVGDLCSVFLVA 288
Qy 251 DWLV-----RHWLIHIDLNRTGTCYLEVPTGIDPGFL--GFIGW---MAGKVEAVIFLTKL 301
Db 289 QLTFSPRRHETVQ-DCN-----CSIYFGHVTGHRMWDMMMNWSTALVVSQ 337
Qy 302 ASQVYAIATMFSVHVYAVGALIYYASRGVQLLALMLYIATSGNPRVPTGCSIA 361
Db 338 L-RIPQVAVDMVAGAHVGLAGLAYYSMVGNWAKVLIWMLIFAGVDGTYV---TGGTMA 393
Qy 362 E-----FCSPLMPCPCHSYLSE 379
Db 394 KNTLGITSLFSGSSQKQLVNTNGSMHINRTALNCNDSLNTGFLAALFY---VHKENS 450
Qy 380 -----NVSEVICYSKPTRPTILEYNSISWVPY-----TIPGARGC----- 416
Db 451 GCPERMASCPIDAFAQGW-GPITYNESHSDQRPYCHWHYAPRPGGIVPAAQVGPVYCP 509
Qy 417 -----WYFKPKNT-----WGCCRIRNVPSY-----C 437
Db 510 TSPGVVVGTTDRFGVPTYSGENETDVLNNTNRPQGNWFGCTWMNSTGTCTKCGGPPC 569
Qy 438 TMG-----TDVWNTNRTTYEACGYTPMLT-----TAWHNSALKALILQ- 477
Db 570 NIGGIGNKTLTCTDCFRKHPEATYTKCGSGPMLTTPRCLVHYVYRLHYPTVNTFTIFKV 629
Qy 478 --YPGSKE--MFKPHNMMSG-HLYFEGSDTPIVVFYDPVNSTLLPWRWRLPGTPPVVR 532
Db 630 RMVVGVEHLEACNWTGERCNLEDRD-----SELSPLLLSTTEWQVLPSC----- 678
Qy 533 GSWLQVPGPYSDVKDLATGLITKDKAWKNYQVLYSATGALSITGVTTKAVVLLGLCG 592
Db 679 -----FTTLPALSTGLIHLHQNVDVQVLYGIGSAVVSFAIKWEVYVLLFLLLAD 728
Qy 593 SKYLILAYCYLSLCFGRASGYPLRPVLPQSQSYLAQWDVLSKAQVAPPALIFPICCYLR 652
Db 729 ARVCACLLMMML-----IAQAEALLENLV----- 753

Db 1376 YKAIPIBAIKGRHLIFCHSKKKCDLAAKLTLGLNAVAYRGLDVSVIPPIGDVVVV 1435
Qy 1347 ATDALCTYCTGDFSVYDCSLWVEGTCHVDLPDPTMGVRVCGVSAIYKQGRGRTGR 1406
Db 1436 ATDALMTGTFDGFSDVDCNTCVTQVDFSLDPTFTIETTTVPQDAVSRRGRTGR 1495
Qy 1407 AGIYVYVDSCTPSGMPPECNIVEAFAAKAWYGLSSTEAQTLIDTYRTQCPGLPAIGANL 1466
Db 1496 SGIYRFVTPGSPGMPDSSVLCYCDAGCAWYELTPAETSURLRAYLNTFGLPCQDHL 1555
Qy 1467 DEWADLFG-MYNPEPSFVNTAKRTADNVLLTAQOLQCHQYGAAPNDAPRWOG-ARLG 1524
Db 1556 EFVESVFTGLTHIDAHFLSQTQAGDNFPYLWAYQATVCARAQAPSPSQWQMKLIRLK 1615
Qy 1525 KK---PCGVLRDLGADACPGPESEV-----TRYQM-CFT--EYVNTSGTAAVAVGV 1571
Db 1616 PTLHGFTPLLYRL-----GAVQNEVILTHPITKYIMACHMSADLEVVTS-TWLVGGVL 1667
Qy 1572 VAMAYLAIDTFCATCVRRCWSITSVPTGATVAPVVDEBEI-----VEECASFIP-LEAM 1624
Db 1668 AALAAAYCLTSGSVIVGR-----IILSGKPAVVPDREVLYQEFDEMEECASQLPIEQG 1721
Qy 1625 VAAIDKLK-----STIT-----TTSPTLEALEKLNFTLFGPHAATILAIIEYCCGLVT 1673
Db 1722 MOLABQFKOKALGLLQATATKQAEAAAP--VWESKWRALFTFWAKHWNFTISGIQYLAGLST 1780
Qy 1674 LPDNPFCVCFAGIITPLPHKIMFLSFGGAIASKLTDARGALAFMAGAAGTALG 1733
Db 1781 LFGNPAIASLAFTASITSPLTQNTLLFNILGGWVAQAAPPSSAASAFVGVAGIAGAAGV 1840
Qy 1734 TWTSGVF---VFDMLGGYAAASSTACTFKCLMGEMWPTMDOLAGLVYSAFNPAAAGVGV 1790
Db 1841 ---SIGLQKLVLDIILAGYAGVAGALVAFKVMSEVPSTEDLVNLLPAILSPGALVGVV 1897
Qy 1791 SACAMFALTAGPD-----HWPNRLLTMLARSNVNCNEYFIATRIDRRKILGLEASTPWS 1846
Db 1898 --CAAILRRHVGPBGGAQVQMMNRLIAFASRGNHVSPTHVPESDAAARVQILSLT--- 1952
Qy 1847 VISACIRMLHPTEDDCGLI---ANGLEIWQVYCNFFVICFNVKAGVQS--WNIIPGCP 1901
Db 1953 -ITQLKRLHQWINEBDCSTPCSGSLRDVDMWICT-----VLTFKTLQSKLLPLPGVP 2007
Qy 1902 FYSQCKYKGWPGWGLQARCPGCAELIFSVEENGFAKLYKGPRTCSNWRGAVPVNARL 1961
Db 2008 FLSCORGKYGWVRGDIQWTTCPCAQIAGHVKNSGMRIV-GPRICSNTHWGTFFINAYT 2066
Qy 1962 CGSARPDT-DWTSLVNVYGRDYCKYKMGDHIIFVTAVSSPNV-CFTQVP----- 2010
Db 2067 TGPCTPSAPNYSRALWRVAABEYVEVTRVGDHFVYVGTMTDNNKVCPCQVPAPEPFTVD 2126
Qy 2011 -----PTLRAAVAVD-----GVQVOCYLGEKPTPWTTSACCYGPDPGKGT 2050
Db 2127 GVRLHRYAPACKPLLEDVTFQVGLNQYLVGSQLPF-----EPD-----PDVTVL 2172
Qy 2051 VKL--PFRVDGHTPGVRMQLNRLDALETND-----CNSTNNTPSDEAAVSALV 2096
Db 2173 SMLTDPSSHITAEATXRRLARGSPPSLASSSSQLSAPSILKATCTTHDSGPDADLLEANLL 2232
Qy 2097 FKQEL-----RRTNQLL-----BAISAGVDTTKLPAPSIIEVVVRKQFRARTGSLT 2144
Db 2233 WRQEMGGNITRVESENKVVILDSFEPFLHAEGDEREISVAA--EILKSRKPPSALPIWAR 2290
Qy 2145 P---PP-----PRSVPGV--SCPESLORSPLLEGPSNLPPSP-----VLQAMP 2185
Db 2291 PDYNNPPLLESWKDPDYVPVPHGCELP-----PTKAPPIPPRRKRTVVLTESNVS 2341
Qy 2186 PLLGAGECNPFITAIGCAMTETGGG---PD-----DLPSY---PP---KKEVSEWS 2226
Db 2342 SALAELATKTTGSSGSSSAVDSGTATALPDLASDDGDKGSDVESYSSMPLEGECPDPLS 2401
Qy 2227 DESMSTATTAGSYVTGPYPKIRGKDSQSAKAPRTKKLKGKSBFCSMSYTTWD-VIS 2285
Db 2402 DGSMTVSEAS-----EDVVCCSMSYTTWTGALIT 2431

Qy 2286 PKTASKVLSATRAITSGFLKORSILVYVTEPRDAELRKQKVTINROPLFPPPSYHKQVRLAK 2345
Db 2432 PCAABESKLPINPUSNLLRHHNNVYATTSASLRKQKVTFDRLQVLDHRYDVLKEMK 2491
Qy 2346 EKASKVVGVMWDYDEVAHAHTPSKSAKSHITGLRGTDVRSKAARKAVLDL----KQCVBAG 2401
Db 2492 AKASTVKAKLLSIEEACKLTPHSAKSKF-GYGAKDVRNLSR-AVNHIRSVWEDLLEDT 2549
Qy 2402 EIPSHYQTVTVPEKEEVFKTPQKPTKPPRLISYPHLEMRCEVKMYGQVADPVVKAAM 2461
Db 2550 ETPF---DTTIMAKSEVFCVQPEKGRKPARLIIVFPDLGVRVCEKMALYDVVSLPQAVM 2606
Qy 2462 GDAYGF-VDPRTVRKRLLSMWSPD--AVGATCDTVCDFSTITPEDIMVETDIYSAAKLSD 2518
Db 2607 GSSYGFQYSPQRQVFEFLVNTWKSKKCPMGFSYDTRCFDSTVIESDIRVEESIYQCCDLAP 2666
Qy 2519 QHRAGIHTIARQLYAGGPMIAYDQREIGYRRCSSGVYTTSSNSLTCWLKVNAAEQAG 2578
Db 2667 EARQAIRSLTERLYIGGPLTNSKGQNCYRCRASGVLTTCGNTLTCLYKATAACRAK 2726
Qy 2579 MKNRFLICGDDCTVIWKSAGADADAKQMRVFAWMKVMGAPQDCVPOPKYSLEBLTSCS 2638
Db 2727 LQDCTMLVNGDDLVIYCESAGTQEDAAALRAFTAMTRYAPPDPPQPEYDLELITSCS 2786
Qy 2639 SNVTSGITKSGKPYVELTRDPIPLGRCSABGLGVNPSAAMIGYLIHHYPCLWVSRLAV 2698
Db 2787 SNVSVAHDASGRVYILTRDPTTFLARAWEATARTHPINSWEGNIIMYAPILWARMILMT 2846
Qy 2699 HFMSQMLFEDKLPETVTFDWTGKNYTVFVDELPSIIAGVHGIEAFSVVRYTNABILRVSQ 2758
Db 2847 HFFSILLAQEQLKALDCQIYGACYSIEPLDLPQIIERLHGLSAFTLHYSYSPGEINRVAS 2906
Qy 2759 SLTDMTHPPLRAWKKARAVLASAKRRGGGAHAKLARFLL-WHATSR-----PLP-----DL 2808
Db 2907 CLRKLGVPPPLTWRHRARSRAKLLSQGGAATCGRYLFNMAVTRKLTLPAPASQJDL 2966
Qy 2809 DKTSVARTTNYCDVYSPEGDVFITPQRRLOKFLVKYLAIVFALGLIAYGLAI 2863
Db 2967 SGWFVAGYS-----GGDIYHLSRARPRW-----FPLCLLLLSVGVGI 3004

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Job time : 93 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2005, 15:36:22 ; Search time 286 Seconds
(without alignments)
4186.277 Million cell updates/sec

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Perfect score: 15376
Sequence: 1 MPVISTQTSVPAPTRKNK.....KYLAVIVFALGLIAGLAIS 2864

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	15317	99.6	2864	8	US-08-424-550B-394
3	14474	94.1	2862	9	US-09-742-659-5
4	13194	85.8	2865	9	US-09-742-659-6
5	7380	48.0	1422	8	US-08-424-550B-83
6	3262	21.2	3010	15	US-10-467-000-1
7	3234.5	21.0	3011	15	US-10-296-734-406
8	3232	21.0	3010	16	US-10-333-449A-34
9	3219.5	20.9	3011	9	US-09-742-659-4
10	3215.5	20.9	3011	20	US-11-126-662-1
11	3214.5	20.9	3011	9	US-09-952-572-9
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					Sequence 394, App
					Sequence 5, Appli
					Sequence 83, Appli
					Sequence 1, Appli
					Sequence 406, App
					Sequence 34, Appli
					Sequence 4, Appli
					Sequence 1, Appli
					Sequence 9, Appli

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14	3214.5	20.9	3011	15	US-10-189-359-14	Sequence 14, Appli
15	3214.5	20.9	3011	20	US-11-006-313-20	Sequence 20, Appli
16	3208.5	20.9	3011	10	US-09-891-894-3	Sequence 3, Appli
17	3208.5	20.9	3011	14	US-10-184-150-3	Sequence 3, Appli
18	3208.5	20.9	3011	15	US-10-328-397-3	Sequence 3, Appli
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20	3208.5	20.9	3012	10	US-09-995-937-2	Sequence 2, Appli
21	3208.5	20.9	3012	10	US-09-917-563-2	Sequence 2, Appli
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23	3204.5	20.8	3011	16	US-10-445-724-2	Sequence 2, Appli
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25	3202.5	20.8	3011	10	US-09-995-937-20	Sequence 20, Appli
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28	3148.5	20.5	2985	14	US-10-259-275-40	Sequence 40, Appli
29	3148.5	20.5	2985	20	US-11-006-313-40	Sequence 40, Appli
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32	3126.5	20.3	3011	13	US-10-104-966-1	Sequence 1, Appli
33	3126.5	20.3	3011	15	US-10-719-619-1	Sequence 1, Appli
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36	3045	19.8	2894	14	US-10-044-995-23	Sequence 23, Appli
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38	2992	19.5	576	14	US-10-211-455-3	Sequence 3, Appli
39	2830.5	18.4	2201	13	US-10-029-907-3	Sequence 3, Appli
40	2830.5	18.4	2201	14	US-10-309-561-3	Sequence 3, Appli
41	2830.5	18.4	2201	16	US-10-789-355-3	Sequence 3, Appli
42	2830.5	18.4	2201	16	US-10-686-835-3	Sequence 3, Appli
43	2795.5	18.2	2201	13	US-10-085-476-2	Sequence 2, Appli
44	2754.5	17.9	1985	14	US-10-259-275-42	Sequence 42, Appli
45	2754.5	17.9	1985	16	US-10-639-150-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-742-659-2
; Sequence 2, Application US/09742659
; Patent No. US20010034019A1
; GENERAL INFORMATION:
; APPLICANT: Hong, Zhi
; APPLICANT: Butkiewicz, Nancy J.
; APPLICANT: Zhong, Weidong
; APPLICANT: Ingravallo, Paul
; APPLICANT: Wright-Minogue, Jacquelyn
; APPLICANT: Lau, Johnson Y.
; APPLICANT: Lemon, Stanley M.
; TITLE OF INVENTION: Chimeric HCV/GBV-B viruses
; FILE REFERENCE: ID01116
; CURRENT APPLICATION NUMBER: US/09/742,659
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/171,469
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2864
; TYPE: PRT
; ORGANISM: GB virus-B
US-09-742-659-2

Query Match 100.0%; Score 15376; DB 9; Length 2864;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPVISTQTSVPAPTRKNKQTQASYPVSIKTSVERGORAKKVKVORDARPNRYKIAGIHD 60
DB 1 MPVISTQTSVPAPTRKNKQTQASYPVSIKTSVERGORAKKVKVORDARPNRYKIAGIHD 60

Qy	61	GLQTLAQAALPAHGWGRQDPRKSRNLGILLDYPILGWIGDVTHHTPLVGLPVAGAVVRPV	120
Db	61		
Qy	121	COIIVRLLEDGVNNAWATGFWGHLFVVCLLSLACPSCGARVTDPTNTTILTNCCQRNOVY	180
Db	121		
Qy	181	CSFSTCLHEPGCVICADECWVPANPYISHPSNWGTDSFLADHIDFVMGALVTCDDALD	240
Db	181		
Qy	241	ELCGACVLVDMLVRHMLIHDINETGTCYLEVPTGIDPGFLGFIQWMAKGVKAEAVIFLTK	300
Db	241		
Qy	301	LASQVPYAIATMFSSVHYLAVALGALIIYASRGWYQLLLALMLYIEATSGNPIRVPTGCSI	360
Db	301		
Qy	361	ABFCSPLMPCPCHSYLSENVSEVICYSPKWTRPITILEYNNISISWPTYIPGARGCMVKF	420
Db	361		
Qy	421	KNTWGCCIRINVPSCYCTWGTDAVMDTRNTYACGVTPWLTTAWHNGSALKLAILQYPG	480
Db	421		
Qy	481	SKEMFKPHNMMSGHLYFEGSDTPIVIFYDPVNSTLLPPERWARLPOTPPVVRGSMLOVPQ	540
Db	481		
Qy	541	GFYSVDKDLATGLITKDKAKWNTQVLYSATGALSGLTGVTTKAVVLLILGLCGSKYILAY	600
Db	541		
Qy	601	LCVLSLCFGRASGYPLRPVLPQSQYLOAGHDVLSKAQVAPFALIFPICVLRCLRLYAAL	660
Db	601		
Qy	661	LGFPVMAAGLPLTFVAAAAAQPDYDWMVRLLVAGLVLMAGRNRGHRILALLVGPWPLVAL	720
Db	661		
Qy	721	LTLHLVTPASAFDTEIIIGLTIIPPVVALVMSRFGFFAHLPRCALVNSYLNQRWENWF	780
Db	721		
Qy	781	WNVTLRPERFVLVCFPGATYDALVTFCHVALLCLTSSAASFFGTDSDRVRARHMLVR	840
Db	781		
Qy	841	LGKCHAWYSHYVLKFFLLVFGENGVPYKHLHGDVLPNDPASKLPLOQEPFFPEGKARVY	900
Db	841		
Qy	901	RNEGRRLACGDTVDGLPVVARLGDLPFAGLAMPDPDGAITAPPTLQCLSERGTLSAMAVV	960
Db	901		
Qy	961	MTGIDPRTWGTIIFRLGSLATSYMGFVCDNVLYTAHSGSKGRRLAHPPTGSIHPITVDAAN	1020
Db	961		
Qy	1021	DODIYQPPCAGSLTRCSGKETGKYLVRGLSLVEVKNKSDDPYWCVCGLPMAVAKGSSG	1080
Db	1021		
Qy	1081	APILCSSGHVIGMFTAARNSSGVSQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYSVQ	1140
Db	1081		
Qy	1141	ILIAPTSGSKSTKLPLSYMQEYEVLVNPSVATTASMPKYMATYGVNPNCFYNGKCTN	1200
Db	1141		

Db	1141	ILIAPTSGSKSTKLPLSYMQEYEVLVNPSVATTASMPKYMATYGVNPNCFYNGKCTN	1200
Qy	1201	TGASLTYSTYGYMLTGACSRNYDVIIICDECHATDATTVLIGIKVLTAPSKNVRLVVLAT	1260
Db	1201		
Qy	1261	ATPPGVIPTPHANITIEIOLTDEGTIPFHGKTKKEENLKKGRHLIPEATKKHCELANELA	1320
Db	1261		
Qy	1321	RKGITAVSYRGCDSIKIPEGDCVVVATDALCTGYTGDFDSVYDCSLMVEGTCHVDLDP	1380
Db	1321		
Qy	1381	FTMGVVRVCVSAIVKQORRGTRGRAGIYYVYVDSCTPSGMVPECNIVEADAAKAWG	1440
Db	1381		
Qy	1441	LSSTEAQTLIDTYRTQPLPAIGANLDEWADLFMSVNPPEPSFVNTAKRTADNYVLLTAAQ	1500
Db	1441		
Qy	1501	LQCHQYGYAAPNDAPRMQGARLGKPCGVLRWLDGADACPGPESEVTRYQMCFTEVNT	1560
Db	1501		
Qy	1561	SGTAAVAVGVGVAMAYLAIDTFGATCVRRCWISITSVPTGATVAPVUDEEIVEECASFIP	1620
Db	1561		
Qy	1621	LEAMVAAIDKLSTITTTTSPFTLETALEKNTFLGPHAATILAIIEYCCGLVTLPNPFA	1680
Db	1621		
Qy	1681	SCVFAPAGITTPPHKIKMFLSLFGGAJASKLTDARGALA PMMAGAAAGTALGTWTSVGF	1740
Db	1681		
Qy	1741	VFDMLGGYAAAASTACLTPKCLMGEPWPTMDLAGLVYSAFNPAAVGVVLSACAMFALTT	1800
Db	1741		
Qy	1801	AGPDHWPRLLTWLAARSNTVCNEYFIATRDIRKKILGILEASTPMSVISACIRWLHTPTE	1860
Db	1801		
Qy	1861	DDCGLLIWGLEIWOYVCNFFVICFNVLKAGVQSMVNIPOGPFYSCQKYGKPGWIGSMLQ	1920
Db	1861		
Qy	1921	ARCPGCAELIFSVENGFAKLYKGPRTCSNYWRGAVPNARLCSGASBPDDTMDTSLVVNYG	1980
Db	1921		
Qy	1981	VRDYCKYKMGDHI FVTAVSSPNVCFQVPTLRAAAVAVDGVQVCYLGEPKTPWTTSAC	2040
Db	1981		
Qy	2041	CYGPDKGKTVKLPFRVDGHTPGVRMQLNRDALETNDCNSTNTTSPSDEAAVSALVPKQE	2100
Db	2041		
Qy	2101	LRTNQLLEAI SAGVDTTKLPAPSIIEVVVRKQFPARTGSLTLPBPPRSVRGVCPESL	2160
Db	2101		
Qy	2161	QRSDPLEGNSLPPSPVLQALMPPLL GAGECNPFTAI GCAMTETGGGDDLPSPYPPKK	2220
Db	2161		
Qy	2221	EVSEWSEDSMTATTASSYVTPGPPYPKIRGKOSTQSAPAKRPTKKLKGSEFCSSMSYTW	2280
Db	2221		

Db 2221 EVSEWDESWSTATASSVYTPGPPIRGKDSQAPAKRPTKKGKSEFSCMSMYTM 2280
QY 2281 TDVISEKTASKVLSATRAITSGFLKORSVYVTEPRDAELRKQKVTINRQPLFPSPYHKQ 2340
Db 2281 TDVISEKTASKVLSATRAITSGFLKORSVYVTEPRDAELRKQKVTINRQPLFPSPYHKQ 2340
QY 2341 VRLAKEKASKVGVMMYDDEVAHAHTPSAKSHITGLRGCTDVRSGAARAVLDLQKCVBA 2400
Db 2341 VRLAKEKASKVGVMMYDDEVAHAHTPSAKSHITGLRGCTDVRSGAARAVLDLQKCVBA 2400
QY 2401 GEIPSHYROTIVLPKEEVFKTPQKTKPPRLISYPHLEMCVEKMYGQVAPDVVKAV 2460
Db 2401 GEIPSHYROTIVLPKEEVFKTPQKTKPPRLISYPHLEMCVEKMYGQVAPDVVKAV 2460
QY 2461 MGDAYGFVDPRTRVKLLSMWSPDVGATCDVCFDSTITTPEDIMVETDIYSAAKLSDOH 2520
Db 2461 MGDAYGFVDPRTRVKLLSMWSPDVGATCDVCFDSTITTPEDIMVETDIYSAAKLSDOH 2520
QY 2521 RAGIHTIARQLYAGGPMIAYDREIGYRCRSGGVYTTSSNSLTCWLKVNAAAQAGMK 2580
Db 2521 RAGIHTIARQLYAGGPMIAYDREIGYRCRSGGVYTTSSNSLTCWLKVNAAAQAGMK 2580
QY 2581 NPRELFCGDDCTVIWKSAGADADKQMRVFAWMKVMGAPQDCVPQPKYSLEELTSCSN 2640
Db 2581 NPRELFCGDDCTVIWKSAGADADKQMRVFAWMKVMGAPQDCVPQPKYSLEELTSCSN 2640
QY 2641 VTSGITKSGKPYFYLTRDPRILPGRCSAEGLVNPSAAMIGYLIHHYPCLWVSRVLAVHF 2700
Db 2641 VTSGITKSGKPYFYLTRDPRILPGRCSAEGLVNPSAAMIGYLIHHYPCLWVSRVLAVHF 2700
QY 2701 MEQMLFEDKLPETVTFDWTGKNTYVPELPSIIAGVHGIEAFSVVRYTNAIILVQSOL 2760
Db 2701 MEQMLFEDKLPETVTFDWTGKNTYVPELPSIIAGVHGIEAFSVVRYTNAIILVQSOL 2760
QY 2761 TDMTPPLPRAWKKARAVLASAKRGGAHAKLARELLWHATSRPLDLDKTSVARYTTFN 2820
Db 2761 TDMTPPLPRAWKKARAVLASAKRGGAHAKLARELLWHATSRPLDLDKTSVARYTTFN 2820
QY 2821 YCDVYSPEGDVFTTPORRLQKFLVKYLAIVIFALGLIAVGLAIS 2864
Db 2821 YCDVYSPEGDVFTTPORRLQKFLVKYLAIVIFALGLIAVGLAIS 2864

RESULT 2

US-08-424-550B-394
; Sequence 394, Application US/08424550B
; Publication No. US2002019447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 394:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-424-550B-394

Query Match 99.6%; Score 15317; DB 8; Length 2864;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2852; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MPVISTQTSVPAPRTRKNKQTOASYPVSIKTSVERGQAKKQVORDARPRNYKIAGIHD 60
Db 1 MPVISTQTSVPAPRTRKNKQTOASYPVSIKTSVERGQAKKQVORDARPRNYKIAGIHD 60

QY 61 GIQTLAQAALPAHGWGRODPRHKSRLGLLDYPLGWIQDVTHTHTPLVGLVAGAVVRPV 120
Db 61 GIQTLAQAALPAHGWGRODPRHKSRLGLLDYPLGWIQDVTHTHTPLVGLVAGAVVRPV 120

QY 121 CQIVRLLEDGQVNWATGFWGVHLFVVCLLSLACPCSGARVTDPTNTTILTNCCQNRQVIY 180
Db 121 CQIVRLLEDGQVNWATGFWGVHLFVVCLLSLACPCSGARVTDPTNTTILTNCCQNRQVIY 180

QY 181 CSPSTCLHEPGCVICADECWVPANPYISHPSNWTGDSFLADHIDFVMGALVTCDAIDIG 240
Db 181 CSPSTCLHEPGCVICADECWVPANPYISHPSNWTGDSFLADHIDFVMGALVTCDAIDIG 240

QY 241 ELGACACVLVGDWLVRHLIHDNETGTCYLEVPTGIDPGFLGFGVWAGKVEAVIFLTK 300
Db 241 ELGACACVLVGDWLVRHLIHDNETGTCYLEVPTGIDPGFLGFGVWAGKVEAVIFLTK 300

QY 301 LASQVPAIATMFSSVHYLAVALGALYYASRGKYYQLLLALMLYIEATSGNPIRVPTGCSI 360
Db 301 LASQVPAIATMFSSVHYLAVALGALYYASRGKYYQLLLALMLYIEATSGNPIRVPTGCSI 360

QY 361 AEFCSPLMPCCHSYLSENSEVICYSPKWTPTITLEYNNISISWYPTIPGARGCWKF 420
Db 361 AEFCSPLMPCCHSYLSENSEVICYSPKWTPTITLEYNNISISWYPTIPGARGCWKF 420

QY 421 KNTWGCRCIRNVPSCYCTMGTDVWMDTRNTYEAAGVTPWLTTHWNGSALKLAILQYPG 480
Db 421 KNTWGCRCIRNVPSCYCTMGTDVWMDTRNTYEAAGVTPWLTTHWNGSALKLAILQYPG 480

QY 481 SKEMFKPHNWSGHLIFYEGSDTPIVYFYDPVNSTLLPPERWARLPCTPPVVRGSMLOVPQ 540
Db 481 SKEMFKPHNWSGHLIFYEGSDTPIVYFYDPVNSTLLPPERWARLPCTPPVVRGSMLOVPQ 540

QY 541 GYISDVKDLATGLITKQKAWKQYQVLSATGALSITGVTTKAVVILLGLGCKSKYLILAY 600
Db 541 GYISDVKDLATGLITKQKAWKQYQVLSATGALSITGVTTKAVVILLGLGCKSKYLILAY 600

QY 601 LCYLSLCFGRASGYPLRPVLPQSQSYLQAGWDVLSKAQVAPFALIEFFICYLCRCRURYAAL 660
Db 601 LCYLSLCFGRASGYPLRPVLPQSQSYLQAGWDVLSKAQVAPFALIEFFICYLCRCRURYAAL 660

QY 661 LCFVPMAGLPLTFFVAAAAAQDPDWMVRLLVAGLVLMWAGNRHRIALLVGPWPLVAL 720
Db 661 LCFVPMAGLPLTFFVAAAAAQDPDWMVRLLVAGLVLMWAGNRHRIALLVGPWPLVAL 720

QY 721 LTLHLVTPASAFDTEITGGTIPPVVALVWNSRFGFFAHLPLPRCALVNSYLWQWENWF 780
Db 721 LTLHLVTPASAFDTEITGGTIPPVVALVWNSRFGFFAHLPLPRCALVNSYLWQWENWF 780

Db 721 LTLHLATPASAFDTBIIIGLTIPTPPVVALVMSRFGFFAHLPRCALVNSYLQWRWENWF 780
Qy 781 WNVTLRPERFFVLVCFPGATYDALYTCVCHVALLCLTSSAASFGTDSRVAHRMLVR 840
Db 781 WNVTLRPERFLVLVCFPGATYDYLTVFCVCHVALLCLTSSAASFFGTDSRVAHRMLVR 840
Qy 841 LGKCHAWYSHYVLKFFLLVFGENGVPFYKHLHGDVLPNDPASKLPJQEPFFPFPEGKARVY 900
Db 841 LGKCHAWYSHYVLKFFLLVFGENGVPFYKHLHGDVLPNDPASKLPJQEPFFPFPEGKARVY 900
Qy 901 RNEGRRLACGDTVDGLPVVARLGDLPFAGLAMPDDGWAITAPTLQCLSERGTLSAMAVY 960
Db 901 RNEGRRLACGDTVDGLPVVARLGDLPFAGLAMPDDGWAITAPTLQCLSERGTLSAMAVY 960
Qy 961 MTGIDPRTWGTFIRLGLSLATSYMGFVCONVLTAHHGSKGRRLAHTGSIHPIITVDAAN 1020
Db 961 MTGIDPRTWGTFIRLGLSLATSYMGFVCONVLTAHHGSKGRRLAHTGSIHPIITVDAAN 1020
Qy 1021 DQDIYOPPCAGSLTRCSCGETKGYLVTRLGSLVEVNKSDDPYWCVCALPMAVAKGSSG 1080
Db 1021 DQDIYOPPCAGSLTRCSCGETKGYLVTRLGSLVEVNKSDDPYWCVCALPMAVAKGSSG 1080
Qy 1081 APILCSSGHVIGMFTAAARNSGGSVQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYSVQ 1140
Db 1081 APILCSSGHVIGMFTAAARNSGGSVQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYSVQ 1140
Qy 1141 ILIAPTSGSKSTKPLSYMQEKEYEVLNPSVATTASMPKYMHAATYGVNPNCFYNGKCTN 1200
Db 1141 ILIAPTSGSKSTKPLSYMQEKEYEVLNPSVATTASMPKYMHAATYGVNPNCFYNGKCTN 1200
Qy 1201 TGAISLYSTYGMVLTGACSRNYDVIIICDECHAYDATTVLIGIKVLTEAPSKNVLVLAT 1260
Db 1201 TGAISLYSTYGMVLTGACSRNYDVIIICDECHAYDATTVLIGIKVLTEAPSKNVLVLAT 1260
Qy 1261 ATPPGVPTPHANITBIQLTDEGTIPPHGKKIKENLKKGRHLIIFEATKKGCDLANELA 1320
Db 1261 ATPPGVPTPHANITBIQLTDEGTIPPHGKKIKENLKKGRHLIIFEATKKGCDLANELA 1320
Qy 1321 RKGITAVSYRGCDISKIPBGDCVAVATDALCTGYTGDEDSVYDCSLMVEGTCHVDLPT 1380
Db 1321 RKGITAVSYRGCDISKIPBGDCVAVATDALCTGYTGDEDSVYDCSLMVEGTCHVDLPT 1380
Qy 1381 FTMGVRVCGVSAIVKQRRGRTGRAGIYYYVDGSCTPSGMVPECNIVAEAFDAKAWYG 1440
Db 1381 FTMGVRVCGVSAIVKQRRGRTGRAGIYYYVDGSCTPSGMVPECNIVAEAFDAKAWYG 1440
Qy 1441 LSSTEATQILDVYRTQPLPAIGANLDEWADLFSMNVNPEPSFVNTAKRTADNTVLLTAAQ 1500
Db 1441 LSSTEATQILDVYRTQPLPAIGANLDEWADLFSMNVNPEPSFVNTAKRTADNTVLLTAAQ 1500
Qy 1501 LQICHQYGYAAPNDAPRWQCARLKKPCGYLWRLDGADACGPEPSEVTRYQMCFTEVNT 1560
Db 1501 LQICHQYGYAAPNDAPRWQCARLKKPCGYLWRLDGADACGPEPSEVTRYQMCFTEVNT 1560
Qy 1561 SGTAAALAVGVAMAYLAIDTFGATCVRRCSWTSVPTGATVAPVDEEBEIVEECASFIP 1620
Db 1561 SGTAAALAVGVAMAYLAIDTFGATCVRRCSWTSVPTGATVAPVDEEBEIVEECASFIP 1620
Qy 1621 LEAMVAADIKLSTITPTTLETALUKNTFLGPHAATILAIIEYCCGLVTLPNPFA 1680
Db 1621 LEAMVAADIKLSTITPTTLETALUKNTFLGPHAATILAIIEYCCGLVTLPNPFA 1680
Qy 1681 SCVFAFTAGITTPHPKIKMFLSIFGGAIAASKLTDARGALAFMWGAAGTALGTWTSVGF 1740
Db 1681 SCVFAFTAGITTPHPKIKMFLSIFGGAIAASKLTDARGALAFMWGAAGTALGTWTSVGF 1740
Qy 1741 VFDMLGGYAAASSTACILTFKCLMGWPTMDQLAGLVYSAFNPAAGVGVGLSACAMFALTT 1800
Db 1741 VFDMLGGYAAASSTACILTFKCLMGWPTMDQLAGLVYSAFNPAAGVGVGLSACAMFALTT 1800
Qy 1801 AGPDHWPNRLLTMLARNTVCNEYFIATRIDIRKILGILBEASTPWSVISACIRWLHTPTE 1860
Db 1801 AGPDHWPNRLLTMLARNTVCNEYFIATRIDIRKILGILBEASTPWSVISACIRWLHTPTE 1860

Qy 1861 DDCGLIANGLEIWOYVCNFFVVICFNVLKAGVQSMVNIPEGCPFYSCQKGYKGPWISGMLQ 1920
Db 1861 DDCGLIANGLEIWOYVCNFFVVICFNVLKAGVQSMVNIPEGCPFYSCQKGYKGPWISGMLQ 1920
Qy 1921 ARCPGCAELIIFSVENGFAKLYKGPRTCSNYMRGAVPVNARLCSARPDPDWTSLVYNG 1980
Db 1921 ARCPGCAELIIFSVENGFAKLYKGPRTCSNYMRGAVPVNARLCSARPDPDWTSLVYNG 1980
Qy 1981 VRDYCKYKMGDHIIFVTAVSSBNVCFTQVPPTLRAAVALDVGVQVOCYLGEPTKPTWTSAC 2040
Db 1981 VRDYCKYKMGDHIIFVTAVSSBNVCFTQVPPTLRAAVALDVGVQVOCYLGEPTKPTWTSAC 2040
Qy 2041 CYGPGDGKTKVLKPRFVDGHTPGVMQNLNRLDALETNDCNSTNNTPSDEAAVSALVFKOE 2100
Db 2041 CYGPGDGKTKVLKPRFVDGHTPGVMQNLNRLDALETNDCNSTNNTPSDEAAVSALVFKOE 2100
Qy 2101 LRRTNQLLEAISAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLPPPSPRSVPGVSCPESL 2160
Db 2101 LRRTNQLLEAISAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLPPPSPRSVPGVSCPESL 2160
Qy 2161 QRSDDLLEGSNLPPSPVLOLAMPPLLGAGECNPFTAIGCAWTETGGGDDDLPSVPPKK 2220
Db 2161 QRSDDLLEGSNLPPSPVLOLAMPPLLGAGECNPFTAIGCAWTETGGGDDDLPSVPPKK 2220
Qy 2221 EYSEWSDESWSATTASSYVTGPPYPKIRGKDSTQSAKAPRPTKKKLGKSEFSCMSYTW 2280
Db 2221 EYSEWSDESWSATTASSYVTGPPYPKIRGKDSTQSAKAPRPTKKKLGKSEFSCMSYTW 2280
Qy 2281 TDVIFSKTASKVLSTRAITSGFLKORSILVYVTEPRDAELRKOKVTINRQPLFPSPYHKQ 2340
Db 2281 TDVIFSKTASKVLSTRAITSGFLKORSILVYVTEPRDAELRKOKVTINRQPLFPSPYHKQ 2340
Qy 2341 VRLAKEKASKVGVWMDYDEVAHAHTPSKSAKSHITGLRGTDVRSKAARKAVLDLQKCEA 2400
Db 2341 VRLAKEKASKVGVWMDYDEVAHAHTPSKSAKSHITGLRGTDVRSKAARKAVLDLQKCEA 2400
Qy 2401 GRIPSHYRQTVIVPKEEVFVKTPQKPTKKPRLISYPHLEMCRCVEKMYIGQVAPDVVKAV 2460
Db 2401 GRIPSHYRQTVIVPKEEVFVKTPQKPTKKPRLISYPHLEMCRCVEKMYIGQVAPDVVKAV 2460
Qy 2461 MGDAGYFVDPTRVRKLLSMWSPDAGATCDTVCFDSTITTPEDIMVETDIYSAAKLSDQH 2520
Db 2461 MGDAGYFVDPTRVRKLLSMWSPDAGATCDTVCFDSTITTPEDIMVETDIYSAAKLSDQH 2520
Qy 2521 RAGIHTIARQLYAGGPMIAYDGREIGYRRCRSGVYTTSSNSLTCWLKVNAAAEQAGMK 2580
Db 2521 RAGIHTIARQLYAGGPMIAYDGREIGYRRCRSGVYTTSSNSLTCWLKVNAAAEQAGMK 2580
Qy 2581 NRPFLICGDDCTVIWKSAGADADKQAMRVFASWKMVGAPQDCVPQPKYSLEBLTSCSSN 2640
Db 2581 NRPFLICGDDCTVIWKSAGADADKQAMRVFASWKMVGAPQDCVPQPKYSLEBLTSCSSN 2640
Qy 2641 VTSGITKSGKPYFYLTRDPRIPLGRCSAEGLYNPSAAWIGYLIHHYPCLWVSRVLAVHF 2700
Db 2641 VTSGITKSGKPYFYLTRDPRIPLGRCSAEGLYNPSAAWIGYLIHHYPCLWVSRVLAVHF 2700
Qy 2701 MEQMLFEDKLPETVTFDWYKNTYVVEDLPSTIAGVHIGIEAFSVVRYTNAETLRVSQSL 2760
Db 2701 MEQMLFEDKLPETVTFDWYKNTYVVEDLPSTIAGVHIGIEAFSVVRYTNAETLRVSQSL 2760
Qy 2761 TDMTMBPLRAWRKARAVLASAKRGAHAHKLARFLLWHATSRPLDLDKTSVARTTFN 2820
Db 2761 TDMTMBPLRAWRKARAVLASAKRGAHAHKLARFLLWHATSRPLDLDKTSVARTTFN 2820
Qy 2821 YCDVYSPGDFVFTPORLQKFLVKYLAIVIFALGLIAVGLAIS 2864
Db 2821 YCDVYSPGDFVFTPORLQKFLVKYLAIVIFALGLIAVGLAIS 2864

RESULT 3
US-09-742-659-5
; Sequence 5, Application US/09742659

; Patent No. US20010034019A1		
; GENERAL INFORMATION:		
; APPLICANT: Hong, Zhi		
; APPLICANT: Butkiewicz, Nancy J.		
; APPLICANT: Zhong, Weidong		
; APPLICANT: Ingravallo, Paul		
; APPLICANT: Wright-Minogue, Jacquelyn		
; APPLICANT: Lau, Johnson Y.		
; APPLICANT: Lemon, Stanley M.		
; TITLE OF INVENTION: Chimeric HCV/GBV-B viruses		
; FILE REFERENCE: ID01116		
; CURRENT APPLICATION NUMBER: US/09/742,659		
; CURRENT FILING DATE: 2000-12-21		
; PRIOR APPLICATION NUMBER: US 60/171,469		
; PRIOR FILING DATE: 1999-12-22		
; NUMBER OF SEQ ID NOS: 16		
; SOFTWARE: PatentIn Ver. 2.1		
; SEQ ID NO 5		
; LENGTH: 2862		
; TYPE: PRT		
; ORGANISM: GBV-B/HCV		
; FEATURE:		
; NAME/KEY: SITE		
; LOCATION: (945)...(1129)		
; OTHER INFORMATION: chimeric region		
; NAME/KEY: SITE		
; LOCATION: (1579)..(1593)		
; OTHER INFORMATION: chimeric region		
US-09-742-659-5		
Query Match		94.1%; Score 14474; DB 9; Length 2862;
Best Local Similarity		94.7%; Pred. No. 0;
Matches 2717; Conservative 39; Mismatches 101; Indels 12; Gaps 5;		
QY	1	MPVISTQTSVPAPRTRKNKQTOASYPVSIKTSVERGQAKVKQDARPNYKTAGIHD 60
DB	1	MPVISTQTSVPAPRTRKNKQTOASYPVSIKTSVERGQAKVKQDARPNYKTAGIHD 60
QY	61	GLQTLAQAALPAHGMGRQDPRHKSRNLGILLDYPLGWI GDNVTHTPVLPVLAGAVVRPV 120
DB	61	GLQTLAQAALPAHGMGRQDPRHKSRNLGILLDYPLGWI GDNVTHTPVLPVLAGAVVRPV 120
QY	121	COI VRLLDGVNWTGFWGHLFVVCLLSLACPCSGARVTDPTNTTILTNCCQRNQVY 180
DB	121	COI VRLLDGVNWTGFWGHLFVVCLLSLACPCSGARVTDPTNTTILTNCCQRNQVY 180
QY	181	CSPSTCLHPGCVICADECWVPANPYISHPSNWTGDSFLADHIDFVMGALVTCDAIDIG 240
DB	181	CSPSTCLHPGCVICADECWVPANPYISHPSNWTGDSFLADHIDFVMGALVTCDAIDIG 240
QY	241	ELCGACVLVGDWLVRRHLHIHDLNETGTCYLEVPTGIDPGFLGFGIMWAGKVEAVIFLTK 300
DB	241	ELCGACVLVGDWLVRRHLHIHDLNETGTCYLEVPTGIDPGFLGFGIMWAGKVEAVIFLTK 300
QY	301	LASQVPIATWPFSSVHYLAVALGIYASRGKWKYQLLLALMLYIEATSGNPIRVPTGCSI 360
DB	301	LASQVPIATWPFSSVHYLAVALGIYASRGKWKYQLLLALMLYIEATSGNPIRVPTGCSI 360
QY	361	ABFCSPLMTPCCHSVLSNSVSEVICSPKWTREPITLVEYNNISISWYPYTIPIGARGCMWKF 420
DB	361	ABFCSPLMTPCCHSVLSNSVSEVICSPKWTREPITLVEYNNISISWYPYTIPIGARGCMWKF 420
QY	421	KNNTWGCCIRINVPSCYCTWGTDAVMDNTRNTYEACGVTPLWTATWANGSALKLAILQYPG 480
DB	421	KNNTWGCCIRINVPSCYCTWGTDAVMDNTRNTYEACGVTPLWTATWANGSALKLAILQYPG 480
QY	481	SKEMFKPHNMGSHLYFEGSDTPIVYFDPVNSTLLPPERWARLPQTTPVVRGSMQLQVPO 540
DB	481	SKEMFKPHNMGSHLYFEGSDTPIVYFDPVNSTLLPPERWARLPQTTPVVRGSMQLQVPO 540
QY	541	GFYSVDKDLATGLITKDKAKWKYQVLYSATGALS LGTVTTKAVWILLGLCGSKYLILAY 600
DB	541	GFYSVDKDLATGLITKDKAKWKYQVLYSATGALS LGTVTTKAVWILLGLCGSKYLILAY 600
QY	601	LCYLSLFCFRASGYPLRPLVPSQSYLQAGWDVLSKAQVAPFALIFFICCYLCRLRYAAL 660
DB	601	LCYLSLFCFRASGYPLRPLVPSQSYLQAGWDVLSKAQVAPFALIFFICCYLCRLRYAAL 660
QY	661	LGFVPMAGLPLTFFVAAAQAQPDYDWMVRLLVAGLVLAGNRGHRHRIALLVGPPLVAL 720
DB	661	LGFVPMAGLPLTFFVAAAQAQPDYDWMVRLLVAGLVLAGNRGHRHRIALLVGPPLVAL 720
QY	721	LTLHLVTPASAFDTEIIGGLTIPVVALVMSRFGFFAHLPRCALVNSYLQWQWENPF 780
DB	721	LTLHLVTPASAFDTEIIGGLTIPVVALVMSRFGFFAHLPRCALVNSYLQWQWENPF 780
QY	781	MNVTLRPERFFLVLCVCPGATYDALVTCVCHVALCLTSSAASFGTDSRVAHRMLVR 840
DB	781	MNVTLRPERFFLVLCVCPGATYDALVTCVCHVALCLTSSAASFGTDSRVAHRMLVR 840
QY	841	LQKCHAWYSHYVLKFFLLVFGENGVPFYKHLHGDVLPNDFAFKLPLOEPPFPPEGKARY 900
DB	841	LQKCHAWYSHYVLKFFLLVFGENGVPFYKHLHGDVLPNDFAFKLPLOEPPFPPEGKARY 900
QY	901	RNEGRRLACGDTVDGLPVVARLGDVLFAGLAMPDPGMAITAPFTLQCLSERGTLSAMAVV 960
DB	901	RNEGRRLACGDTVDGLPVVARLGDVLFAGLAMPDPGMAITAPITAYAOQTRGLGCIITS 960
QY	961	MTGIDPRTWTGTIFRLGSLATSYMGVCDNVLYTAAHSGKRRRLAHTPGSIHPITVDAAN 1020
DB	961	LTGRDNQVGEVQIVSTATOTFLATCINGVCTVYHGAGTRTIA SPKGPV--IQMYTVV 1018
QY	1021	DDDI--YQPPCAGSLTRCSGETHKGYLVTRLGSLVENVKSDDPYWCVCALPMAVAKS 1078
DB	1019	DDDLGWPAPOGSRSLTPTCTCGSSDLYLVTRHADVIPVRRRGDSRGLSLSPISYLGKS 1078
QY	1079	SGAPILCSGSHVIGMFTAA---RNSGGSVQIRVRPLVCAGYHPOYTAHATLDTKTPVN 1135
DB	1079	SGGPLLCPAGHAGLFPRAVCTRGVAKAVDFIPVENLETTMRSVPFTDMS---SKPTVFN 1135
QY	1136	EYSVQILIAPTGSGKSTKPLPSYMQEKEYELVLPNSVATTASMPKYMHATYGVNPNCPN 1195
DB	1136	EYSVQILIAPTGSGKSTKPLPSYMQEKEYELVLPNSVATTASMPKYMHATYGVNPNCPN 1195
QY	1196	GKNTGTGASLTYSTYGMVLTGACSNRYDVIICDECHATTATTVLIGIKVLTAPSKNRL 1255
DB	1196	GKNTGTGASLTYSTYGMVLTGACSNRYDVIICDECHATTATTVLIGIKVLTAPSKNRL 1255
QY	1256	VVLATATPPGVIPTPHANITEIQLTDEGTIPPHGKKIKEENLKKGRHLIFEATKKHCDL 1315
DB	1256	VVLATATPPGVIPTPHANITEIQLTDEGTIPPHGKKIKEENLKKGRHLIFEATKKHCDL 1315
QY	1316	ANELARKGITAVSYVRGCDISKIPEGDCVWATDALCTGYTGDFSDSVYDCSLMVEGTCHV 1375
DB	1316	ANELARKGITAVSYVRGCDISKIPEGDCVWATDALCTGYTGDFSDSVYDCSLMVEGTCHV 1375
QY	1376	DLDPFTMGVRVCGVSAIVKGORRGTGRGAGIYIYVDGSCCTPSGMVPECNIVEAFDA 1435
DB	1376	DLDPFTMGVRVCGVSAIVKGORRGTGRGAGIYIYVDGSCCTPSGMVPECNIVEAFDA 1435
QY	1436	KAWYGLSSTEAQTIIDTYRTOPLPAIGANLDEWADLFMSVNPPEPSFVNTAKRTADNYVL 1495
DB	1436	KAWYGLSSTEAQTIIDTYRTOPLPAIGANLDEWADLFMSVNPPEPSFVNTAKRTADNYVL 1495
QY	1496	LTAALQLCHOYGYAAPNDAPRWQGARLKGKPCGYLWRLDGDACPGPEPSVTRYQMC 1555
DB	1496	LTAALQLCHOYGYAAPNDAPRWQGARLKGKPCGYLWRLDGDACPGPEPSVTRYQMC 1555
QY	1556	TEVNTSGTAAALAVGVGAMAYLAIDTFGATCVRRCSWITSVPTGATVAPVWDEEIVEBC 1615
DB	1556	TEVNTSGTAAALAVGVGAMAYLA--STGCWIVGRVILSGKPTGATVAPVWDEEIVEBC 1613
QY	1616	ASFIPLEAWAAIDKLSKSTITTTTSPFTLEALEKNTFLGPHAATILATIEYCCGLVLP 1675
DB	1614	ASFIPLEAWAAIDKLSKSTITTTTSPFTLEALEKNTFLGPHAATILATIEYCCGLVLP 1673

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QY 1676 DNPFCSCVAFIAGITTPPHKIKMFLSLFGGAIASKLTDARGALAFMMAGAGTALGTW 1735
Db 1674 DNPFCSCVAFIAGITTPPHKIKMFLSLFGGAIASKLTDARGALAFMMAGAGTALGTW 1733
QY 1736 TSVGVFVDFMLGGYAAASSTACITFKCLGEMWPTMDLAGLVTSAFNPAAGVGVLSACAM 1795
Db 1734 TSVGVFVDFMLGGYAAASSTACITFKCLGEMWPTMDLAGLVTSAFNPAAGVGVLSACAM 1793
QY 1796 FALTAGPDHWPNRLLTMTLARSNTVCNEYFIATRDIRRKILGILBEASTPWSVISACIRWL 1855
Db 1794 FALTAGPDHWPNRLLTMTLARSNTVCNEYFIATRDIRRKILGILBEASTPWSVISACIRWL 1853
QY 1856 HPTPTDDCGLIAGLEIOWVQCNFFVICFNVLKAGVQSMVNPICPCPFYSCQKGYKGPWIG 1915
Db 1854 HPTPTDDCGLIAGLEIOWVQCNFFVICFNVLKAGVQSMVNPICPCPFYSCQKGYKGPWIG 1913
QY 1916 SGMLOARCPGCAELIFSVENGFAKLYKGPRTCNSYWRGAVPVNARLCGSARPDPTDWTSL 1975
Db 1914 SGMLOARCPGCAELIFSVENGFAKLYKGPRTCNSYWRGAVPVNARLCGSARPDPTDWTSL 1973
QY 1976 VVNYGVDRDYCKEYKMGDHI FVTAVSSPNVCFTQVPTLRAAAVADGVQVQCYLGEKPTW 2035
Db 1974 VVNYGVDRDYCKEYKMGDHI FVTAVSSPNVCFTQVPTLRAAAVADGVQVQCYLGEKPTW 2033
QY 2036 TTSACCYGPDGKGTVKLPFRVDGHTPGVRMQLNLRDALETNDCNNTNTPSDEAAVSAL 2095
Db 2034 TTSACCYGPDGKGTVKLPFRVDGHTPGVRMQLNLRDALETNDCNNTNTPSDEAAVSAL 2093
QY 2096 VFQKQLRRNTQLLEAISAGVDTTKLPAPSEIEVVVRKQFRARTGSLTLP PPPRSVPGVS 2155
Db 2094 VFQKQLRRNTQLLEAISAGVDTTKLPAPSEIEVVVRKQFRARTGSLTLP PPPRSVPGVS 2153
QY 2156 CPESLQSRDPLEGPNLPPSPVQLAMPMLLIGACENPFTAI GCAMTETGGPDLDLPS 2215
Db 2154 CPESLQSRDPLEGPNLPPSPVQLAMPMLLIGACENPFTAI GCAMTETGGPDLDLPS 2213
QY 2216 YPPKKEVSEWSDSWSTATTASSYVTPGPYKTRGKDSQSAKAPKPTKKLKGKSFSCS 2275
Db 2214 YPPKKEVSEWSDSWSTATTASSYVTPGPYKTRGKDSQSAKAPKPTKKLKGKSFSCS 2273
QY 2276 MSYTWTDVTSFKTASVLSATRAITSGFLKQSLVYVTEPRDAELRKQKVTINRQLFPP 2335
Db 2274 MSYTWTDVTSFKTASVLSATRAITSGFLKQSLVYVTEPRDAELRKQKVTINRQLFPP 2333
QY 2336 SYHKQVRLAKEKASKVGVWMDYDEVAHAHTPSKASHITGLRGTDVRSGAARKAVLDLQ 2395
Db 2334 SYHKQVRLAKEKASKVGVWMDYDEVAHAHTPSKASHITGLRGTDVRSGAARKAVLDLQ 2393
QY 2396 KCVEAGEI PSHYRQTVI VPKEEVFKTPOKPTKKPRLISYPHLEMRCEVMKYGVAPD 2455
Db 2394 KCVEAGEI PSHYRQTVI VPKEEVFKTPOKPTKKPRLISYPHLEMRCEVMKYGVAPD 2453
QY 2456 VVKAVMGDAYGFVDPRTRVRKLLSWSMDVAGATCDTVCFDSTITTPEDIMVETDIYSAAK 2515
Db 2454 VVKAVMGDAYGFVDPRTRVRKLLSWSMDVAGATCDTVCFDSTITTPEDIMVETDIYSAAK 2513
QY 2516 LSDQHRAGIHTIARQLYAGGPMIAYDGREI GYRRCSRSGVYTTSSNSLTCWLKVNAAE 2575
Db 2514 LSDQHRAGIHTIARQLYAGGPMIAYDGREI GYRRCSRSGVYTTSSNSLTCWLKVNAAE 2573
QY 2576 QAGMKQPRFLICGDDCTVIWKSAGADADKQAMRVFASWKMVGAPQDCVPQPKYSLELT 2635
Db 2574 QAGMKQPRFLICGDDCTVIWKSAGADADKQAMRVFASWKMVGAPQDCVPQPKYSLELT 2633
QY 2636 SCSSNTSGITKSGKPYFFLTRDPRIPGLRCSAEGGLGNPSAAWIGYLIHHYPCLMWSRV 2695
Db 2634 SCSSNTSGITKSGKPYFFLTRDPRIPGLRCSAEGGLGNPSAAWIGYLIHHYPCLMWSRV 2693
QY 2696 LAVHFMQMLFEDKLPETVTFDMYGNKYTVPVEDLPSIIAGVHGIEAFSVVRYTNAEILR 2755
Db 2694 LAVHFMQMLFEDKLPETVTFDMYGNKYTVPVEDLPSIIAGVHGIEAFSVVRYTNAEILR 2753
QY 2756 VSQSLDTMTWTPPLRAWRKARAVLASAKRGGAHAKLARFLWLHATSRPLDLDKTSVAR 2815
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Db 2754 VSQSLDTMTWTPPLRAWRKARAVLASAKRGGAHAKLARFLWLHATSRPLDLDKTSVAR 2813
QY 2816 YTTFNCDVYSPGDFVITPQRRLOKFLVKYLAVIVFALGLIANGLAIS 2864
Db 2814 YTTFNCDVYSPGDFVITPQRRLOKFLVKYLAVIVFALGLIANGLAIS 2862

RESULT 4
US-09-742-659-6
; Sequence 6, Application US/09742659
; Patent No. US20010034019A1
; GENERAL INFORMATION:
; APPLICANT: Hong, Zhi
; APPLICANT: Butkiewicz, Nancy J.
; APPLICANT: Zhong, Weidong
; APPLICANT: Ingravallo, Paul
; APPLICANT: Wright-Minogue, Jacquelyn
; APPLICANT: Lau, Johnson V.
; APPLICANT: Lemon, Stanley M.
; TITLE OF INVENTION: Chimeric HCV/GBV-B viruses
; FILE REFERENCE: ID01116
; CURRENT APPLICATION NUMBER: US/09/742,659
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/171,469
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 6
; LENGTH: 2865
; TYPE: PRT
; ORGANISM: GBV-B/HCV
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2275)..(2865)
; OTHER INFORMATION: chimeric region
; US-09-742-659-6

Query Match      85.8%; Score 13194; DB 9; Length 2865;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 2496; Conservative 98; Mismatches 241; Indels 52; Gaps 12;

QY 1 MPVISTQTSFVPAPRTRKNKQTOASYPVSIKTSVERGQAKRVQRDARPRNYKIAIHD 60
Db 1 MPVISTQTSFVPAPRTRKNKQTOASYPVSIKTSVERGQAKRVQRDARPRNYKIAIHD 60
QY 61 GLQTLAQAALPAHGWGRQDPRHKSRNLGILLDYPPLGWI GDTVTHHTPLVGLVAGVVRPV 120
Db 61 GLQTLAQAALPAHGWGRQDPRHKSRNLGILLDYPPLGWI GDTVTHHTPLVGLVAGVVRPV 120
QY 121 CQTVRLLEDGVNWATCHFVHLLSVCLLSLACPCSGARVTDPTNTTILTNCCORNOVIY 180
Db 121 CQTVRLLEDGVNWATCHFVHLLSVCLLSLACPCSGARVTDPTNTTILTNCCORNOVIY 180
QY 181 CSPSTCLHBPCCVICADECWVPANPYISHPSNNWTGDSFLADHIDFVMGALVTCDALDIG 240
Db 181 CSPSTCLHBPCCVICADECWVPANPYISHPSNNWTGDSFLADHIDFVMGALVTCDALDIG 240
QY 241 ELCGACVLVDMLVRHWHLIHIDLNETGTCTYLEVPTGIDPGFLFIGMAGKVEAIVPLTK 300
Db 241 ELCGACVLVDMLVRHWHLIHIDLNETGTCTYLEVPTGIDPGFLFIGMAGKVEAIVPLTK 300
QY 301 LASQVPIATATWESSVHYLAAGALIVYASRGWYQLLLALMLYIATSGNPIRVPTGCSI 360
Db 301 LASQVPIATATWESSVHYLAAGALIVYASRGWYQLLLALMLYIATSGNPIRVPTGCSI 360
QY 361 AEFCSPLMTPCPCHSYLSNSENSEVICYSPKWTPTPILEYNNNSISWYPYTTIPGARGCMVKF 420
Db 361 AEFCSPLMTPCPCHSYLSNSENSEVICYSPKWTPTPILEYNNNSISWYPYTTIPGARGCMVKF 420
QY 421 KNNTWGCCIRNVPSTCTGTGTDVAMNDTRNTYBACGVTPMLTTAWHNGSALKALILQYPG 480
Db 421 KNNTWGCCIRNVPSTCTGTGTDVAMNDTRNTYBACGVTPMLTTAWHNGSALKALILQYPG 480
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QY	481	SKEMFKPHNMGGHLYFBGSDTPIVYFYDPVNSTLLPPERWARLPCTPPVVRGSMQLQVPQ	540	QY	1561	SGTAALAVGVGVAMAYLAIDTFGATCVRRCSWITSVPTGATVAPVVDDEBEIVEECASFIP	1620
Db	481	SKEMFKPHNMGGHLYFBGSDTPIVYFYDPVNSTLLPPERWARLPCTPPVVRGSMQLQVPQ	540	Db	1561	SGTAALAVGVGVAMAYLAIDTFGATCVRRCSWITSVPTGATVAPVVDDEBEIVEECASFIP	1620
QY	541	GFYSVDKDLATGLITKDKAKWQVLYSATGALSUTGVTTKAVLILGLCGSKYILAY	600	QY	1621	LEAMVAADKLKSTTTTSPFTLEALEKNTFLGPHAATILAIIEYCCGLVTLDPNPEA	1680
Db	541	GFYSVDKDLATGLITKDKAKWQVLYSATGALSUTGVTTKAVLILGLCGSKYILAY	600	Db	1621	LEAMVAADKLKSTTTTSPFTLEALEKNTFLGPHAATILAIIEYCCGLVTLDPNPEA	1680
QY	601	LCYLSLCFRASGYPLRPVLPQSYLQAGWDVLSKAQVAPFALIIPFICCYLRCRLRYAAL	660	QY	1681	SCVFAPFAGITTPPLPHKIMFSLFSGGAIASKLTDARGALAFMMAGAACTAGTWTSVGF	1740
Db	601	LCYLSLCFRASGYPLRPVLPQSYLQAGWDVLSKAQVAPFALIIPFICCYLRCRLRYAAL	660	Db	1681	SCVFAPFAGITTPPLPHKIMFSLFSGGAIASKLTDARGALAFMMAGAACTAGTWTSVGF	1740
QY	661	LGFPVMAAGLPTTFVFAAAAQPDYDWMVRLLVAGLVLWAGNRGHRIRIALLVGPMPPLVAL	720	QY	1741	VPDMLGGVAAASSTACLTFFKCLMGWEPWQDLAGVLVSAFNPAAAGVGVVLSACAMPALTT	1800
Db	661	LGFPVMAAGLPTTFVFAAAAQPDYDWMVRLLVAGLVLWAGNRGHRIRIALLVGPMPPLVAL	720	Db	1741	VPDMLGGVAAASSTACLTFFKCLMGWEPWQDLAGVLVSAFNPAAAGVGVVLSACAMPALTT	1800
QY	721	LTLHLVTPASAFDETEIIGGLTIPVVALVMSRFGFFAHLPRCALVNSYLWQRENWF	780	QY	1801	AGPDHWPRLLTMLARSNTVCNEYFIATRDIRRKTLGILEASTPMSVTSACIRWLHTPTE	1860
Db	721	LTLHLVTPASAFDETEIIGGLTIPVVALVMSRFGFFAHLPRCALVNSYLWQRENWF	780	Db	1801	AGPDHWPRLLTMLARSNTVCNEYFIATRDIRRKTLGILEASTPMSVTSACIRWLHTPTE	1860
QY	781	WNVTLRPERFFVLVCFPGATYDALVTFVCVHALLCLTSSAASFGTDSRVRAHRMLVR	840	QY	1861	DDCGLIANGLEIWOVCNFFVICFNVLKAGVQSMVNIIPGCPFYSCQKGYKGPWIGSGMLQ	1920
Db	781	WNVTLRPERFFVLVCFPGATYDALVTFVCVHALLCLTSSAASFGTDSRVRAHRMLVR	840	Db	1861	DDCGLIANGLEIWOVCNFFVICFNVLKAGVQSMVNIIPGCPFYSCQKGYKGPWIGSGMLQ	1920
QY	841	LQKCHAWSHYVYLKPFLLVFGENGFFYKHLHGDVLPNDPASKLPLOEBPFFPFEKGARVY	900	QY	1921	ARCPCGABELIFSVENGFAKLYKGPRTCSNYWRGAVPVNARLCSARPDPTDWTSLVYVYG	1980
Db	841	LQKCHAWSHYVYLKPFLLVFGENGFFYKHLHGDVLPNDPASKLPLOEBPFFPFEKGARVY	900	Db	1921	ARCPCGABELIFSVENGFAKLYKGPRTCSNYWRGAVPVNARLCSARPDPTDWTSLVYVYG	1980
QY	901	RNEGRLACGDTVDLGVVVARLGDVLVAGLAMPDGGWAITAPTLOCLSERGTLSAMAVV	960	QY	1981	VRDYCKYKMGDHI FVTAVSSBNCVCTQVPTLRAAVDGVQVOCYLGEKPTPMTTSAC	2040
Db	901	RNEGRLACGDTVDLGVVVARLGDVLVAGLAMPDGGWAITAPTLOCLSERGTLSAMAVV	960	Db	1981	VRDYCKYKMGDHI FVTAVSSBNCVCTQVPTLRAAVDGVQVOCYLGEKPTPMTTSAC	2040
QY	961	MTGIDPRTWTGTIFRLGSLATSYMGFVCDNVLYTAHSGSKGRRLAHPGTGSIHPITVDAAN	1020	QY	2041	CYGPDGKGTVKVLPFRVDGHTPGVRMQLNLRDALETDCNSTNTNTPSDEAAVSALVFQOE	2100
Db	961	MTGIDPRTWTGTIFRLGSLATSYMGFVCDNVLYTAHSGSKGRRLAHPGTGSIHPITVDAAN	1020	Db	2041	CYGPDGKGTVKVLPFRVDGHTPGVRMQLNLRDALETDCNSTNTNTPSDEAAVSALVFQOE	2100
QY	1021	DQDIYQPPCGAGSLTRCSCGETKGLVTLRLGSLVEVNSKDDPYWCVCVCGALPMAVAKGSSG	1080	QY	2101	LARTNQLLEASAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLPPLPPRSPFVGVSCPESL	2160
Db	1021	DQDIYQPPCGAGSLTRCSCGETKGLVTLRLGSLVEVNSKDDPYWCVCVCGALPMAVAKGSSG	1080	Db	2101	LARTNQLLEASAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLPPLPPRSPFVGVSCPESL	2160
QY	1081	APILCSSGHVIGMFTAAARNSGSGVQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYSVQ	1140	QY	2161	QRSDPLEGPNLPPSPVVLQAMPPLGAGECNPTAIGCAMTETGGGDDLPSPYPPKK	2220
Db	1081	APILCSSGHVIGMFTAAARNSGSGVQIRVRPLVCAGYHPQYTAHATLDTKPTVPNEYSVQ	1140	Db	2161	QRSDPLEGPNLPPSPVVLQAMPPLGAGECNPTAIGCAMTETGGGDDLPSPYPPKK	2220
QY	1141	ILIAPTGSGKSTKLPLSYMOEKYEVLLNPSVATTASMPKYMHTVGVNPNVCYFNGKCTN	1200	QY	2221	EYSEHSDESWSATTASSYVTGPPYKIRGKOSTQSAKAPRTKKKLGKSEFSCMSYTW	2280
Db	1141	ILIAPTGSGKSTKLPLSYMOEKYEVLLNPSVATTASMPKYMHTVGVNPNVCYFNGKCTN	1200	Db	2221	EYSEHSDESWSATTASSYVTGPPYKIRGKOSTQSAKAPRTKKKLGKSEFSCMSYTW	2280
QY	1201	TCASLTYSTYGMVLTGACSRNDVLIICDECHATDATTVLIGIKVLTAPSKNVRVLVLAT	1260	QY	2281	TD-VISFKTASKVLSATRAITSGFLQKRSLVYVTEPRDAELRKQKVTINRQPLFPSPYHK	2339
Db	1201	TCASLTYSTYGMVLTGACSRNDVLIICDECHATDATTVLIGIKVLTAPSKNVRVLVLAT	1260	Db	2281	TGALITPCAABESKLPINALSNLRRHNMVYATTSRAGLRQKQVTFDLQLVDDHYRD	2340
QY	1261	ATPPGVIPTPHANITETIQLTDEGTIPFGHKIKIENLKKGRHLIIFEATKKHCELANELA	1320	QY	2340	QVRLAKEKASKVGVMDYDEVAHPTPSKASHITGLRGTDVRSAGARKAVLIDLQKCYE	2399
Db	1261	ATPPGVIPTPHANITETIQLTDEGTIPFGHKIKIENLKKGRHLIIFEATKKHCELANELA	1320	Db	2340	QVRLAKEKASKVGVMDYDEVAHPTPSKASHITGLRGTDVRSAGARKAVLIDLQKCYE	2399
QY	1321	RKGITAVSYRGCDSKIPGEGCVVATDALCTGYTDFDSYVDCSLMVEGTCVLDLPT	1380	QY	2341	VLKEMKAKASTYKAKLSVBEACKLTPPHSAKSF-GYGAKDVRN-LSSKAV-----	2399
Db	1321	RKGITAVSYRGCDSKIPGEGCVVATDALCTGYTDFDSYVDCSLMVEGTCVLDLPT	1380	Db	2341	VLKEMKAKASTYKAKLSVBEACKLTPPHSAKSF-GYGAKDVRN-LSSKAV-----	2399
QY	1381	FTMGVVRVCGVSAIVKQRRGRTGRAGIYIYVVDGSCPTSPGMVPECNIVAEAFDAKAWYG	1440	QY	2400	AGEI PSHVR-----QTIVIPKEEVFKVTPKPTKPPRLISYPHLEMRCEVEMKY	2449
Db	1381	FTMGVVRVCGVSAIVKQRRGRTGRAGIYIYVVDGSCPTSPGMVPECNIVAEAFDAKAWYG	1440	Db	2400	AGEI PSHVR-----QTIVIPKEEVFKVTPKPTKPPRLISYPHLEMRCEVEMKY	2449
QY	1441	LSSTEAQITLTYRQPLPAIGANLDEWADLFSMVNPBPSFWNTAKRTADNYVLLTAAQ	1500	QY	2449	-NHHSWKDILLEDVTPIDTTIMAKNEVFCVQPEKGRKPARLLIVFDLGVVCEKMAL	2499
Db	1441	LSSTEAQITLTYRQPLPAIGANLDEWADLFSMVNPBPSFWNTAKRTADNYVLLTAAQ	1500	Db	2449	-NHHSWKDILLEDVTPIDTTIMAKNEVFCVQPEKGRKPARLLIVFDLGVVCEKMAL	2499
QY	1501	LQCHQYGAAPNDAPRWQAGRLKPCGVLRWLDGADACPGPEPSEVTRYQMCFTVNT	1560	QY	2509	YDVVSTLPOVWVGSGYFQYSGFQVRVEFLVNTWKSKNPMGFSYDTRCFDSVTENDIRV	2509
Db	1501	LQCHQYGAAPNDAPRWQAGRLKPCGVLRWLDGADACPGPEPSEVTRYQMCFTVNT	1560	Db	2509	YDVVSTLPOVWVGSGYFQYSGFQVRVEFLVNTWKSKNPMGFSYDTRCFDSVTENDIRV	2509
QY	1561	LQCHQYGAAPNDAPRWQAGRLKPCGVLRWLDGADACPGPEPSEVTRYQMCFTVNT	1560	QY	2566	ETDIYSAAKLSDOHPAGIHTIARQIYAGCPMIAYDGRBIGYRRCRSSGVYVTTSSNSLTC	2566
Db	1561	LQCHQYGAAPNDAPRWQAGRLKPCGVLRWLDGADACPGPEPSEVTRYQMCFTVNT	1560	Db	2566	ETDIYSAAKLSDOHPAGIHTIARQIYAGCPMIAYDGRBIGYRRCRSSGVYVTTSSNSLTC	2566
QY	1627	PKYSLEELTSCSSNVTSGITKSGKPYFYLTRDPRIPILGRCSAEBGLGYNPSPAAMWIGYLIHH	2686	QY	2569	WLVNAAAQAGMKMFRFLICGDDCTVIWKSGADADQKQARVFAFMWKMGAQDCVQ	2626
Db	1627	PKYSLEELTSCSSNVTSGITKSGKPYFYLTRDPRIPILGRCSAEBGLGYNPSPAAMWIGYLIHH	2686	Db	2569	WLVNAAAQAGMKMFRFLICGDDCTVIWKSGADADQKQARVFAFMWKMGAQDCVQ	2626

Db 2630 PEYDLEITSCSSNVSAHDASGRVYVYLTRDPTTLARAAMETARHTPTPNWLGNIIMY 2689
QY 2687 YPCLVSVRLAVHFMQMLFEDKLPRTVTFDWYKQYVTPVEDLPSIIAGVHGIEAFSVV 2746
Db 2690 APTLWARMILMTHFFSIIAQEOLKALDCQIYGACYSIEPLDLPQIIIRLHGLSAFSLH 2749
QY 2747 RYTNARILVQSQTDMTPPLRAWRKARAVLASAKRGGAHAKLARFLL-WHATSR-- 2803
Db 2750 SYSPGEINRVASCLRLKGVPPPLVWRHRAVSUPARILLSGGRNATCGKYLFWAVKTKLK 2809
QY 2804 --PLP-----DLDKTSVARYTTFNYCDVYSPGDFVFTTPQRRLQKFLVKYLAVIVPALGL 2856
Db 2810 LTPIPAASQLDLGWFVAGVS-----GGDIVHLSLRAPRW-----FMLCLLL 2852
QY 2857 IAVGLAI 2863
Db 2853 LSVGVGI 2859

RESULT 5

US-08-424-550B-83
; Sequence 83, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAMSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEBHOF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESSES: 716
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1422 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-83

Query Match 48.0%; Score 7380; DB 8; Length 1422;
.Best Local Similarity 97.3%; Pred. No. 0;
Matches 1392; Conservative 2; Mismatches 27; Indels 10; Gaps 2;

QY 1005 AHPTGSIHPITVDAANDODIYQPPCAGSLTRCSCGETKGYLVTRLGSLVEYNKSDDPYV 1064
Db 1 AHPTGSIHPITVDAANDODIYQPPCAGSLTRCSCGETKGYLVTRLGSLVEYNKSDDPYV 60
QY 1065 CVCGALPMAVAKGSSGAPILCSSGHVIGMFTAAHNSGGSVSQIRVRPLVCAHYHPOYTAH 1124
Db 61 CVCGALPMAVAKGSSGAPILCSSGHVIGMFTAAHNSGGSVSQIRVRPLVCAHYHPOYTAH 120
QY 1125 ATLDTKPTVPNEYSVQIILIAPTGSGKSTKLPLSYMQEKEVVLNPSVATTASMPKYMHA 1184
Db 121 ATLDTKPTVPNEYSVQIILIAPTGSGKSTKLPLSYMQEKEVVLNPSVATTASMPKYMHA 180
QY 1185 TYGVNPNVCYFNGKCTNTGASLTYSYGMVLTGACSRNYDVIIICDECHATTATTVLGIGKV 1244
Db 181 TYGVNPNVCYFNGKCTNTGASLTYSYGMVLTGACSRNYDVIIICDECHATTATTVLGIGKV 240
QY 1245 LTEAPSKNVLVVLATATPPGVIPTPHANITIBIQLTDEGTIPFHGKKIKEENLKKGRHLI 1304
Db 241 LTEAPSKNVLVVLATATPPGVIPTPHANITIBIQLTDEGTIPFHGKKIKEENLKKGRHLI 300
QY 1305 FEATKKHCDLANELARKGITAVSYRGCDISKIPEGDCVVVATDALCTGYTGDPSVDYD 1364
Db 301 FEATKKHCDLANELARKGITAVSYRGCDISKIPEGDCVVVATDALCTGYTGDPSVDYD 360
QY 1365 CSLMVEGTCHVDLDPFTFTMGVRVCGVSAIVKQRRGRTGRGAGIYVYVDSGCTPSGMVP 1424
Db 361 CSLMVEGTCHVDLDPFTFTMGVRVCGVSAIVKQRRGRTGRGAGIYVYVDSGCTPSGMVP 420
QY 1425 EGNIVEAFDAKAWYGLSSTEATQITLDYTRTQPLPAIGANLDEWADLFMSWNPESFVN 1484
Db 421 EGNIVEAFDAKAWYGLSSTEATQITLDYTRTQPLPAIGANLDEWADLFMSWNPESFVN 480
QY 1485 TAKRTADNVLLTAAQLQCHQYGAAPNDAPRWQARGKPCGVLRDLGADACPGPE 1544
Db 481 TAKRTADNVLLTAAQLQCHQYGAAPNDAPRWQARGKPCGVLRDLGADACPGPE 540
QY 1545 PSEVTRYQMCFTVNTSGTAALAVGVGAMAYLAIDTFGATCVRRCWSITSVPTGATVAP 1604
Db 541 PSEVTRYQMCFTVNTSGTAALAVGVGAMAYLAIDTFGATCVRRCWSITSVPTGATVAP 600
QY 1605 VDDEEIVEECASFIPLEAMVAIDKLKSTITTSPTTLEALEKNTFLGPHAAITLAI 1664
Db 601 VDDEEIVEECASFIPLEAMVAIDKLKSTITTSPTTLEALEKNTFLGPHAAITLAI 660
QY 1665 IEYCCGLVTLDPNPFASCVFAFIAGITTPPHKIKMFLSLFGGAIASKLTDARGALAFMM 1724
Db 661 IEYCCGLVTLDPNPFASCVFAFIAGITTPPHKIKMFLSLFGGAIASKLTDARGALAFMM 720
QY 1725 AGAAGTALGTWTSVGVFDMLGAGYAAASSTACLTFFKLMGEMWPTMDLAGLVYSAPNPAA 1784
Db 721 AGAAGTALGTWTSVGVFDMLGAGYAAASSTACLTFFKLMGEMWPTMDLAGLVYSAPNPAA 780
QY 1785 GVVGVLSACAMFALTTAGDPHNPRLLTMLARSNTVCNEYFIATDIRRKLIGLEASTP 1844
Db 781 GVVGVLSACAMFALTTAGDPHNPRLLTMLARSNTVCNEYFIATDIRRKLIGLEASTP 840
QY 1845 WSVISACIRWLHPTDEDDCGLTAWGLEIWOYVCNFFVICFNLKAGVQSMVNPVPGCPFYS 1904
Db 841 WSVISACIRWLHPTDEDDCGLTAWGLEIWOYVCNFFVICFNLKAGVQSMVNPVPGCPFYS 900
QY 1905 CQKGYKGPWITGSMQLQARCPGAEILIFSVEENGFAKLYKGPRTCSNYWRGAPVNPVNLKCGS 1964
Db 901 CQKGYKGPWITGSMQLQARCPGAEILIFSVEENGFAKLYKGPRTCSNYWRGAPVNPVNLKCGS 960
QY 1965 ARPDPTDWTSLVNVYGVDRYCKYKMGDHI FVTAVSSPNVCFTQVPTTLBAAVADVQV 2024
Db 961 ARPDPTDWTSLVNVYGVDRYCKYKMGDHI FVTAVSSPNVCFTQVPTTLBAAVADVQV 1020
QY 2025 QCYLGEKPTWTTSSACCYGDGKGTVKLPFRVDGHTPGVRMQLNLRDALETNDCNSTNN 2084
Db 1021 QCYLGEKPTWTTSSACCYGDGKGTVKLPFRVDGHTPGVRMQLNLRDALETNDCNSTNN 1080

```
QY 2085 TSDDEAAVSALVFKQELRRTNQLLEAISAGVDTTKLPAPS-IEVVVVRKQFRARTGSLT 2143
DB 1081 TSDDEAAVSALVFKQELRRTNQLLEAISAGVDTTKLPAPSQIEVVVVRKQFRARTGSLT 1140
QY 2144 LPPPPRSVGVSCPELQSDPLEGPSNLPPLPPVQLQAMPPLLGAGCNPFTAIGCAM 2203
DB 1141 LPPPPRSVGVSCPELQSDPLEGPSXLPSPFPVQLQAMPPLLGAGCNPFTAIGCAM 1200
QY 2204 TETGGGDDLPSPYPPKKEVSESDSWSTATTASSYVTPGPKINGKDSQSAKAPRPT 2263
DB 1201 TETXGXPXLPSPYPPKKEVSESDSWSTTTTASSYVTPGPKINGKDSQSAKAPRPT 1260
QY 2264 KKKLKGSESCMSYMTWDVIFSKTASKVLSATRAITSGFLKQSLVYVTEPRDAELRQ 2323
DB 1261 KKKLKGSESCMSYMTWDVIFSKTASKVLSATRAITSGFLKQSLVYVTEPRDAELRQ 1320
QY 2324 KVTINRQPLPPSYHKQVRLAKEKASKVGVWMDYDEVAHAHTPSKSAKSHITGLRGTDVR 2383
DB 1321 KVTINRQPLPPSYHKQVRLAKEKASKVGVWMDYDEVAHAHTPSKSAKSHITGLRGTD-- 1378
QY 2384 SGAARKAVLDLQKCEAGBIPSHYRQTVIVPKEEVFVKTPOKPTKKPPRLI 2434
DB 1379 -----VLDLQKCEAGBIPSHYRQTVIVPKEEVFVKTPOKPTKKPPRLI 1422

RESULT 6
US-10-467-000-1
; Sequence 1, Application US/10467000
; Publication No. US20040067486A1
; GENERAL INFORMATION:
; APPLICANT: De Francesco, Raffaele
; APPLICANT: Migliaccio, Giovanni
; APPLICANT: Paonessa, Giacomo
; TITLE OF INVENTION: HEPATITIS C VIRUS REPLICONS AND REPLICON
; TITLE OF INVENTION: ENHANCED CELLS
; FILE REFERENCE: ITR0003P
; CURRENT APPLICATION NUMBER: US/10/467,000
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: PCT/EP02/00526
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/263,479
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3010
; TYPE: PRT
; ORGANISM: Con 1 HCV isolate nucleic acid
US-10-467-000-1

Query Match
Best Local Similarity 29.8%; Pred. No. 1.3e-238;
Matches 970; Conservative 452; Mismatches 1183; Indels 648; Gaps 116;

QY 8 TSPVPAPTRKKNQKQTAQSPVSIK-----TSVERGQRAKRVQRRDARPR 51
DB 3 TNPKPQKTKRNTNR--PQDVKFGGQIVGVVLLPRRGPRLGVRATRKTSERSQPR 59
QY 52 NYKIAGIHGLOTLQAALP-----AHGKGROD 79
DB 60 GRR-----QPIPKARQPEGRAMAQPGYPMPLVNEGHWAGMULLSPRGSRPSWGPTD 111
QY 80 PRHKSRLNGLIDYPLGMDVTHTPPLVGLVAGAVRVPVQIIVRLLEDGVNWTG--- 136
DB 112 PRRSRNLCVIDTLTCGADLMGYIPLVGA PLGGA-ARALAHGVRLVLEDGVNATGNLP 170
QY 137 WFGVHLFVVCLLS-LACPGSGARVTDPTNTILNCCORNVYICSPSTCLHBPCCVIC 195
DB 171 GCSFSIFLLALSCLTIPASAYEVRNV-SGVYHVTNDCSNASIVYEAAIMHMTGCVPC 229
QY 196 ADE-----CWVPANPVISHPSNWTGDSFLADHIDPVMGALVTCDALDIDGCGACVVG 250
DB 230 VRENNSSRCWALTPTLA--ARNASVPTTIRRHVDLLVGAALCSAMYVDLCGSFVLVA 288
```

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QY 251 DWLV-----RHWLIHIDLNETGTCYLEVPTGIDPGFL--GFICW---MAGKVEAVIFLTKL 301
DB 289 QLFTEPSRRHETVQ-DCN-----CSIYFGHVTGHRMAWDMWMMNSPTAALVVSQ 337
QY 302 ASQVPAIATMFESSVHYLAVGALIYYASRGKWQVLLALMLYIEATSGNPPIRVPTCSIA 361
DB 338 L-RIPOAVDMVAGAHGVLAGLAYYSWGNWAKVLIIVMLLFAGVDGGTVY---TGGTWA 393
QY 362 E-----FCSPLMPCPCHSYLS 379
DB 394 KNTLGIITSLFSGSOKIQLVNTNGSWHINRTALNCNDSLNTGFLAALFY---VHKFNSS 450
QY 380 -----NVSEVICVSPKWRPITILEYNNISWYYP-----TIFGARGC----- 416
DB 451 GCPERMASCPIDAFQGW-GPITYNESSHSDQRPYCMHYAPRPGCIVPAAQVCGPVYCF 509
QY 417 -----WVKFKNT-----WGCCRIRNVPSY-----C 437
DB 510 TSPVWVGTDRFQVPTYSWGENETDVLNLRNPPQGNWFGCTWNNSTGFTKTCGGPPC 569
QY 438 TMG-----TDAVWMDTRNTYEACGVTPLT-----TAWHNGSALKLAILQ- 477
DB 570 NIGGIGNKTLCTDCPRKHPEATYTKCGSGPWLTPRCLVHYPYRLWHYPCTVNFIFKV 629
QY 478 --YPGSKE--MPKPHNMMSG-HLYFEGSDTPIVFYDPVNVSTLLPPEWARLPPTPVVR 532
DB 630 RMYGVGVHRELEACNWTGERCNLEDRD-----SELSPLLLSTTEQVLPSC----- 678
QY 533 GSWLQVPOGFYSVDKDLATGLITKQKAMQVQVLYSATGALSLTGVTTKAVVLLILGLCG 592
DB 679 -----FTTLPALSTGLIHQNVVDVQVLYGIGSAVVSFAIKWYVLLLFULLAD 728
QY 593 SKYLILAVLYLSLFCGRASGYPLRPVLPQSQVLAQWMDVLSKAQVAPALFFICCYLR 652
DB 729 ARVCACLMMLL-----IAQEAALLENLV----- 753
QY 653 CRLRYAALLGFVPMAGLPLTFFVAAAQAQPDYDMWVR--LLVAGLVLMAGRNRGHRIAL 711
DB 754 --LNAASVAG---AHGI-LSFLVFFCAA---NVKGRLVPGAAY-----AL 790
QY 712 VGPWPLVALLTLHLVTPASAFDTEI---IGGLTTPPVVALVVMSPRPGFAHLLPRCALV 768
DB 791 YGVWPL--LLLLLALPPRAYAMDREMAASCGGAVFVGLILLTLSPHYKLFLARL----- 842
QY 769 NSYLWQRWENFWNVTLRPERFLVLCFP-----GATYDALVTCVCHVALL--CLTSSA 822
DB 843 ---IW-----WLOYFITRAEAHLQWVI--PPLNVTRGGRDAVILLICAHPHIFTITKL 892
QY 823 ASFFG-----TDSRVRAHR-----MLVRLGKCHAWYSHYVLFLLVFGNGVVF 866
DB 893 LAILGLPLVLOAGITKVPYFVRAHGLIRACMLVR---KVAGGHVYQMALMKLAALTGT 948
QY 867 FYKHL-----HGDLVNDPASKLPLOEPFFPFEGKARVYRNEGRRLACGTDVGLPV 919
DB 949 VYDHLTPLRDWAHAGL--RDLAVAV---EPVVFSDMETKVTIWTGADTAACGDIILGPS 1003
QY 920 ARLGDLVPAGLA--NPPDGAITAPFTLQCLSERGTLSAMVVMVTGIDPRTWTGTIFRLG 977
DB 1004 ARGREIHLGPADSLLEGQGWRLLAIPITAYSQOTRGLGCIITSLTRDRNQVEGEVQVVS 1063
QY 978 SIATSYMGFVCDNVLYTAHHSKGRRLAHTGSIHPITVDAAN--DQDI---YQPPCGAGSL 1034
DB 1064 TATQSFATCATCVNGVCMWTVYHGAGSKTLGAPKG---PITQMTNVDOQLVGMQAPPGARSL 1120
QY 1035 TFCSCGETGKYLIVRLGSLVEVKNKSDDPYWCVCALPMAVAKSSGAPILCSCSHVIGMF 1094
DB 1121 TPTCTCGSDLYLIVTRHADVIPVRRRGDSRGSLLSPRVSYLKSGGGLLPCSGHAGVIF 1180
QY 1095 TAA---RNSGGSVSOIRVRPLVACGYHPQYTAHATLDTKPTVPNEYSVQIIAPTSGSGKS 1151
DB 1181 RAAVCTRGVAKAVDFVPVSMETTWRSVFTDMS---SPPAVPQTFQVAHLHAPTSQSGKS 1237
```

Qy	1152	TKLPLSYMQBKEVVLVLPNSVAITAMPKYMHAHYGVNPNCYENGKCTNGASLTVTSTYG	1211
Db	1238	TKVPAAYAAQGYKVLVLPNSVAATLFGFAMKHAIGIDNIRTVGRTITTTGAPITYSTYG	1297
Qy	1212	MYLT-GACSRN-YDVIICDSCHATDATTVLIGIKVLTEAPSKNVRVLVLTATATPGVIPT	1269
Db	1298	KFLADGCSGGAVDIIICDCHSDSTSTIIIGITVDLQOASTAGARVLVLTATATPPGSVTV	1357
Qy	1270	PHANITEIQLTDEGTTIPPHGKKIKEENLKKGRHLIPEATKKHODELANELARKGITAVSY	1329
Db	1358	PHENIEEVALSSTGEIPFYKAIPIETIKGRHLIFCHSKKKCDELAALKSLGLGNAYV	1417
Qy	1330	YRGCDISKIP-EGDCVVVATDALCTGYTGFDSYDCSLMVEGTCHVDLDPPTMTGMVRVC	1388
Db	1418	YRGLDVSVIPTSGDVIWATDALMTGTFGDFSDVIDCNTCVTQTVDFSLDPTFTETTTV	1477
Qy	1389	GVSAIVKQGRGRTGRAGIYYVVDGSCPTPSGMVPECNIVEAFDAKAWYGLSSTEAOQT	1448
Db	1478	PQDAVSRQSRGRTGRMGIGYRFTVGERPSGMFDSVLCCEYDAGCAWYELTPAETS	1537
Qy	1449	ILDTYRTQPLPAIGANLDEWADLFS-MVNPEPSFVNNTAKRTADNVVLLTAAQLQCHQY	1507
Db	1538	RLRAYLNTPLPCODHLEFWESVFTGLTHIDAHFLSQTQAGDNFPYLVAQYATVCARA	1597
Qy	1508	GYAAPNDAPRWQ-ARLGKK---PCGVLMRLDGADACPGPEPSEVTRYQM-CFT---EVN	1559
Db	1598	QAPPPSDQMWKCLIRLKPTLHGPTPLLYRL-GAVQNEVTTTHPIKTIYIMACMSADLEVV	1656
Qy	1560	TSGTAALAVGVGVMAYLAIDTGTACVRCNSITSVPTCAATVAPVUDEBEI-----VE	1613
Db	1657	TS-TWLVGVGLAALAAAYCLTTCGSVIVGR-----IILSGKPAIIDPREVLRYRFEDE	1709
Qy	1614	ECASFIP-LEAMVAADDKL-----STIT-----TTSPTTLETALEKNTFLPGAHAATI	1661
Db	1710	ECASHLPYIEQGHQLABQFKQALGLQYATKQABAAAP-VVSGKRTLEAFWAKHWNFF	1768
Qy	1662	LAIIEYCCGLVTLFPNDPFPASCVFAFTAGITTPHPKIKMFLSLFGGAIAKSLTDARGALA	1721
Db	1769	ISGIQYLAGLSTLPGNPAIASLMAFTASITSLPTTQHTLLFNILGGVWAAQLAPPASA	1828
Qy	1722	FMAGAAGTALGTWTSVGF--VFDMLGGVAAASSSTRACLTFKCLMGSEWPTMDQLAGLVYS	1778
Db	1829	FVGAGTAGAAGV---SIGLGKVALDILAGYGAGVAGALVAFKVMGSEMPSTEDLVNLLPA	1885
Qy	1779	AFNPAAGVGVLSACAMFALTTAGD---HWPNRLLTLMARSNTVCNEYFIATRIDIRK	1834
Db	1886	ILSPGALUVGV--CAAILRRHVGPBGAVQWMNRLLJAFASRGNHVSPTHYVESDAAAR	1943
Qy	1835	ILGILEASTPWSVISACIRWLHTPTEDDCGLI---AWGLEIWOYVCNFFVICFNVLKAGV	1891
Db	1944	VTQILSLT---ITQLLKRHLQWINEDCSTPCSGWLRLVDWDWICT---VLTDFTKWL	1995
Qy	1892	QS--MVNIPGCPFYSCQKYGKBPWIGSMLOARCPGAEILFSVENGFAKLYKGPRTCSN	1949
Db	1996	QSKLLPLRPGVPFFSCQRYKGVWRGDGIMQTTCTPCGAQITGVXONGSMRIV-GPRTCSN	2054
Qy	1950	YMRGAVPNARLCSARPDT-DWTSLVVNYGVDRDYCKYKMGDHFVTAVSSPNV-CFT	2007
Db	2055	TWHTGTFPINATYTCPTPSAPNYSRALWRVAABEYVEVTRVDFHVYGMTDNNVKCP	2114
Qy	2008	QVP-----PTLRAAVA-----VDGVQVQCYLGEPEKPTWTT	2038
Db	2115	QVPAPEPTEVDGVLRLHRYAPACKPLLREEVTFVLGLNOYLVGSQLPC---EP-----	2165
Qy	2039	ACVGPDPGKTKVL--PFRVDGHTPGVRQMLNRLDALETND-----CNSTNN	2084
Db	2166	-----PDVAVLTSMLTDPHSITAEAKRRLARGSPPSLASSSASQLSAPSLKATCTRHD	2220
Qy	2085	TPSDEAAVSALVFKQEL-----RRTNQLL-----EASAGVDVTKLPAPSTEIEVVVRK	2132
Db	2221	SPDADLTEANLLMRQENGMINTRVESNKKVYLDSPFLQAEDEBERVESVA--EILRR	2278
Qy	2133	RQFRARTGSLTLPPPRSVPVCSP-----BSLQRSD-----PUEGSPNLPPSP	2176

[illegible]

```

RESULT 7
US-10-296-734-406
; Sequence 406, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; CURRENT APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 406
; LENGTH: 3011

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[illegible]

Db	463	DKFDQGW-GPITVDEGFDLQDRPYCHWYAPRSCGIVPASPQVCPVYCFPTSPVPVVGTTDR	521
Qy	417	-----MVKFKNNT-----WGCCRIRNVPSY-----CTMG-----	440
Db	522	TGAPTYRWGENETDVLINNTPPQGNWFGCTWMSSTGFTKTCGGPPCNIIGAGNNTLVC	581
Qy	441	-TDVAVNDTRNTYEACGVTPWLT-----TAMHNGSALKALILQ-----YFGSKB--MF	485
Db	582	PTDCFRKHPKPEATYTKCGSGFWLTPRCMDVDPYRPMWHPYPCVTNFTIPKVRMYVGGVEHRLN	641
Qy	486	KPHNMWSG-HLYFEGSDTIVFYDPVNSTLLPPERWABLPGCTPPVVRGSLQVQGFYS	544
Db	642	AARNTRGRCDLEDRD-----SELSPLLSTTEWQILPCS-----PT	680
Qy	545	DYKDLATGLITKDKAKWNTQVLYSATGALSGLGVTTKAVVLLILGLGCSKYLILAYLCYL	604
Db	681	TLPALSTGLIHLHQNIVDVQVLY-----GIGSVVSVLIKW-----EYVLLSFF---	724
Qy	605	SUCFRASGYPLRVLPSOSYLOAGWDVLSKAQVAPFALIFPICCYLRCRLRYAALLGVF	664
Db	725	-----LLADARVCACILMMMLLIAQEAALLENVLVNA	757
Qy	665	PMAA--GLPLTFEFAAAAQPDYDMWR--LLVAGLVLMAGRNRGHRIALLVGFWPLVALL	721
Db	758	SVAGAHGI-LTLFLVFCFA--WYIKGRLVFGAAY-----AFYGVWFL--LL	798
Qy	722	TLLHLVTPASAFDTEI---IGGLTIPPVVALVMSRFGFFAHLPRCALVNSYLWQRMEN	778
Db	799	LLLLALPPRAYANDREMAASCGANFGLVLLTSLPHYKVFLARL-----IW-----	844
Qy	779	WFNVNLTBRERFVLVLCFP-----GATYDALVTEFCVCH-----VALLCLTSSAASF	825
Db	845	WLQYFTTAEAILHVMV--PPLNVRGGRDAVILLTCAVHPDLIFDITKLLAVLGLPMVF	902
Qy	826	FGTDSR---VZAHRLM--VRLGKCHAWSHYVLFELFLVFGENGVFVFKHL-----H	872
Db	903	LAGITRVPFVRAOGLIRACALARKVAG--GHYIQMALMKLAALTGTLYLDHLTPLRDWAH	961
Qy	873	GDVLNDFASKLPLOEPPFPFEGKARVYRNEGRRLACGTVDPGLPVVARLGDPLVAGLA-	931
Db	962	AGL--RDLAVAV--EPVVFSDMETKIITWADTAACGDIIIGLPSVARGREIILGPAD	1016
Qy	932	-MPPDGAITAPFTIQCUSERGTLSAMAVMTGIDPRTWTGTIFRLGSLATSYMGVCDN	990
Db	1017	SLEGOQWRLAPITAYSQOQTRGLLGCIIITSLGRDKNOVEGVBQVSTATQSFATCVNG	1076
Qy	991	VLYTAHSGKGRRLAHPGTSIHPIITDAAN--DODI--YOPPCGASLITRCSGCTGYLV	1047
Db	1077	VCMTVPFHGAGSKTLAGPKG--PITQMTYNDVDQLVGMQAPPGARSLTPTCTCGSSDLV	1133
Qy	1048	TRLGLSVEYNKDDPYWCVCGALPMAVAKGSSGAPILCSSGHVIGWFTAA--RNSGGSV	1104
Db	1134	THADVIVPVRGDRNGSLSPRPVSYLKGSSGGLLCPGSHAVGIFRAAVCTRGVAKAV	1193
Qy	1105	SOIRVRPLVCAGHPQYTAHATLDKTPVNPBYSVOIILIAPTGSGKSTKPLPSYMOEKYE	1164
Db	1194	DFIPVESMETTWRSPVFTDNS--SPPAVPQFQVAHLHAPTSGSKSTKVPAAYAAQGYK	1250
Qy	1165	VVLVNPVSATTASMPKMYHATYGVNPNCFYNGKCTNTGASLTYSYGMVLT--GACSRN--Y	1222
Db	1251	VVLVNPVAAATLGFGTYSKAYGVDPNIRTVRTITTTGAPITYSTYKFLADGGSGGAY	1310
Qy	1223	DVIIICDECHATTVGLIGKVLTEAPSKNVRLVVLATATPPGVIPTPHANITEIQLTDE	1282
Db	1311	DIIMDCHECHSTUSTTVLGLTVDQAEATAGARLVVLATATPPGVTVPHPNIEELALNT	1370
Qy	1283	GTIPFHGKKIKENLKGRRHLIFEATKKHCDLANELARKGITAVSYRGCDISKIP--BG	1341
Db	1371	GEIPFYGAIPJETIKGRRHLIFCHSKKCDLAAKLSGLGLNAVAYRGLDVSVIPTSG	1430
Qy	1342	DCVVATDALCTGYTGDFFDSVDCSLMVBEGTCHVDLDPFTFMGVRGCVSAIVKQRRGR	1401
Db	1431	DYVVVATDALMTGFTGDSVSDCNCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRQRGR	1490
Qy	1402	TGRGRAGIYVYVDSCTPTSGMWPECNIVEAFDAAKAWYGLSSTEAOITILDTRYTOPGLPA	1461
Db	1491	TGRGRGGIYRVFTVPCGRPSGMFSSVLCYDAGCAWVELTPAETSVRRLAYLNTPLGLPV	1550
Qy	1462	IGANLDEWADLPS--MWNPEPSFVNTAKRTADNYVLLTAAQLOLCHQYGAANDAPRWOG	1520
Db	1551	CODHLEFVESVFTGLTHIDAHFLSQTKOAGDNFPYLVAQVATVCARAQAPPSWQMWKS	1610
Qy	1521	-ARLCKK--PCGVLRILDGADACGPBPSE-----VTRYOM-CFT---EYNTSSTAAL	1566
Db	1611	LIRLXPTLHGTPPLLYRL-----GTQSEITLTHPTVKYIMACHSADLEVVTS--TWVL	1662
Qy	1567	AVGVGVMAYLAIDTFGATVRRCHWSITSVPTGATVAPVUDEEBI-----VEECASFTP	1620
Db	1663	VSGVLAALAAVCLTTGTSVVIVGR-----IILSGKPAVIPDREVLVREPEDEMECASHLP	1716
Qy	1621	-LEAMVAIDKUK-----STIT-----TTSPTTLETALEKUNTFGLGPHAATILAIIEYC	1668
Db	1717	YIEQGMQLAEQPKQKALGLLOTATKOABAAA--VVESEKMRALAEAFWAKHMNFISGIOYL	1775
Qy	1669	CGLVTLDPNPAPASCVPFAFIAGITTPHKKIMFSLFGAIAASKLTDARGALAFMMAGAA	1728
Db	1776	AGLSTLHGNPAIASLMAFTASITSLTQHTLLFNILGWNVAQAAPPASAASAFVAGAGIA	1835
Qy	1729	GTALGTWTSVGF--VFDMLGYYAAASSTACLTFFKCLMGWPTMDQLAGLVYSAFNPAAG	1785
Db	1836	GAAVG--SIGLGVKLVLDVLAGYGAGVACALVAFKVMSEGVSESTEDLVNLLPAVLSPGAL	1892
Qy	1786	VVGVLUSACAMPALITAGPD----HWPNRLLTLMARSNTVCNEYFIATRDIRKILGILEA	1841
Db	1893	VVGWV--CAAILRRHVGPGEAGVQMMNRLLIAPASRGNHVSPTHYVVPESDAAAARVQILSS	1950
Qy	1842	STPWSVISACIRMLHTPTDDCGLI---AWGLEIMQVVCNPPVICFNVLKAGVQS--MVN	1896
Db	1951	LT-----VTQLRRLHQWINEDECSTPCSGSWLRDVMWMICT-----VLTDFKTWQSKLLPR	2002
Qy	1897	IPGCPFYCQKGYKGFPIGSGMLQACPCGAELIFSEVNGFAKLYKGPRTCNRYRGAVP	1956
Db	2003	LPGVFFPFCQRYRGVWRGDMGIMQITTCPGAQISGHVKNXGSMRIV--GPRSCSNTWHGTTP	2061
Qy	1957	VNARLCGSARDPT--DWTSLVNVYGVRYCKYKMGDHI FVTAVSSPNV--CTQVP----	2010
Db	2062	INAYTTGCTPAPAPNYSRALRVAAEBYVEVTRVGDVHYVTGMTTNDNVKPCOVPAPEF	2121
Qy	2011	-----PTLRAAAVAVD-----GVQVCYVLGPRKPTPWTTSACCCYGD	2045
Db	2122	FTEVDGVLHRYAPACKPILLREEVTFQVGLNOYLVGSOLPC---BPE-----PD	2167
Qy	2046	KGKTKVKL--PFRVDGHTPGVRMQLNLRDALETND-----CNSTNNVTPSDEAA	2091
Db	2168	VAVLTSMLTDPHSHTAETAKRRLDRGSPPLSSASSASQLSAPSKATCTTRHSDPDAGLI	2227
Qy	2092	VSALVFKQEL-----RRTNQLL-----EASAGVDTTKLPAPSEIEVVVVRKQPRART	2139
Db	2228	EANLLRWGEMGNITRVESENKVNILDSFEPLRAEBEDEREVSVA--EILKSRKPPRAM	2285
Qy	2140	GSLTLP---PP-----PRSVPGV--SCPESLQSRDPLGSPSNLPPSP-----VLQ	2180
Db	2286	PIWARPDPNPPLESWKNPDPVPPVHVGCP-----LPPIKG-----PPIPPPRKRTVLUT	2336
Qy	2181	LAMPNPLLAGECNPFITAIGCAWETG--GGPDDLPSPYPPKKEVSEWSDESTATTASS	2238
Db	2337	ESTVSSALAEALATKTFGSGSSAVDSGTASAPDQPS-----DNGDAGSDAES	2384
Qy	2239	YVTGPPYPIKRG--DSTQSAKAPRPTKKUKGSEFSCSMSTYTTD--VISFTASKULBA	2295
Db	2385	YSSMPP---LEGEPPDPLSDGSMSTVSEASED VVCCSMSTYTTWCALITPCAABESKLP	2441
Qy	2296	TRAITSGFLQORSLVYVTEPRDAELRKOKVTINRQLPFPSVHKQVRLAKEKASVVGVM	2355
Db	2442	INALNSNLLRHHNMVYATTSSASQKQKVTFDRLOVLDHDDYRDLVKEMKAKASTYKAKL	2501

Qy	991	VLYTAHUGSKGRRRLAHPTGSIHPIITVDAANDQDI--YOPPCGAGSLTRCSCGETKGVLVT	1048
Dz	:	: : : :	:
Dz	1077	VCWTWTHGAGRTTASPKGPV-IQMTYNVDQDLVGWPA PQGRSRLTPCTCGSDLLVLT	1134
Qy	1049	RLGSLVEVNRKSDDPYWCVC GALPNAVAKSGGAPILCSSGHVICMFTAA--RNSGGSVS	1105
Dz	:	: : : :	:
Dz	1135	RHADVIPRRRGDSRGSLSPRPISYLXSGGGPLCPAGHAVGLFAAVCTRGVAKADV	1194
Qy	1106	QIRVRPLVCAGHPQYTAHAFLDTPKVPNEYSQIILIAPTGGSKSTKLPLSYMQEKYEY	1165
Dz	:	: : : :	:
Dz	1195	FIPVENLETTMRSPVFTDNS---SPPAVPOSFQVAHLHAPTGGSKSTKVPAAYAAQYKV	1251
Qy	1166	LVLNPSVATTASMPKMKHATYGVNPNVCYFNKGCTNTGASTYSTYGYMYLT-GACSRN-YD	1223
Dz	:	: : : :	:
Dz	1252	LVLNPSVAATLFGAYMSKAHGVDPNRTGTVRTITTGSTPYTYSGFKFLADGGCSGGAYD	1311
Qy	1224	VIIICDECHATDATTVLGIGVKLVTEAPSKNRLVLVLATAPPGVPTPHANTETOLTDEG	1283
Dz	:	: : : :	:
Dz	1312	IIIICDECHSTDATSILGITGVLDQRETAGARLVVLATATPPGSTVVPHPNIEEVALSTTG	1371
Qy	1284	TIPFHKKIKREENLUKGRHLIFEATKKHKHDELANELARKGITAVSYRGCDISKIP-BGD	1342
Dz	:	: : : :	:
Dz	1372	EIPFYKAIPLVIKGRHLIFCHSKKKKDELAALVALGINA VAYYRGLDVSVIPITSGD	1431
Qy	1343	CVVVATDALCTGYTDGFDSYVDCSLMWEGTCHVDLDPTFTMGVRCVGSIVAIVGORRGRT	1402
Dz	:	: : : :	:
Dz	1432	VVVVATDALMTGTFGDFSDVIDCNTCTVTQTVDFFSLDPTFTIETTLTPQDAVSRTORRGRT	1491
Qy	1403	GRGRAGIYYVVGSGCTSGMWPECNIVEAPDAAKAWGLSSTEQAQTILDTRYTOPGLPAI	1462
Dz	:	: : : :	:
Dz	1492	GRGPGIYRVAPGERSGMFDSSVLCBCEYDAGCAWYELTPAETTVELRAYMTPTGPLPVC	1551
Qy	1463	GANLDEWADLFS-MVNPESPFWNTAKRTADNYILLTAAQLQCHQYGAAPNDAPRWQG-	1520
Dz	:	: : : :	:
Dz	1552	QDHLEFEWEGVFTGLTHIDAFLSQTKSGENFPYLVAYQATVCARAQAPPESDMOMWKCL	1611
Qy	1521	ARLGKK---PCGVLRWLDGADACGPPBPSEV-----TRYQM-CFT---EVNTSGITAALA	1567
Dz	:	: : : :	:
Dz	1612	IRLKPTLHGPTPLLRYL-----GAVONEVTLTHPTIKYIMTCMSADLSEVWTS-TWVLV	1663
Qy	1568	VGVGMAYAILADTFGATCVRRCWSIITSVPTGATVAPVVDDBEI-----VEECASFIPL	1621
Dz	:	: : : :	:
Dz	1664	GSVLAALAAVCLSTGCVVIGR-----IVLSGKPAILPREVLVYQEFDEWECSOHLPY	1717
Qy	1622	--EAMVAA---IDLKSTITTTTS-----PFTLETALEKLNTFLGPHAATIILAIHEYCC	1669
Dz	:	: : : :	:
Dz	1718	IEQGMMLAEQPKQKALGLLOLTASROAEVITP-AVOTNMWQLEVFWAKHMWNFISGIQYLA	1776
Qy	1670	GLVTLPDNPASCVFPIAGITTPLPKHIMFISLFPGAASKUTDARGALAFWMAGAAG	1729
Dz	:	: : : :	:
Dz	1777	GLSTLPGNPAIASLMATTAATVTSPLTTGOTLLFNILGGWAAQLAAPGAATAFVGAGLAG	1836
Qy	1730	TALCTWTSVGEF--VFDMLGYYAAAASSTACLTFKCLMGEMWPTMDQLAGLVVSAFNPAAGV	1786
Dz	:	: : : :	:
Dz	1837	AAIG--SVGLGKVLVDILAGYGAGVAGALVAFKIMSGEVPSFTEDLVNLPLAILSPCALV	1893
Qy	1787	VGVLSACAMPALTITAGPD----HWPNRLTWLARSNVTCNEYFIATRDRIKRKILGLEAS	1842
Dz	:	: : : :	:
Dz	1894	VGUV-CAAILRRHVGPGEQAVQMNRLIAFASRGHNHSPTHVVPESDAAARVTAILLSL	1951
Qy	1843	TPWSVISACIRWLHTPTEDDOGLIANGLETWQYYCNFVFCFNVVLKAGVOSWNI PCGPF	1902
Dz	:	: : : :	:
Dz	1952	TVTOLLRLRHQWISSECTTPCS-GSWLRUDLWDWITCEVLSDFKTWLKA-KLIMPOLPGIPP	2008
Qy	1903	YSCOKYKGWPIGWGMLQARCPPCAELIFSVEENGFAKL YKGPRCTSNYMRGAVPVNARLC	1962
Dz	:	: : : :	:
Dz	2009	VSCORG YGVWRGDGMHTRCHCBAEITHGVKNGTMRIV-GPTRCRNMWSGTTPINAYTT	2067
Qy	1963	GSARPDT-DWTSILVNVYVRDYCKYBKMGDHI FVTAVSSPNV-CFTQVP-----	2010
Dz	:	: : : :	:
Dz	2068	GPCTPLPAPNYKFALWBSAEYVEIRRVDGFHYVSGMTTDLNKPCQIIPSPBFFTELDQ	2127

RESULT 10
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; Publication No. US20050221297A1

QY	8	TSPVPAPRTRKNKQOASYPVSIK-----TSVERGQRAKKVQORDARPR	51
Db	3	TNPQORKTKRNTNRR---PODVKFPGGQOIVGGVYLLPRRGPRLGVRATRKTSERSQPR	59
QY	52	NYK-----IAGIHGLOTLAQAALP-----AHGWRQDPRHKSRN	86
Db	60	GRQPIPKARRPEG-RTWAQPGYPMWLYGNECGGWAGWLLSPGRSRPSWGPTDPRRRSRN	118
QY	87	LGTLIDYPLGWIQDVTHTPPLVPLVAGAVRPVCOIVRLLEDGWNWATG---WFGVHLF	143
Db	119	LKVIDTLTCGADLNGYIPLVGAPELGA-ARALAHGVRVLEDDGVNYATGNLPCCSFIP	177
QY	144	VVCLLS-LACPCSGARVTDPTNTILTNCCORNOVIYCSFSTCLHEPGCVIC-----AD	197
Db	178	LLALLSCLVPASAYQVRN-SSGLYHVINDCPNSSIVVEAADAIIHTEGCPVCVCREGNAS	236
QY	198	ECWVPANPYISHPNSWNTGDSFLADHIDPVMGALVTCDAIDIGELCGACVLVGWLV---	254
Db	237	RCWAVTPTVATRDGKLPPTQ-LRRHIDLLVGSATLCSALYVGDLGCSVFLVGQLFTFSP	295
QY	255	RHWLHIDINETGICYLEVPRTGIDPGFLGFGW---NAGKVEAVIFLTKLASOVVPAIA	310
Db	296	RRHW-----TTQDCNCSIYPGHITGHR---NAWDMNMWNSPTAALVVVAQLL-RIPQAIM	345
QY	311	TMFSSVHYLAVALGALYYASRGKWYQULLALMLY-----IBATSGNPTRV-----	354
Db	346	DMIAAGHWGLAGIAYFMSVGNWAKVVLVLLFAGVDAETHVTGNGAGRTTAGLVGLLTP	405
QY	355	-----PTGC-----SI	360
Db	406	GAQNITQLINTNGSWHINSTALNCNESLNTGWLGLFYQHKFNSSGCCPERLASCRRLTDF	465
QY	361	AERCSPIMI-----PCCHSVYSENV-SEVICYSPKWTRPITILEYNN--	401
Db	466	AQGWGPISYANGSGLDERYCWHYPRPGCIVPAKSVCGPVYCFTPS-----PVVYGTDRS	522
QY	402	---SISWYPTYPGARGCMVKFNNT-----WGCCRINRNPYS-----CTWG---	440
Db	523	GAPYSW-----GANDTDVFLVNTRPPLGNWFGCTWNSTGTFTKVCGAPPCVILGGVN	576
QY	441	-----TDVMDNTRNTYBACGVTPWLT-----TAWNGSALKALILQ-----YPGSK	482
Db	577	NTLLCPTDCFRKHPEATYSRCSGPMWITPRCMVDYPYRLMHYPCTINYTIKRWYVGGV	636
QY	483	B--MPKPHNMWSG-HLYPEGSTPIVYFYDPVNSTLLPPERWARLPGTPPVVRGSMQLVP	539
Db	637	EHRLEAACNWRGERCDLEDRD-----SELSPLLSTQWQLPCS-----	678
QY	540	QGFYSVDKOLATGLITKDXAKNYOVLYSATGALSITGVTKAVVLIILLCGSKYLILA	599
Db	679	---FTTLPALSTGLIHILHQNIVDVQYLVGVGSSIASWAIKWYVVLFLLLADARVCSCL	735
QY	600	YLCYLSLCFGRASGYPLRPVLPFSQSYLQAGWDVLKSAQVAPPALIFFCCYLCRLRYAA	659
Db	736	MMWLL-----ISQAEAALENLVI-----LNAAS	758
QY	660	LLGFVPMAGLP--LTFVFVAAAAQDDYDWVRLVLVAGLVVLWAGNRGHRITALLVGPWL	717
Db	759	LAG-----THGLVSFLVFFCFA-----WYLK-----GRWVPGAVVYALYGMWPL	796
QY	718	VALLTLHLVTPASAPDTEI-----IGSLTIPPVVALVWMSRGEFFAHLPRCALVNSYLMQ	774
Db	797	--LULLLALPQRAYALDTEVAASCGGVU---VGLMALTSPYKYRYISWCWMLQVFLT	851
QY	775	RWEN-----WPNVTLRPERFFLVLCVFGGATYDALVTECVCHVALLC-LTSSAASPFGT-	828
Db	852	RVEAQLHVWVPLNVRGGRDAVILL-----MCVVHPTLVFDITKLLLAIFGPL	899
QY	829	-----DSRVRAHRMLVRLOKCHAWTSHYVLKFLFLVFGENGUVFFYKHLH--GD	874
Db	900	WILQASLLKVPYVRVQGLLRICALKARKIAG-GHYVQMAIKGLGALTGYTYNNHILTPLRD	958
QY	875	VLPNDFASKLPLOEP--FPFPEGKARYVRNEGRRRLACGDTVDGLPVVARGLDLVFAGLA-	931
Db	959	WAHNGRLDLAVAVEPWFVSERMETKLITWGD--TAAACDIIINGLVPARRGQOELLGPAD	1016
QY	932	-MPPDGMALTAPFTLQCLSERGTLISAMAVVMWTDPRTWGTGIPRLGSLATSYMGFVCDN	990
Db	1017	GMVSKGWRLLAPITAYAOQTRGLGCCIITSUTGRDKNOVEGEVOIVSTATQTFLATCING	1076
QY	991	VLYTAHHSKGRRLAHPGTSGIHPITVDAANDQDI--YQPPCGAGSLTRCSCGETKGYLVT	1048
Db	1077	VCMTYVHGAGTRTITASPKGPV--IQMYTNVDQDLVGMWPAPOGSRSLTPTCTGSSDLYLVT	1134
QY	1049	RUGSLVENKSDDPYWCVCAGALPMANAVAKSGSGAPILCSSGHVIGMTAA---RNSGGSVS	1105
Db	1135	RHADVIPVRRRGDSRGSLLSPRISYLGSSGGPLCLPAGHAVGLFAAAVCTRGVAKAVD	1194
QY	1106	QIRVRPLVCAGVHPQYTAHATLDTKPTVPNEYSVQIILAPIGSCSKTKLPLSYMOEQEYV	1165
Db	1195	FIPVENLGTWMSRPSVFTDNS---SPPAVPSQFQVAHLHAPTGSKGSKTKVPAPYAAOQYKV	1251
QY	1166	LVLPNSVATTASMPKYMHTYGVNPNCTYFNGKCTNCTGASLTYSYGMYL--GACSRN-YD	1223
Db	1252	LVLPNSVAATLFGAYMSKAHGVDPNIRTVGRTITTTGSPITYSYTKFLADGGCSGGAYD	1311
QY	1224	VIIICDECHATTATVLGKVLTEAPSKNVRVLVLATATPPGVIPTPHANITEQLTDEG	1283
Db	1312	IIICDECHSTDATSTILGIGTVDLQDAETAGARVLVLATATPGSVTVVSHPNIEEVALSTTG	1371
QY	1284	TTPFHGKKIKEENLKKGRHLIFEATKKHCHDELANELARKGITAVSYVRGCDISKIP--EGD	1342
Db	1372	EIPFYGKAIPLEVIKGRHLLIFCHSKKCKDELAALKVALGINAVAYVRGDLVSVIPTSGD	1431
QY	1343	CVVWATDALCTGYTGDPSDVVDCSLWVEGTCVHVDLPTFTMGVRVCGVSAIVKQGRGRT	1402
Db	1432	VVVSTDALMTGTFDPSVDICHTCVTQTVDFSLDPTFIETITLLPQDAVSRTORGRT	1491
QY	1403	GRGRAGIYYVYDGSCTPSGMPPECNIVBFAADAAKAWYGLSSTEAGTILDTYRTOPGLPAI	1462
Db	1492	GRGKPGIYRFYVAPGERPSGMFDSVLCBICYDAGCAWYELTPEATTVRLRAYMNTPGLPVC	1551
QY	1463	GANLDEWADLFS-MYNPEPSFWNTAKRTADNVNVLTTAAQLQCHQYGYVAAPNDAPRQW-	1520
Db	1552	QDHLFEWEGVFTGLTHIDAHFLSQSGENFPFLVAYQATVCARAQAPPSWDMWKCL	1611
QY	1521	ARLGKK---PCGVLRWLDGADACQPEPSEV-----TRYQM-CFT---EYVNTSGTAALA	1567
Db	1612	IRLKPFTLHGPTLLVRL-----GAVQNEVTLTHPTIKYIMTCHSADLEVVTS-TWVLV	1663
QY	1568	VGVGVAMAYLAIDTFGATCVRRCWSITSVPTGATVAPVVDDEEI-----VEECASFIPL	1621
Db	1664	GGVLAALAAYCLSTGCVVIVGR-----IVLSGKPAIIPDREVLVYQBEDMEECQHLPY	1717
QY	1622	--BAMVAA---IDKUKSTIITTSPP-----TLETALEKMTPLGPHAAATILALIEVCCG	1670
Db	1718	IEQGMWLAEPQFKQKALGILLQTLASRAHEVITPAVQTNMQKLEVPFWAKHMMNFIISGIOYLAG	1777
QY	1671	LVTLPDNPASCVFAFIAGITTELPKHIMFSLFGGAIAISKLTDARGALAFMMAGAAGT	1730
Db	17		

Db 2010 SCQRYGVWVRGDMHTRCHCAEITGHVXNGTMRIV-GRPTCRNMMSGTPEPINAYTTG 2068
Qy 1964 SARPPPT-DWTSLVVNYGVDRCKEKGMDHIFVTAVSPNV-CFTQVP- 2010
Db 2069 PCTPLPAPNYKALNRVSAEEVEIRVGDFFHVSGMTDNKPCQIPSPFFFTELDGV 2128
Qy 2011 -----PTLRAAVD-----GVQVCYLGEPTKPTWTTSSACCYGDGKGTVK 2052
Db 2129 RLHREAPPCKLLREBVSFVLGHEVPVGSQLP-EBE-----BDVAVLISM 2174
Qy 2053 L--PRVDGHTGVRMQLNRLDALEND-----CNSTNTPSDEAAVSAVFK 2098
Db 2175 LTDPSHITAEAGRRLARGSPSSASSASQSLKATCTANHSDPSDAELIEANLLWR 2234
Qy 2099 QEL-----RRTNOLL-----EASAGVDYTKLPAPSEIEVVVRKQFRARTGSLTLP- 2145
Db 2235 QEMGNGNITRVESENKVVILDSFDPLVAEDEDEVSPA--EILKRSRRFARALPFWARP 2292
Qy 2146 -----PPRSVP----- 2152
Db 2293 YNPPLVETWKKPDYBPVVHGCPLPPRSPPPVPPRKKRTVVLTSTLSTALAEATKSF 2352
Qy 2153 -----GVSCPESLQSDPLEGPNLPPSPVVLQAMPPLLGACECPFTAGCAMTET 2206
Db 2353 GSSSTSGITGDNNTTSSEP--APSGCPSDDESYSMPPLEG-----E 2394
Qy 2207 GGGPDPLPSYPPKKEVSEMSDESMTATTASSVVTGPPPKIRGKDSTQSAKAPKPTKK 2266
Db 2395 PGDPD-----LSDGSNVTSS-----GADT----- 2414
Qy 2267 LKSFSCMSMYTWDVLSFKTASVLS--ATRAITSGFLKQSLVVTPEPRDAELKQKV 2325
Db 2415 --EDVCCSMSYSYTGALVTPCAEBEQPLIPALNSLLRHHNLVYTTSTRSACQKQV 2472
Qy 2326 TINRQPLPPSYHKQVRLAKEASKVGVVMWDYDEVAHTPSKAKSHITGLRGTDVRS 2385
Db 2473 TFDRLQVLDSDHYQVLYKEYKAASKVKANLLSVEEACSLTPPHSAKSF-GYGAKDVRC- 2530
Qy 2386 AARKAVLDL-----QKCEAGEIPSHYROTIVVPKEEVFKTPQKTKPPRLISYPHLEM 2441
Db 2531 HARKAVAHINSVWKLLDESVTPI---DTTINAKNEVFCVQPEKGRKPARLIVFPDLGV 2587
Qy 2442 RCVEKMYGQVADVVVKAVMGDAYGF-VDPTRVRKLLSMW--SPDAVGATCDTVCFDST 2498
Db 2588 RVCERKALVDVVSXKLPLAVMGSSYGFQYSPGQVFLVQAWKS KKTTPMGFSYDTRCFDST 2647
Qy 2499 ITPEDIMWETDIYSAKLSQHRAGIHTTARQLYAGGPMIADGREIGYRRCSSGVYTT 2558
Db 2648 VTESDIRTEEA1YQCCDLDPOARVAIKSLTERLYYGGPLTNSRGNGCYRRCRASGVLT 2707
Qy 2559 SSSNSLTCLWKVNAAEQAGMKNPRFLICGDDCTVIWKSAGADADKQAMRVFASNMKVMG 2618
Db 2708 SCGNLTCTVYIKARACRAAGLQDCTMLVCGDDLVCICESAGVOEDAAASURAFTEAMTRY 2767
Qy 2619 APQDCVPOPKYBLELTSCSNVTSITGKSGPYFLTRDRIPLRGCSAEGLGNPSAA 2678
Db 2768 APPGDPPQPEYDLELITSCSNVSVAHADGAGRVVYLTREDPTTLARAWEATARTPVNS 2827
Qy 2679 WLYGILHHPCLWRSVLAVHMEQMLFEDKLPETVTFDWTGKNTVTPVEDLPSIIAGVH 2738
Db 2828 WLGNIIMFAPTLWARMILMTHFESSVLARDQEQALNCEIYGACYSIEBPLDLPPIQRLH 2887
Qy 2739 GTEAFSVRYTNAETILRVSOQLTDMTPPLRAWRKARAVLASAKRGGAHAKLARFL-- 2797
Db 2888 GLSASLSHSYSGEINRVAACRLKGLVPLPRAWRHAKSVRARLLSRGGRAICOKILFN 2947
Qy 2798 WHATSR-----PLPDLDKTSVARYTTFNVCYDVSPEGDVFIPTQRLQKFLKYLAVIVFA 2853
Db 2948 WAVRTKCLKLTPIAAAGRLDLSGMFTAGYSG-----GDIYHSVSHARPRW-----FWFC 2995
Qy 2854 LGLIANGLAI 2863

Db 2996 LLLLAAGVGI 3005
RESULT 12
US-09-747-419-20
; Sequence 20, Application US/09747419
; Patent No. US2002015582A1
; GENERAL INFORMATION:
; APPLICANT: Yi, MinKyung
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
; FILE REFERENCE: 265.0007 0101
; CURRENT APPLICATION NUMBER: US/09/747,419
; CURRENT FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/171,909
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polyprotein
US-09-747-419-20
Query Match 20.9%; Score 3214.5; DB 9; Length 3011;
Best Local Similarity 29.4%; Pred. No. 5.6e-235;
Matches 956; Conservative 440; Mismatches 1213; Indels 641; Gaps 107;
Qy 8 TSPVPAPTRKKNKQTOASYPVSIK-----TSVERGORAKRKVQRDARPR 51
Db 3 TNPKEPQRTKGTNRR---PDVKPPGGQIVGGVYLLPRRGPRLGVRATRTKTSRSQPR 59
Qy 52 NYK-----TAGIHGQLTQAALP-----AHGGRQDPRHKS 86
Db 60 GRQPIPKARRPEG-RTWAQPGYPMPLVNEGCGWAGWLLSPRSGRSPSGPTDPRRRSRN 118
Qy 87 LGILLDYPLGIDGVYTHTPLVGLVAGAVRVCQIVRLLEDGVNWTG---WFGVHLF 143
Db 119 LGKVIDTLTCGFADLMGYIPLVGAPLGA-ARALAHGVRLVEDGVNYATGNLPGCSFSIF 177
Qy 144 VVCLLS-LACPCSGARVTDPTNTTILNCCORNQVIVCSPTCLHEPCVCIC-----AD 197
Db 178 LLALLSCLTVPASAYQVRN--SSGLYHVTNDCPNSSIVVEAADAILHTPGCVPCVRBNAS 236
Qy 198 ECWVPANPYISHPSNWTCTDSFLADHIDFVMGALVTCALDIDIGELCGACVLVDMLV--- 254
Db 237 RCWAVTPTVATRDGKLPPTQ-LRRHIDLVLGVSATLCSALYVGDLCGSVFLVGQULFTFSP 295
Qy 255 -RHMLIHIDLNETGTCYLEVPTGIDPGFLGFIG---NAGKVEAVIFLTKLASQVPAIA 310
Db 296 RRHW-----TTQDCNCIYPGHITGHR--MAWDMMNWSPTAALVVAQLL-RIPOAIM 345
Qy 311 TMFSSVHYLAVGALYYASRGKWYQLLALLMLY-----IEATSGNPIRV----- 354
Db 346 DWIAGAHGVLAGIAYFNSVGNWAKVVLVLLFAGVDAETHVTGNGRAGRTAGLVGLLTP 405
Qy 355 -----PTGC-----SI 360
Db 406 GAKQNIQLINTNGSMHINSTALNCNESLNTGWLAGLFYQHKFNSSGCPERLASCRRLTDF 465
Qy 361 AEFCSPLMI-----PCCHSVLSNV--SEVICYSPKMTPTTLBYNN-- 401
Db 466 AQGWGPIYANGSGLDERPCHYHPPRCGIVPAKSVCGPVYCFTPS----PVVGTGTD 522
Qy 402 ---SISWYPTTIPGARGCMVKFNNT-----WGCCRINRVPSY-----CTWG---- 440
Db 523 GAPTYSW-----GANDTDVFLNTRPPLGNWFGCTWKNSTGFTKVCGAPPCVIGVGN 576
Qy 441 -----TDAVNDTRNTYEACGVTPWLT-----TAWNGSALKUALIQ---YPSK 482
Db 577 NTLCLPTDCFRKHPAETYSRCGSGPWITPRCMVDVYPRMLWHYPTINTYTFIKVRMYGVG 636

QY	483	E--MFKPHNMMSG-HLYFEGSDTPIVYFYDPVNSTLLPPERWARLPCTPPVVRGSMQLQVP	539	QY	1521	ARLGKK---PCGVLRWLDGADACPGPEPSEV-----TRYQM-CFT-----EVTNSTGTAALA	1567
Db	637	EHRLEAACNWTGERCDLDRD-----SELSPLLSTTQOVLPSCS-----	678	Db	1612	IRLKTPLHGPTLLXRL-----GAVQNEVTLTHPTIKYIMTCMSADLEVVTSTWVLV	1663
QY	540	QGFYSVDKDLATGLITKDKAWKNYQVLYSATGALSITGVTTKAVLILILGLCGSKYLILA	599	QY	1568	VGVGVAMAYLAIDTGTGATCVRRCWSITSVPTGATVAPVVUDEEI-----VEECASFPL	1621
Db	679	---FTTLPALSTGLIHLHQNIVDQVLYGVGSSIASMAIKWEVVLFLLLADARVCSCUL	735	Db	1664	CGVLAALAAYCLSTGCVVIVGR-----IVLSGKPAIIPDREVLYQBFDEMECQHLBPY	1717
QY	600	YLCYLSLCPGRASGYPLRPLVPSQSYLQAGMDVLSKAQVAPFALIPFICCYLRCLRURYAA	659	QY	1622	--EAMVAA---IDKLKSTITTTSPF-----TLETALEKINTFLGPHAAATILAIYCCG	1670
Db	736	WMMLL-----ISQAEAALENLVI-----LNAAS	758	Db	1718	IBQGMMLAEQKQKALGQLQTSRRAEVIPTPAQVNTWQLEVFVWAKHWNFISGTYLAG	1777
QY	660	ILGFPVMAAGLP--LTFVVAANAAPDDYDWVRLLVAGLVWAGNRGHRHIALLVCPWPL	717	QY	1671	LVTLPDNPFASCVFAFIAGITTPHPKIKMFLSLFGGAIAASKLTDARGALAFMMAGAAGT	1730
Db	759	LAG-----THGLVSFLVFCFA-----WYLK-----GRWPGAVVALLYGMWPL	796	Db	1778	LSTLPNPAIASLMAFTAATVTSPLTTGTQTLNLLGWWAAQLAAPGAATAFVGAGLAGA	1837
QY	718	VALLTLLHLVTPASAFDTI-----IGGLTIPPVVALVMSRFGFFAHLPRCALVNSYLWQ	774	QY	1731	ALGTWTSVGF---VFDMLGGYAAASSTACTLTKCLMGWPTMDQLAGLVYSAFNPAGVU	1787
Db	797	--LLLLLALPQRAYALDTEVAASCGVVL---VGLMALTLSPYKEYVISWCMWMLQYFLT	851	Db	1838	AIG---SVGLGKVLVDILAGYGAGVAGALVAFKIMSGEVPTEDLVNLLPAILSPGALVV	1894
QY	775	RVEN-----MFMNVTLRPERFELVCFPGATYDALVFCVCHVALLC-LTSSAASPFGT-	828	QY	1788	GVLSCAMPALTTAGPD---HWPNRLLTMLARSNTVCNEYFIATRIDIRRKILGILEAST	1843
Db	852	RVEAQLHVWVPLNVARGGRDAVILL-----MCVHPHTLVFDITKLLLAIFGPL	899	Db	1895	GVV--CAAILRRHVGPGEVAGVOMMRLLIAFASRGHNHVSPTHVPESDAAARVTAISSLIT	1952
QY	829	-----DSRVRAHRMLVRLCKCHAMYSHYVVKFLLVFGENGVFYFKHLH--GD	874	QY	1844	PWSVISACIRWLHTPTEDDCGLIANGLEIWOYVCNFFVICFNVLKAGVQSMVNIPOCPFY	1903
Db	900	WILQASLLKVPYFVRQGLRICALARKTAG-GHYVQMAIILKLGALTGYVYNHLTPLRD	958	Db	1953	VTQLLRLLHQWISSECTTPCS--GSMRLRDIMDICEVLSDFKTWKA--KLMPQLPGIPFV	2009
QY	875	VLPNDFASKLPLOEP--FFPFEGKARVYRNEGRRLACDGTVDGLPVVARLGDLVFAGLA-	931	QY	1904	SCOKYKGPMWIGSMLQARPCGABELIFSVENGPAKLYKGPRTCSNYWRGAVPVNARLCG	1963
Db	959	WAHNGRLDLAVAVEPVVFSRMEKLTWGD--TAACGDIINGLPPVSARRGQEILLGPAD	1016	Db	2010	SCQRYGVWVRGDMHTRCHCGAEITGHVKNGTMRIV--GPTRCNMWSGTFPINAYTTG	2068
QY	932	-MPPDGWALTAPTLOCLSERGTLSAMVVMTCIDPRTWGTITFRIGSLATSVMGVCDN	990	QY	1964	SARPOPT-DWTSLVVNYGVDRDYCKYKMGDHLFVTAVSSPNV-CFTQVP-----	2010
Db	1017	GMVSKWMLLAPITAYAAQTQRLGGLCIITSLTRDKNQVEGEVQIVSTATQTLATCING	1076	Db	2069	PCTPLPAPNPKFALMRVSAEYVEIRRGDFHVSGMTIDNLKCPQIESPBEFTLDGV	2128
QY	991	VLYTAHSGKGRLAHPTGSIHPTVDANDODI--YQPCGAGSTRCSGCTKGYLYT	1048	QY	2011	-----PTLRAAAVAD-----GVQVCYLGEPKTPMTWSACCYGDGKGKTVK	2052
Db	1077	VCMTVYHAGTRTIASPKGPV--IQMTNVQDLVGWPAPQGRSLTTPCTCGSSDLYLYT	1134	Db	2129	RLHRRAPPCKPLREEVSFRVGLHEYPVGSQLPCL--EPE-----PDVAVLTSM	2174
QY	1049	RLGSLVEVNSDDPYWCVCALPMVAKSSGAPILCSSHVIGCMFTAA---RNSGGSVS	1105	QY	2053	L--PFRVGDHTPGVRMQLNRDALETND-----CNSTNTPDDEAAVASLVFK	2098
Db	1135	RHADVIPVRRRGDSRGLSPRISYLVKSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVD	1194	Db	2175	LTDPSHITAEAAGRRLARGSPSSMASSASQLSAPSLKATCTANHDSPPDAELTEANLLWR	2234
QY	1106	QIRVRPLVCAGYIPIQTAHATLDTKPTVPNEYSVQILIIAPTSGKSTKPLSLTMQEKYEV	1165	QY	2099	QEL-----RRTNOLL-----EALSAGVDTTKLPAPEEVEVVRKQFRARTGSLTP-	2145
Db	1195	FIPVENLGTITMRSPVFTDNS---SPPAVQSQFVAHLHAPTSGKSTKVPAAVAAQGYKV	1251	Db	2235	QEMGGNITRVESENKVVIILDSFDPLVAEDEDREVSVPA--EILRKSRFFARALPVWARP	2292
QY	1166	LVLNPSVATTASMPKYMHTYGVNPNICYFNGKCTNTGASLTYSTYGMWLT-GACSRN-YD	1223	QY	2146	-----PPRSVP-----	2152
Db	1252	LVLNPSVAATLGFAGYMSKAHGVDPNIRTVGRIITTSPIITYGKFLADGGCGGAYD	1311	Db	2293	YNPPLVETWKPDYEPVHVHGCPLPPPPSPPPPPPRKRTVVLTESTLSTALAEATKSF	2352
QY	1224	VITCDECHATDATVTLGIGKVLTEAPSKNVLVLATATPPGVIPTPHANITEIQLTDEG	1283	QY	2153	-----GVSCPSLQSRDPLEGPNLPPSPFPVLQLAMPMPLLGAGCENFTALGCAMTET	2206
Db	1312	IIICDECHSDATSIILGIGVLQDAETAGARLVVLATATPPGVSIVSHPNIEEVALSTTG	1371	Db	2353	GSSTSGITGDNITTSSEP--APSGCPDSDVESYSMPPLEG-----E	2394
QY	1284	TIPFHOKKIKEENLKGRHLIIPRATKKGCDLANELARKGITAVSYVYRGCDISKIP-EGD	1342	QY	2207	GGGPDDLPSYPPKKEVSEWSDSSTATTASSVYTPGPKIRKIDSTQSAKAPRTKKK	2266
Db	1372	EIPFYGKAIPLEVIKGRHLIFCHSKKCDLAKLVALGINAVAYVYRGLDVSVIPTSGD	1431	Db	2395	PGDPD-----LSDGSMSTVSS-----GADT-----	2414
QY	1343	CVVVATDALCTGTGDPDSVYDCSLMVEGTCHVDLDPFTMGVVRVCGVSAIVKQRRGRT	1402	QY	2267	LKSEFSCMSYTWTDVIFSFTASKVLS-ATRAITSGFLKQRLSVVYVTEPRDAELRKQV	2325
Db	1432	VVVSTDALMTGTGDPDSVIDCNCVTQTVDFSLDPTFTIETTLTPODAVSRQRRGT	1491	Db	2415	--EDVVCCSMSYSWTGALVTPCAABEQKLPIINALSNLLRRHNLVYSTTSRSACQOKKV	2472
QY	1403	GRGRAGIYVVDGSCTPSGMVPPECNIVEAFDAKAWYGLSSTBAQTILDTYRQPLPAI	1462	QY	2326	TINRQPLFPSPYHKQVRLAKEKASKVVGWMDYDEVAANTPSKSAKSHITGLRGTVRS	2385
Db	1492	GRCKPGIYRFAVGERPSGFMDSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLGPVC	1551	Db	2473	TFDRQLVLDHSYQDLVKEVKAASKYKANLLSVEEACSLTPPHSAKSKF-GYGAKDVR-	2530
QY	1463	GANLDEWADLFS--WNPDPFSVNTAKTADNYVULLTAAQLCHQYGYAAPNADPRWQ-	1520	QY	2386	AARKAVLDL---OKCWEAGEIPSHVROTIVIPKEEVFVKTPOKTKKPPRLISYPHLEM	2441
Db	1552	QDHLFEWEGVFTGLTHIDAHFLSQTKOSGENFPYLVAYQATVCARAQAPPPSDQMWKCL	1611	Db	2531	HARKVAHINSWKOLLEDSVTPI-----DTTIMAKNEVFCVQPEKGGKPARLVFPDLGV	2587
				QY	2442	RCVERMYGQVAPDVVVKAVMGDAYGF-VDPRTVRKRLLSMW--SPDAVGATCTDTCVCFDST	2498

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2588  RVCKRMALYDVVSKLPLAYMGSSYGFQSPGQRVFLVQAWKSKTTPMGFSYDTRCFDST 2647
2499  ITPEDIMVETDIYSAAKLDQHRAGHTHTAROLYAGGPMIAYDREIGYRRRCRSGVYTT 2558
2648  VTESDIRTEAIYQCDDLPQARVAIKSLTERLYVGGPLTNSRGECGYRRCRASGVLT 2707
2559  SSSNLSUTCLWLVNAAEQAKMKNRFLICGDDCTVIWKSAGADADQAMRVFASWKMVNG 2618
2708  SCGNTLTCTIKARACRAAGLQDCTMLVCGDDLVVICSAGVQEDAAASLRAFTEAMTRY 2767
2619  APQDCVPOPKYSLEELTSCSNVTSGITKSGPYFLTRDPRIPLCRCAEGLYNPSAA 2678
2768  APQDPPQPEYDLELITSCSNVSVVAHDGAGKRVYLTDPDTPPLARAAWETARTHPVNS 2827
2679  WICYLIHYPCLVSVRLVAHFVMEQMLFEDKLPETVTFDYGKNTVTPVEDLPSIIAGVH 2738
2828  WLGNIIMFAPTLWARMILMTHFVSJLIARDQLEQALNCEIYACYSIEPLDLPPIQRLH 2887
2739  GIEAFSVRYTNAEILRVQSUTDMTPPLRAWRKARAVLASAKRRGGAHAKLARFLL- 2797
2888  GLSAFSLHSYSGEINRVAACLKLGVPPLRAWRHARSVRALLSRGGRAAICGKYLFN 2947
2798  WHATSR----PLPDLDKTSVARYTTFNYCDVYSPEDGVFIPQRLQKFLVLYLAVIUPA 2853
2948  MAVRTKLLKLTPIAAAGRLDLSGNTAGYSG-----GDIYHSVSHARPRW-----FWFC 2995
2854  LGLIAVGLAI 2863
2996  LLLLAAGVGI 3005

RESULT 13
US-10-259-275-20
; Sequence 20, Application US/10259275
; Publication No. US20030125541A1
; GENERAL INFORMATION:
; APPLICANT: Lemon, Stanley M.
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
; FILE REFERENCE: 265, 0007 0120
; CURRENT APPLICATION NUMBER: US/10/259,275
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/171,909
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 09/747,419
; PRIOR FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/325,236
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/338,123
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Polyprotein
US-10-259-275-20

Query Match      20.9%; Score 3214.5; DB 14; Length 3011;
Best Local Similarity 29.4%; Pred. No. 5.6e-235;
Matches 956; Conservative 440; Mismatches 1213; Indels 641; Gaps 107;

QY      8 TSPVPAFRKKQKQOASVPVSIK-----TSVERGQRAKRVKQDRAPR 51
DB      3 TNPKEQRTKRNTRR---PQDVKPPGGQIVGGVYLLPRRGRGLGVRAIRKTSRSQPR 59
QY      52 NYK----IAGIHDLGLQTLAAALP-----AHGWRGDDPRKSRN 86
DB      60 GRRQPIKARRREG-KTWAQPGYVPLVYGNCGGAGWMLLSRGRSPSGMPTDPRRRRN 118

87  LGILIDYPLMGIDVTHTPLVPLVAGAVRVPCQIVRLLEDGYNMATG-----WFGVHLF 143
119  LCKVITLTCGFADLIGYIPLVGAPLGA-ARALAHGVRVLEDGVNYATGNLPGCSFSIF 177
144  VVCLLS-LACSCSGARVTDPTNTITLNCORNQVIYCSPTCLHEPCVCIC-----AD 197
178  LLALLUSCUTVPASAYQVRN-SSGLYHVTDNCPNSSIVYEAADAI LHTPGCVPCVREGNAS 236
198  ECWVPANPYI SHSPSNWMTGDSPLADHIDFVMGALVTCDALDIGELCGACVLVDLWLV--- 254
237  RCWVAVTPTVATROCKLPTQ-LRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSP 295
255  -RHWLIHIDNETGTCYLEVPTGIDPGFLGIGW---MAGKVEAVIFLTKLASQVPIYA 310
296  RHHW-----TTQDCNGSIYPGHITGHR--MAWDMNMWSPATAALVVAOQL-RIPQAIM 345
311  TMFSSVHYLAVGALYASRGKMYOLLALMLY-----IEATSGNPIRV----- 354
346  DMIAGHVGVLAGIAYFSWGNWAKVLVLLFAGVDAETHVTGAGRTTAGLVGLLTP 405
355  -----PTGC----- 360
406  GAKQNIQLINTNGSHWINSTALNCNESLNTGWLACLFYQHKFNSSGCPERLASCRLLTDF 465
361  AEFCSPLMI-----PCPCHSYLSENV-SEVICYSPKWTPTILEYNN-- 401
466  AQGMGPISYANGSGLDERPCHWYPPRCGIVPAKSVCGPVYCTPS---PVVVGTTDRS 522
402  ---SISWYPTIIPGARGCMVKFKNNT-----WGCCRIRNVPSY-----CTWG--- 440
523  GAPTYSW-----GANDTDVFLVNNTRPLGNMFCGTWMNSTGTFTKVCAGPCCVGGVGN 576
441  -----TDAVNDTRNTYEACGVTPWLT-----TAWHNGSALKLAILQ---YPSGK 482
577  NTLCLPTDCFRKHGPEATYSCSGSPWITPRCMVDYPRYLWHYPCITINTIFKRVMYGVG 636
483  E--MFKPHNMSG-HLYPEGSDTPIVIFYDPVNSTLLPPEKWARIPGTPPVVRGSLQVP 539
637  EHRLEAACNWRGERCDLEDRD-----SELSPLLLSTTQWQVLPFS----- 678
540  QGFYSVDKDLATGLITKDKAKNQVLYSATCALSLTGVTTKAVVLI LLGLCGSKYLLIA 599
679  ---FTTLPALSTGLIHLHQNIVDQVLYGVGSSIASMAIKWEYVVLLFLLADARVCSCL 735
600  YLCYLSLCFGRASGYPLRPVLPVLSQSYLQAGWDVLSKAQVAPFALIFFICCYLRCLRVA 659
736  WMLL-----ISQAEAALENLVI-----LNAAS 758
660  LIGFVPMAGLP--LTFVFAAAAOQPDYDWMVRLVAGLVWAGNRGHR IALLVGPWPL 717
759  LAG-----THGLVSFLVFFCFA-----WYLK-----GRWVPGAVVALYGMWPL 796
718  VALLTLHLVTPASAFDTEI---IGGLTIPVVALVMSRFGFFAHLPRCALVNSYLWQ 774
797  --L LLLALPQRAYALDTEVAASCGVVL---VGLMALTLSPYKRYISWCMWMLQYFLT 851
775  RWEN---WFNVNVLPRPFFLVLCFPGATVDALVTCVCHVALLC-LTSSAAAGFFGT- 828
852  RVEAQLHVVPPLNVRGGRDAVILL-----MCVVHPTLVFDITKLLLAIFGPL 899
829  -----DSRVRAHMLVRIGKCHANYSHVYLKFFLLVFGENG VFFYKHLH--GD 874
900  WILQASLLKVPFVRVQGLLRICALARKIAG-GHYVQMAIILKLGALTGTYYVYNHLTPLRD 958
875  VLPNDFASKLPLOEP--FPFPEGKARVYRNGRRLLACGDTV DGLPVARLGDVLFAGLA- 931
959  WAHNGLRDLAVAVEPWFSPFMRMETKLTITWGD--TAACGDIINGLPVSARRGOEILLGPA 1016
932  -MPDQGWAITAPPTLQCLSERGTLISAMAVMTGTIDPRTWTGTIFRLGLSATSYMFCVFN 990
1017  GNVSGWGLLAPITAYAOQTGLGCIITSLTGRDNQVGEVQIVSTATOTFTLATCING 1076
991  VLYTAHSGSKRRLAHPGTGSIHPITVDAANDQDI--YQPPCAGSLTRCSCGETKGYLVT 1048
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Db 1077 VCMWYHAGTRTIASPKGV--IQMYTVDDQLVGMPPAQGSRSLTPTCGSSDLIYVT 1134
QY 1049 RUGSLVENKSDDPYWCVCALPMAVAKSSGAPILICSSGHVIGMTAA---RNSGGSVS 1105
Db 1135 RHADVIPVRRRGDSRGSLLSPRISYLKSSGGPLLCAGHAGVLPRAAVCTRGVAKAVD 1194
QY 1106 QIRVRPLVACAGYHPQTAHATLDTKPTVNEYSVQIILIAPTGSGKSTKLPLSVMOEKYEV 1165
Db 1195 FIPVENLGTMRSPVETDMS---SPPAVPSQFOVHLHAPTGGKSTKVPAAAYAAOGYKV 1251
QY 1166 LVNLPSVATTASMPKTMHATYGVNPNCFNGKCTNGTASLTYSTYGYMLT-GACSRN-YD 1223
Db 1252 LVNLPSVAATLFGGAYMSKAHGVDPNIRTCVRITITGSPITYSTYKFLADGGCSGAYD 1311
QY 1224 VIICDECHADATTVLIGIKVLTEAPSKNVRVLVLTATATPPGVIPPHANITEIQLTDEG 1283
Db 1312 IIIICDECHSDATSIILGIVLDQAEATAGARLVLTATATPPGSAVTVSHPNIEVALSTTG 1371
QY 1284 TIFPHGKKIKEENLKKGRHLIFBATKHCDELANELARKGITAVSYVRGCDISKIP-EGD 1342
Db 1372 EIPFYKALPLEVIKGRHLIFCHSKKKCDELAAKLVAGINAVAYRGUDVSVIPTSGD 1431
QY 1343 CVVATDALCTGYTGDFDSVYDCSLMVEGTCHVDLPTFTMGVRVCGVSAIVKGQRGRGT 1402
Db 1432 VVVSTDALMTGTFGDFDSVIDCNTCTVTQVDFSLDPTFTIETTLTLPQDAVSRTQRRGT 1491
QY 1403 GGRAGIYVYVDSCTPSGMVPCNIVEAPDAKAWGLSSTBAQIILDTYRTQGLPAI 1462
Db 1492 GRGKPIYFVAPGERPSGMFDSVLCECYDAGCAWYELTPAETTVLRLAYMNTPLGPLVC 1551
QY 1463 GANLDSWADLFS-MVNPESFVNTAKRTADNVLLTAAQLOLCHOYGYAAPNDAPWQG- 1520
Db 1552 QHLEFEWEGFTGLTHIDAHFLSQTQSGENFPYLVAYQATVCARAAQAPPPSWDQWKCL 1611
QY 1521 ARLGKK---PCGVMLRLDGADACGPEPSEV-----TRYQM-CFT---EVNTSGTAALA 1567
Db 1612 IRLKPTLHGPTPLLYRL-----GAVQNEVTLTHPTIKYIMTCSADLEVTS-TWVLV 1663
QY 1568 VGVGVAMAYLAIDTFGATCVRRCWSTSVPATGATVAPVVDDEBI-----VEECASFPL 1621
Db 1664 GGVLAAALAYCLSTGCVCWIVGR-----IVLSGKPAIIPDREVLVQEFDEMECSOHLPY 1717
QY 1622 --BAMVAA---IDKLSTITTTSPF-----TLETALEKNTFLGPHAATILAIIEVCCG 1670
Db 1718 IEQGMMLAEQFKOKALGLLQTAGRAHEVITPAVQTNWQKLEVFWAKHMNFISGIIQLAG 1777
QY 1671 LVTLPNPASFVAFIAGITTPPLPHKIMFLSFGAIAASKLTDARGALAFMMAGAAGT 1730
Db 1778 LSTLPGNPAIASLWATTAATVTSPLTTGQTLFLNLGSGWAAALAAPGAATAFVGAGLAGA 1837
QY 1731 ALGTWTSVGF---VFDMLGYAAASSTACLTFFKCLMGWEFTMDQLAGLVYSATNPAGVV 1787
Db 1838 AIG---SVGLGKVLVDILAGYAGVAGALVAFKIMSGEVPSSTEDLVNLLPAILSPGALVV 1894
QY 1788 GVLSSACAMPALTATAGD---HWPNRLLTMLARSNTVCNFEYFIATDRIRKILGILEAST 1843
Db 1895 GVV---CAAILRRHVGPGEVAGVQMNRLIAPASGNHVSPHYPPESDAAAARVTAISSLT 1952
QY 1844 PMSVISACTIRLWLTPTDEDDCGLIANGLEIMQVYCNFPFVICFNLKAGVQSMVNPICPPFY 1903
Db 1953 VTQLLRLLHQMISSECTTPCS-GSWLRDINDWICEVLSDFKTLKA---KLMPQLPGIPFV 2009
QY 1904 SCQKGYKGPWIGSMLOARCPGAELIFSVEGFAKLYKGPRTCSNVWRGAVPNARLCG 1963
Db 2010 SCQRGYGVNRGDMHTRCHCAEITGHVKNGTMRIV-GPRTCRNMWSGTFFINAYTTG 2068
QY 1964 SARPDPT-DWTSLVNNGVDPDYCKYKMGDHI FVTAVSSPNV-CFTQVP----- 2010
Db 2069 PCTPLPAPNTKFLMRVBSAEYVEIRKVGDFHYVSGMTTDLNLCPCQIPSPPEFTELDGV 2128
QY 2011 -----PTLRAAAVAVD-----GVQVQCYLGEKPTPTWTTSCCYGPGDKGKTVK 2052

RESULT 14

US-10-189-359-14

; Sequence 14, Application US/10189359

; Publication No. US20040019187A1

; GENERAL INFORMATION:

; APPLICANT: MARTIN, Annette

Db 2129 RLHREAPPCKPLLRBEVSFRVGLHEYPVGSQULPC---BPE-----PDVAVLTSM 2174
QY 2053 L--PRVDCGHTPCVPMQNLNRDALETND-----CNSTNNTPSDEAAVASALVFK 2098
Db 2175 LTDPSHITAEAAAGRLARGSPSPMASSASQLSASPLKATCTTANHSDPDALIEANLLWR 2234
QY 2099 QEL-----RRTNQLL-----EASISAGVDTTKLPAPSIIEVVVRKQFRARTGSLTLP- 2145
Db 2235 QEMGGNITRVESENKVILDSFDPLVAEDEDEVSVPA--EILRKSRRRPARALPVWARDP 2292
QY 2146 -----PPRSVPP----- 2152
Db 2293 YNPPLVETWKKPDYBPVVHGCPLPPRSPPPVPPRKRKTIVVLTSTLSTALAEATKSF 2352
QY 2153 -----GVSCPSLQSORPLEGPSNLPPSPVQLQAMPPLLAGAGECNFTTALGCAMTET 2206
Db 2353 GSSSTSGITGDNNTTTSSEP--APSGCPPDSDESYSMMPLLEG-----E 2394
QY 2207 GGGPDDLPSPYPPKKEVSWSDESWSSTATTASSYVTGPPYKIRGDKDSTQSAKAPKRTKK 2266
Db 2395 PGDPD-----LSDGSMSTVSS-----GADT----- 2414
QY 2267 LKGSFSCMSYMTDVISFKTASKVL-S-ATRAITSGFLKQKSLVVTPEPRDAELRKQKV 2325
Db 2415 --EDVVCCSMSYSWTGALVTPCAABEQKLPIINALSNLLRHHNLVYSTTSRACQKQV 2472
QY 2326 TINRQPLFPSPYHKQVRLAKKASKVGMWDYDEVAHTTPSKSAKSHITGLRGTDVRSG 2385
Db 2473 TFDRLQVLDSSHQDVLKEVKAASAKVKANLLSVEEACSLTTPHSAKSKF-GYGAKDVRC- 2530
QY 2386 AARKAVLDL-----QKCEVAGEIYPSHYRVTIVPKEEVFKTPQKPTKPPRLISYPHEM 2441
Db 2531 HARKAVAHINSVMKOLLEDSVTPI---DITIANKNEVFCVQPEKGRKPARLIVPDLGV 2587
QY 2442 RCVKXMYQVQAPDVVYKAVMGDAYGF-VDPTRVYKRLLSMW--SPDAVQATCDTVCFDST 2498
Db 2588 RVCEKMALYDVVSKLPLAVMGSSYGFQVSPGQVBFVLQAWKSKKTPMGFSYDTRCFDST 2647
QY 2499 ITPEDIMVETDIYSAAKLSDOHRAGIHTTAROLYAGGPMIAYDGREIGYVRRCRSSGVTT 2558
Db 2648 VTESDIRTEEAIIYQCDDLPQARVAIKSLTERLYVGGPLTNSRGENCYGRRCCKASGLTT 2707
QY 2559 SSSNSLITCLWKVNAAEQAGMKNRPLICGDDCTVIWKSAGADADKQAMRVFASMMKVMG 2618
Db 2708 SCGNTLITCYIKARAACRAAGLQDCTMLVCGDDLWICESAGVQEDAAASLRAFTEAMTRY 2767
QY 2619 APQDCVPQPKYSLEELTSCSSNVTSGITKSGPYPLTRDPRIPLCRCSAEGLYNPSAA 2678
Db 2768 APPGDPQPEYDLELITSCSSNVSAHDGAGKRVYVLTDRPTTPLARAAMETARHTPVNS 2827
QY 2679 WIGYLIIHYPCLVWSRVLAHFMEQMLFEDKLPEVTVFDWYGNVTVPVVEDLPSIIAGVH 2738
Db 2828 WLGNIIMFAPTUWARMILMTHFFSVLIARDQLEQALNCBIYGACYSIEPLDLPILQRLH 2887
QY 2739 GIEAFSVRYTNAEILURVSQSLTDMTPPLRAWRKARAVLASAKRGGGAHAKLARPLL- 2797
Db 2888 GLSASFSLHSYSGEINRVAACLKLGVPPLRAWRHARSVRARLLSRGGRAALCGKYLEN 2947
QY 2798 WHATSR-----PLPDLDKTSVARYTTTNYCDVTSPEGDVITPORRLOKFLVKLVAVIPA 2853
Db 2948 WAVRTKLTLPITAAAGRLDLGSMFTAGYSG-----GDIYHSVSHARPRW-----FWFC 2995
QY 2854 LGLIIVGLAI 2863
Db 2996 LLLLAAGVGI 3005

```

; APPLICANT: SANGAR, DAVID V.
; APPLICANT: LEMON, STANLEY M.
; TITLE OF INVENTION: Chimeric GB Virus B (GBV-B)
; FILE REFERENCE: UTSG:258US
; CURRENT APPLICATION NUMBER: US/10/189,359
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: .10/189,359
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 3011
; TYPE: PRF
; ORGANISM: Hepatitis C virus
; US-10-189-359-14

Query Match      20.9%; Score 3214.5; DB 15; Length 3011;
Best Local Similarity 29.4%; Pred. No. 5.6e-235;
Matches 956; Conservative 440; Mismatches 1213; Indels 641; Gaps 107;

QY 8 TSPVPAPTRKKNQTOQASYPVSIK-----TSVERGQRAKRVQORDARPR 51
DQ 3 TNPKEQKTRKNTNR--PODVKPGGQIVGGVYLLPRRGPRGLGVRAKTRKTSERSQPR 59
QY 52 NYK-----IAGIHGLOTLQAALP-----AHGWRQDPRHKSNN 86
DQ 60 GRQPIPKARRPEG-RTWAQPGYPWPLFYGNCGGWAGWLLSPRGRSPSGMPTDPRRRSRN 118
QY 87 LGILLDYPGLMGDVTHTPLVPLVAGAVRPVCOIVRLLEDGYNWATG---WFGVHLF 143
DQ 119 LKQVIDTLTCGFADLMGYIPLVGAFLGGA-ARALAHGVRLVDGYNATGNLPGCSFSIF 177
QY 144 VVCLLS-LACPCSGARVTDPTNTTILNTCCORNOVIYCSPTCLHEPCVCIC-----AD 197
DQ 178 LLALLSCLTVPASAVQVRN-SSGLYHVTNDCNPNSSIVYEADAAILHTPCVPCVREGNAS 236
QY 198 ECWVPANPVIHSPSNWGTDSFLADHIDFVGMALVTCDAIDTGEICGACVLVGDMLV--- 254
DQ 237 RCWVAVPTVTRDGKLPPTQ-LRRHIDLLVGSATLCSALYVGDLCGSVFLVQLFTFSP 295
QY 255 -RHWHLIHDLNETGYLEVPTGIDPGFLFGW--MAGKVEAVIFLTKLASOVPYATA 310
DQ 296 RRHW-----TTQDCNCSIYEGHITGHR--NAWDMNMNWSPTAALVVAQLL-RIPQAIM 345
QY 311 TMFSSVHYLAVGALYIYASRGKWOQLLLALMLY-----IEATSGNPIRV----- 354
DQ 346 DMIAGAHGVLAGIAYFSVMGNWAKVVLVLLFAGVDAETHVTGNGAGRTTAGLVGLLTP 405
QY 355 -----PTGC-----SI 360
DQ 406 GAKQNIQLINTNGSWHINSTALNCNESLNTGWLAGIFYQHKFNSSGCPERLASCRRLTDF 465
QY 361 AEFCSPLMI-----PCCHSYLSENV-SEVICSPKTRPITLEYNN-- 401
DQ 466 AQGWGPISVANGSGLDERPCHYPRPCGIVPAKSVCGPVYCFTPS---PVVGTGTRS 522
QY 402 ---SISWYPTTTPGAGCMVKFNNT-----WGCCRIRNVPSY-----CTMG--- 440
DQ 523 GAPTYSW-----GANDTDVFLNTRPPLGNWFGCTWNNSTGFTKVCGAPPCVIGGVGN 576
QY 441 -----TDAVNDTNTYECAGVTPLWT-----TAWHNGSALKUAILQ---YPSGK 482
DQ 577 NTLCLPTDCFRKHPEATYSCSGEPMITPRCMVDVYPRMLWHYPCTINVTIFKVRMYGVG 636
QY 483 E--MFKPHNMMSG-HLYFEGSTPIVYFVDPVNSTLLPPEWARLPPTPPVVRGSLQVP 539
DQ 637 EHRLEAACNWTGERCDLEDRD-----SELSPULLSTTQWVLPCS----- 678
QY 540 QCFYSDVKDLATLITKOKAMKNYQVLYSATGALSITGVTTKAVVLLILGLCGSKYLILA 599
DQ 679 ---FTTLPALSTGLHLHLHQNIVDVQVLYGVGSSIASWALKWEYVVLFLLLADARVCSCL 735
QY 600 YLCYLSLFCGRASGYPLRPLVLPSPQSYLQAGWDVLSKAQVAPPALLIFFICCYLRCLRYAA 659

736 WMML-----ISQAEAALENLVI-----LNAAS 758
QY 660 LLGFVPMAGLP--LTFVAAAAAQPDYDWMVRLVAGLVWAGNRGRHRIALLVCPWPL 717
DQ 759 LAG-----THGLVSFLVFCFA-----WYLK-----GRWPGAVVALVGMWPL 796
QY 718 VALLTLHLVTPASAFDTEI---IGGLTIPPVVALVMSRFGFFAHLPRCALVNSYLWQ 774
DQ 797 --LLLLLALPQRAYALDTEVAASCGGVVL--VGLMALTSPYKRYISWCMWMLQYFLT 851
QY 775 RHEN-----WFWNVTLRPERFFLVLCFPGATYDALVTCVCHVALLC-LTSSAASFFGT- 828
DQ 852 RVEAQLHVWVPLNVRGGRDAVILL-----MCVWHPTLVFDITKLLLAIFGPL 899
QY 829 -----DSRVAHRMLVRLGKCHAWYSHYVLKFFLLVFGENGWFFVKHLH--GD 874
DQ 900 WILQASLLKVPFVRVQGLLRICALARKIAG-GHIVQMAIKLGALTGTGYVNNHLTPLRD 958
QY 875 VLPNDPASKLPLEP--FPFPEGKARVYRNEGRRLACGDTVDGLPVVARLGDVLFAGLA- 931
DQ 959 WAHNGLRDLAVAVEPVVFSRMEETKLITWAD--TAACGDIINGLPVSARRGOEILLGPAD 1016
QY 932 -MPPDGMAITAPFTLOCLSERGTLSAMAVMTGIDPRTWTGTIFRLGSLATSYMGFVCDN 990
DQ 1017 GNVSGMRLAPITAYAAQOTRGLLGCITSLTRDKNQVEGEVQIVSTATOTFLATCING 1076
QY 991 VLYTAHSGSKRRLLAHPGSIHPITVDAANDQD1--YOPPCGAGSLTRCSCGETKGLVT 1048
DQ 1077 VCWTYHAGATRTIASPKGPV--IQMYTNVDODLVGWPAPOGSRSLTPTCTCGSSDLYLT 1134
QY 1049 RLGLSVENKSDDPYWCYCGALPMVAVAKSGGAPILCSSGHVIGMFTAA--RNSGGSVS 1105
DQ 1135 RHADVIPVRRGRDGRSLLSPRISYLSGSGGGLPCPAGHAVGLFRAAVCTRGVAKAVD 1194
QY 1106 QIRVPLVACGVHPQYTAHATLDTPKTPVNEYSVOILIAPTGSGSKSTKPLSYMGEKYBV 1165
DQ 1195 FIPVENLGTTRSPVFTDNS---SPPAVQSFQVAHLHAPTGSKSTKVPAAAYAAQYKV 1251
QY 1166 LVLNPSVATTASMPKYMATYGVNPNCYFNKCTWGTASLTSTYTGMYLT-CACSRN-YD 1223
DQ 1252 LVLNPSVAATLFGGAYMSKAHGDVDPNIRGTWRTTGTGTPITYTYSTYKFLADGCGSGGAYD 1311
QY 1224 VIICDECHATTATVLGIGKVLTEAPSKNVLWLATATPPGVIPTPHANTIEIOLTDGB 1283
DQ 1312 IICDECHSTDATSILGIGTGLDQAEATAGARLVLATATPGSVTVSHPNIEEVALSTTG 1371
QY 1284 TIPFHGKIKKENLKKGRHLIFEATKKGDELANELARKGITAVSYRGCDSKIP-EGD 1342
DQ 1372 EIPFYGKAIPLEVIKGGRHLLIFCHSKKKCDELAALVALGINAVAYYRGLDVSIVTSGD 1431
QY 1343 CVVATDALCTGYTGDPDSVYDCSLWVBGTCHVDLDPFTTGMGRVVCVSAIVKGGRRGT 1402
DQ 1432 VVVSTDAIMTGTGDFSDVDCNTCVQTQTVDFSLDPTFTTETTLPODAVSRTOORGT 1491
QY 1403 GRGAGIYVYVYDGSCTPSGMVPECNIVEAFDAKAWYGLSSTEAQTIILDTYRTOPLCPAI 1462
DQ 1492 GRGEGIVRFVAPGPRPSGMFDSVSLCEYDAGCAWYELTPAETTVRLRAYMNTPLGPVC 1551
QY 1463 GANLDEWADLFS-MVNPEPSFWNTAKRTADNVLLTAAQLQLOLCHOYGYAAPNDAPRWG- 1520
DQ 1552 QDHLFEWEGVFTGLTHIDAHFLPQTKQSGENFPVLVAYQATVCARAQAPPPSWDQMKCL 1611
QY 1521 ARLGKK---PCGVLRWLDGADACPGPBPSEV-----TRYQM-CFT---EVTNSTGAALA 1567
DQ 1612 IRLKPTLHGPTPLLYRL-----GAVQNETVLTHTPTIKYIMTMSADLEVVVTS-TWLV 1663
QY 1568 VGVGVAMAYLAIDTFGATCVRRCMSITSVPTGATVAPVVDDEEI-----VEECASFPL 1621
DQ 1664 GGVLAALAAAYCLSGCVVIVGR-----IVLSGRPAIIPDREVLVQEFDEMECSQHLPY 1717
QY 1622 --EAMVAA---IDKLKSTITTTSPF-----TLETALKLWTFPLGPHAAATLAIETCCG 1670
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QY 198 ECWVPANPVI SHSPSNWGTDSFLADHIDFVMGALVTCDAOLDIGELCGACVLVGDMLV--- 254
DB 237 RCWVAVTPTATRDGKLPTTO-LRRHIDLLVGSATLCSALYVGDLCGSVFLVQGLFTSP 295
QY 255 -RHMLJHIDNETGTCYLVPTGIDPGFLGFGW---MAGKVEAVFLTKLASOVPYATA 310
DB 296 RHHW-----TTQDCNCSYIPGHITGHR--NAMDMMNWSPTAALVVAQLL-RIPOAIM 345
QY 311 TMFSSVHYLAVALYIYASGRWYQALLALMLY-----IEATSGNPIRV----- 354
DB 346 DMIAGAHMGVLAGIAYFSVGNWAKVLVLLFAGVDAETHYTGNGAGRTTAGLVGLLTP 405
QY 355 -----PTGC-----SI 360
DB 406 GAKONIQLINTNGSWHINSTALNCNESLNTWGLAGLFYQHKFNSSGCPERLASCRLLTDF 465
QY 361 AEFCSPLMI-----PCCHSYLSENV-SEVICYSPKWRTPITLEVNN-- 401
DB 466 AOGWPIISVANGSGLDERPCHYPPRCGIIPAKSVCGPVVCFTPS---PVVGTTRDS 522
QY 402 ---SISWYPTITPGARGCMVKFNNT-----WGCCRIRNVPSY-----CTMG----- 440
DB 523 GAPTYSW-----GANDTDVFLNTRPPLGNWFGCTWNNSTGFTKVCGAPPCVIGGVGN 576
QY 441 -----TDAVNDTRNTYEACGVTPWL-----TAWNGSALKLAILQ---YPSK 482
DB 577 NTLCLPTDCFRKHPEATSRCSGSPWITPRCMVDYPYRLWHYPCTINYTIFKRVMYGVG 636
QY 483 E--MEKPHNMMSG-HLYPFGSDTPIVYFDVYNSTLLPPERWARLPGTPPVVRSWMLQVP 539
DB 637 EHLRBAACNWTGRCDEDRD-----SELSPULLSTTQMOVLPCS----- 678
QY 540 QGFYSDVKDLATGLITKRAWKYQVLSATGALSITGVTTKAVVLLILGLCGSKYLIIA 599
DB 679 ---FTPLPALSTGLIHLHQINVDQYLVGVGSSIASWAIKWEVVLFLLLADARVCSCL 735
QY 600 YLCYLSLCEGRASGPLRPLVPSQSYLQAGWDVLSKAQVAPFALLFFCCYURCLRVA 659
DB 736 WMMLL-----ISQAEAALENLVI-----LNAAS 758
QY 660 LAGFVPMAGLP--LTFEFAAAAQPDYDWMVRLVAGLVLAGNRGHRHIALLVGPHPL 717
DB 759 LAG-----THGLVSLVFFCFA-----WYLUK-----GRWPGAVVLYGMPL 796
QY 718 VALLTLLHLVTPASAFDTEI-----IGGLTTPPVVALVWMSRFGFFAHLPRCALVNSYLWQ 774
DB 797 --LLLLLALPORAYALDTEVAASCGVL---VGLMALTSLPYKYKXYSWCMWMLQYFLT 851
QY 775 RWEN-----WFMNVTLRPERFVLVCFPGATYDALVFCVCHVALLC-LTSSAAFFGT- 828
DB 852 RVEAQLHVNVPLNVRGGRDAVILL-----MCVVHPTLVFDITKLLLAIFGPL 899
QY 829 -----DSBRAHMLVRLGKCHAWYSHVULKEFLLVFGENGVPFYKHLH--GD 874
DB 900 WILQASLLKVPYFVRVQGLLRICALARKIAG-GHYVQMAIHKLGALTGYVYNHILTPLRD 958
QY 875 VLPNDFASKLPQEPP--FPFEGKARVYRNEGRRLACGDTVDGLPVARLGLDLPVAGLA- 931
DB 959 WAHNGLRDLAVAPVVFVRSMETKLITWGD--TAACGDIINGLPVSARRGQEIILGPAD 1016
QY 932 -MPPDGWAIATFTLOCLUSERGTLSAMAVMTGIDPRTWTGTIFRLGSLATSYMGFVCDN 990
DB 1017 GNVSGWRLAPITAYAOQTRGLLGCIIITSLTRDKNOQVEGVEQIVSTATQFLATCING 1076
QY 991 VLYTAHSGKRLAHPTGSIHPIITVDAANDODI--YQPPCAGSLITRCSCETKGYLVT 1048
DB 1077 VCMWYHAGRTIASPKGPV--IQWYTNVDQDLVGMWPAQPSRSLTPTCTGSSDLYLVT 1134
QY 1049 RLGSLEVNKSDDPYWCVCALPMAVAKGSCAPILCSGHVIGMFTAA---RNSGGSVS 1105
DB 1135 RHADVIVPVRRGDSRGSLSPRI SYLKGSSGGPLCPAGHAVGLFRAVCTRGVAKAVD 1194
QY 1106 QIRVRPLVCAGYHPQYTAHATLDTKPTVPEYSVQILIAPTGSGKSTKLPLSYMOKYEV 1165
DB 1195 FIPVENLCTMRSPVFTDNS---SPPAVPOSFQVAHLHAPTSGSGKSTKVPAAYAAQGYKV 1251
QY 1166 LVLNPSVATTASMPKYMATYGVNPNCFNGKCTWTGASLTYSTYGMVLT-GACSRN-YD 1223
DB 1252 LVLNPSVAATLFGAYMSKAHGVNDNIRTVRTITGSPITYTYGKFLADCGCGGAYD 1311
QY 1224 VIIICDECHATTATVILGIGKVLTEAPSKNVLWLATATPPGVIPTPHANITEIOLTDSE 1283
DB 1312 IIIICDECHSTDATSILGIGTAVLQAEATAGARLVLATATPPGSVTVSHPNIEVALSTTG 1371
QY 1284 TIPPHGKKIKENLKKGRHLIFEATKCHDELANELARKGITAVSVYRGCDISKIP-BGD 1342
DB 1372 EIPFYGKAIPLEVIGKGRHLIFCHSKKCKDELAALVALGINAVAYYRGLDVSIVPTSGD 1431
QY 1343 CVVATDALCTGYTGDGDFSDVDCSLMWEGTCHVDLDPTFTMGVRVCGVSAIVKGORRGRT 1402
DB 1432 VVVSTDALMTGFTGDFSDVDCNTCVQTVDFSLDPTFTTETTLPODAVSRTOGRT.1491
QY 1403 GRGAGIYYVYDGSCTPSGMVPECNIVEAFDAKAWYGLSSTEATQIILDTYRTQGLPAI 1462
DB 1492 GRGKPGIYRFVAPGERSPGMFDSSVLCYDAGCAWYELTPAETTVRLRAYMNTGCLPVC 1551
QY 1463 GANLDEWADLPS-MVNPSPSVNTAKRTADNADNVLLTAAQLQLCHOYGYAAANDAPRWQ- 1520
DB 1552 QHLEFWEVGTGLTHIDAHFLSOTKQSGENFPYLVAYQATVCARAQAPPPSWDQWCKL 1611
QY 1521 ARLGKK---PCGVLRWLDGADACPGPESEV-----TRYOM-CFT--EVTSTGTAALA 1567
DB 1612 IRLKPTLHGPTLLVRL-----GAVONEVTLTHPTIKYIMTCSADLEVVTS-TWVLV 1663
QY 1568 VGVGVAMAYLAIDTFEGATCVRRCMSITSVPTGATVAPVVDEEEI-----VEECASFPL 1621
DB 1664 GSVLAALAAAYCLSTGCVVIVGR-----IVLSGKPAIIPDREVLVQOEDEMEECQHLPV 1717
QY 1622 --EAWAA---IDKLKSTITTTSPF-----TLEALEKLTNTFLGPHAATILAIYCCG 1670
DB 1718 TEQGMMLAEQFKQKALGILLQATASHRAEVITPAVQTNWQKLEVFNAKHMNFISGQYLAG 1777
QY 1671 LVTLPDNPFASCVPAFIAGITTPPLPHIKMFLSLFGGAIASKLTDARGALAPMAGAACT 1730
DB 1778 LSTLPGNPAIASLMAFTAAVTSPLTTGQTLFNLILGHWAAQALAAPGAATAPVAGLAGA 1837
QY 1731 ALGTWTSYGF---VPDMLGGYAAASSTACLTFKCLMGEMPTMDQLAGLVYSAPNPAAGV 1787
DB 1838 AIG---SVGLGKVLVDIILAGYGAGVAGALVAFKIMSGEVSPSTEDLVNLLPALSPCALV 1894
QY 1788 GVLSCAMFALTAGPD-----HWPNRLLTMLARSNTVCNEFIATRDTRRKILGILEAST 1843
DB 1895 GVV--CAAILRRHVPGEGAGVQWNRLLIAPASRGNHVSPTHYVPESDAAARVTAISSLT 1952
QY 1844 PWSVISACIRMLHTPTEDDCGLIANGLEIWOYVVCNFFVICFNVLKAGVQSMVNIIPGCPY 1903
DB 1953 VTQLRRLRHOMISSECTTPCS-GSWLRDIWDWICEVLSDFKTWLKA--KLMQLPGIIPV 2009
QY 1904 SCQGYKGPWIGSGMLQARCPGABLI ESVENGFALYKGPRTCSNYWRGAPVFNARLCG 1963
DB 2010 SCQRYGVWRGDDGIMTHRCHGAEITGHVKNGTMRIV-GPRTCRNMMSGTFFINAYTTG 2068
QY 1964 SARDDPT--DWTSLVVYGVROYCKYKMGDHI FVTAVSPNV-CFTQVP----- 2010
DB 2069 PCTPLPAPNYKFAWRVSAEBYVEIRRYGDPHYVSGMTDNLKCPQIPSEFFTEL DGV 2128
QY 2011 -----PTLRAAAVAD-----GVQVOCYLGEPKPTWTTTACCYGDGKGKTVK 2052
DB 2129 RLHRFAPCKPCLLREVSFRVGLHEYVPGSQUPC---EPE-----PDVAVLTSM 2174
QY 2053 L--PFRVDGHTPGVRMQLNRLDALETND-----CNSTNTPTSDEAAVSAVFK 2098
DB 2175 LTDPSHITAEAGRRLARGSPPSMASSASQLSAPSKATCTANHDSDAELIEANLWR 2234
QY 2099 QEL-----RRTNOLL-----EALSAGVDTTKLPAPSIEEVVVRKROFRARTGSLTLP- 2145

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Db 2235 QEMGGNITRSESNKVILDSFDPLVAEEDEREVSVA--EILRKSRFFARALPVWARD 2292
Qy 2146 -----PPRSVP----- 2152
Db 2293 YNPPLVETWKKPDYEPVHVGCPLPPRPPPPPRKKRTVVLTESTLTAELATKSF 2352
Qy 2153 -----GVSCPSLQSDPLEGPSNLPPSPVLIQLAMPPLLGAGECNPFTAIGCAMTET 2206
Db 2353 GSSSTSGITGDNTTTSEP--AFSGCPCPDSDVESYSMPLEG-----E 2394
Qy 2207 GGGPDDLPSYPPKKEVSEWSDSWSTATTASSYVTPGPPYKIRGDKOSTOSAPAKRPTKK 2266
Db 2395 PGDPD-----LSDGSWSTVSS-----GADT----- 2414
Qy 2267 LGKSEFSCSNYTWTDVIFSKTASKVL-ATRAITSGFLKQRLSVVTEPRDAELRKQV 2325
Db 2415 --EDVVCCSMYSWTCALVTPCAAEBQKLPINALSNLRRHNLVYSTTSRSACQKQV 2472
Qy 2326 TINRQPLFPSPYHKQVRLAKEKASKVGVVMWDYDEVAHTPSKASHITGLRGTDVRS 2385
Db 2473 TFDRLQVLDHYQDVLKEVKAASKKANLLSVEEACSLTPPHSAKSF-GYGAKDVRC- 2530
Qy 2386 ARKAVLDL-----OKVEAGEIPSHYRQTVIVPKEEVFKTPOKTKKPPRLISYPHLEM 2441
Db 2531 HARKAVAHINSVMKDLLEDSVTPI---DTTIMAKNEVFCVQPEKGGKPARLIVFPDLGV 2587
Qy 2442 RCVEKMYGQVAPDVVKAVMGDAYGF--VDPRTVRKLLSMW--SPDAVGATCDTVCFDST 2498
Db 2588 RVCERKALYDVWSKLPFLAVNGSSYGFQYSPGQVFEVLQAWKSKKTPMGFSYDTRCFDST 2647
Qy 2499 ITPEDIMVETDIYSAAKLSQHRAGIHTIARQLYAGGPMIAYDGRBIGYRRCRSSGVYTT 2558
Db 2648 VTESDIRTEEAIIQCCDLDPQARVAIKSLTERLYVVGPLTNSRGNGCYRRCSRASGLTT 2707
Qy 2559 SSSNSITCWLKVNAAEQAGKNPRLICGDDCTVIWKSAGADADQOAMRVFASWKMVG 2618
Db 2708 SCGNTLTCVIKARAACRAAGLODCTMLVCGDDLWVICSAGVQVEDAAASLRAFTEAMTRY 2767
Qy 2619 APQDCVPOPKYSLEELTSCSNVTSGITKSGKPYFLTRDPTPLGRCSAEGLYGNPSAA 2678
Db 2768 APGDPPEYDELELTSCSNVSVAHGAGKRVYLTDRPTPLARAAMETARHTPVNS 2827
Qy 2679 WIGYLIIHVPCLWVSRVLAVHFMEOMLFEDKLPETVTFDWYGNKYTVPVEDLPSIIAGVH 2738
Db 2828 WLGNIIMEAPTILWARMLTHTFFSVLIARDQLEALNCEIYGACYSIEPLDLPPIQLRH 2887
Qy 2739 GIEAFSVRYTNAEILRVOSLTDMTMPPLPAWRKKARAVLASAKRRGGGAHAKLARPLL- 2797
Db 2888 GLSAFSLHSYSPGEINRVAACLKGLGVPLPAWRHRARSVRARLLSRGGRAAICGKYLEN 2947
Qy 2798 WHATSR---PLPDLDKTSVARVTTFNKYCDVSPGDDVEITPQRRLOKPLVKYLAVIFA 2853
Db 2948 WAVRTKLKLTPIAAAGRLDLSGWMFTAGYSG-----GDIYHSVSHARPRW-----FWFC 2995
Qy 2854 LGLIAGLAI 2863
Db 2996 LLLAAGVI 3005
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Search completed: October 27, 2005, 15:54:11
Job time : 323 secs

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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 08:53:15 ; Search time 2934 Seconds
(without alignments)
18963.752 Million cell updates/sec

Title: US-10-009-002-1
Perfect score: 9399
Sequence: 1 accacaaactcagtttg.....cccgcttggaataaaact 9399

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9399	100.0	9399	4	Aaf23484 GBV-B vir
2	9386.2	99.9	9399	12	Adj56732 Genome le
3	9386.2	99.9	9399	12	Adj64244 GB virus
4	9338.6	99.4	9397	9	Ada77752 Genomic h
5	9131.4	97.2	9139	4	Aaf23485 GBV-B vir
6	9059.8	96.4	9143	2	Aat00130 Hepatitis
7	9059.8	96.4	9143	3	Aaa55376 Hepatitis
8	9059.8	96.4	9143	3	Aaa55379 Hepatitis
9	9037.4	96.2	9143	2	Aat59785 Hepatitis
10	8692.6	92.5	8912	3	Aaa55280 Hepatitis
11	8691.4	92.5	8912	2	Aat00040 Hepatitis
12	6088	64.8	8069	9	Ada77751 Hepatitis
13	4159	44.2	4268	2	Aat00052 Hepatitis
14	4159	44.2	4268	3	Aaa55298 Hepatitis
15	449.8	4.8	479	2	Aat00045 Hepatitis
16	449.8	4.8	479	3	Aaa55378 Hepatitis
17	449.8	4.8	479	3	Aaa55291 Hepatitis
18	319.6	3.4	337	2	Aat00127 Hepatitis
19	319.6	3.4	337	2	Aat00049 Hepatitis
20	319.6	3.4	337	3	Aaa55371 Hepatitis

C	21	319.6	3.4	337	3	AAA55295	Hepatitis
	22	307.8	3.3	362	5	AAS15946	3' nontra
	23	307.4	3.3	309	4	AAC92010	GBV-B 3'X
	24	279.4	3.0	281	3	AAA55285	Hepatitis
	25	279.4	3.0	281	3	AAA55286	Hepatitis
	26	278.4	3.0	9405	2	AAQ40426	Full-leng
	27	273.6	2.9	9402	2	AAQ41345	Human hep
	28	273.2	2.9	9444	2	AAT13279	CDNA to g
C	29	270.4	2.9	9711	4	Aaf23486	Infectio
	30	270.4	2.9	9711	4	AAC86937	Nucleotid
	31	270.4	2.9	9711	5	AAC86644	Nucleotid
	32	269.6	2.9	3564	2	AAQ32442	HCV NS2-N
	33	265.6	2.8	9589	2	AAQ38218	NANBH vir
	34	262.4	2.8	3970	2	AAQ38219	NANBH vir
	35	262.4	2.8	5211	4	AAC83408	DNA encod
	36	260.2	2.8	9502	2	AAQ74770	Hepatitis
	37	257.4	2.7	259	4	AAC91998	GBV-B 3'X
	38	256	2.7	8385	13	ADQ26514	Hepatotro
	39	256	2.7	9609	6	ADQ31038	HCV-S1 fu
	40	255.6	2.7	9436	2	AAQ63499	Blood tra
	41	254.4	2.7	260	12	ADJ56731	3' termin
	42	254.4	2.7	260	12	ADJ64243	GB virus
	43	253.4	2.7	7911	2	AAQ32436	HCV antig
	44	252.8	2.7	3564	2	AAQ32501	HCV NS2-N
	45	252.6	2.7	2061	6	ADQ34500	Hepatitis

ALIGNMENTS

RESULT 1	
AAF23484	
ID	AAF23484 standard; DNA; 9399 BP.
XX	
AC	AAF23484;
XX	
DT	11-SEP-2003 (revised)
DT	21-MAR-2001 (first entry)
XX	
DE	GBV-B virus genome.
XX	
KW	GBV-B; hepatitis C virus; HCV; vaccine; ds.
XX	
OS	Hepatitis GB virus B.
XX	
PN	WO200075337-A1.
XX	
PD	14-DEC-2000.
XX	
PF	02-JUN-2000; 2000WO-US015293.
XX	
PR	04-JUN-1999; 99US-0137694P.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Bukh J, Yanagi M, Emerson SU, Purcell RH;
XX	
DR	WPI; 2001-091214/10.
XX	
PT	New infectious nucleic acids of the GB virus-B clone, useful for
PT	indirectly studying the molecular properties of hepatitis C virus (HCV)
PT	and in developing vaccines and therapeutics for HCV.
XX	
PS	Claim 3; Page 60-63; 96pp; English.
XX	
CC	The present invention relates to GB virus-B. The nucleic acid molecules
CC	of the invention are useful for indirectly studying the molecular
CC	properties of hepatitis C virus (HCV). The infectious nucleic acid
CC	sequence of the GB virus-B clone and the HCV/GBV-B chimera may be used
CC	in the development of vaccines and therapeutics for HCV. (Updated on 11-
CC	SEP-2003 to standardise OS field)
XX	
SQ	Sequence 9399 BP; 2125 A; 2326 C; 2430 G; 2518 T; 0 U; 0 Other;

Query Match				Score 9399; DB 4; Length 9399;			
Best Local Similarity 100.0%; Pred. No. 0;							
Matches 9399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
QY	1	ACCAAAACATCCAGTTTGTATACACTCGCTAGGAATGCTCCTCGAGACACCCCCCTAG	60				
DB	1	ACCAAAACATCCAGTTTGTATACACTCGCTAGGAATGCTCCTCGAGACACCCCCCTAG	60				
QY	61	CAGGCGTGGGGATTTCCCTGCGGCTGCGAGAGGTGGAGCAACCACTTAGTAT	120				
DB	61	CAGGCGTGGGGATTTCCCTGCGGCTGCGAGAGGTGGAGCAACCACTTAGTAT	120				
QY	121	GTAGCGCGGGACCTCATGACGCTCGCGTGTATGACAGCGCCCAAGCTTGATGGC	180				
DB	121	GTAGCGCGGGACCTCATGACGCTCGCGTGTATGACAGCGCCCAAGCTTGATGGC	180				
QY	181	CCTGATGGCGTTCAATGGTTCCGTTGCGTGTGGCGCTTTAGGCAAGCTTCAAGCCCA	240				
DB	181	CCTGATGGCGTTCAATGGTTCCGTTGCGTGTGGCGCTTTAGGCAAGCTTCAAGCCCA	240				
QY	241	CCTCCAGATAGACGGCGGCACTGTAGGGAAGACGGGGACCGGTCACTACCAAGGAC	300				
DB	241	CCTCCAGATAGACGGCGGCACTGTAGGGAAGACGGGGACCGGTCACTACCAAGGAC	300				
QY	301	CAGACCTCTTTTGTAGTATCAGCGCTCGGAAGTAGTTGGGCAAGCCCACTTATGTGT	360				
DB	301	CAGACCTCTTTTGTAGTATCAGCGCTCGGAAGTAGTTGGGCAAGCCCACTTATGTGT	360				
QY	361	TGGGATGTTGGGTTAGCCATCCATACCGTACTGCTGATAGGTCTCTCGAGGGGAT	420				
DB	361	TGGGATGTTGGGTTAGCCATCCATACCGTACTGCTGATAGGTCTCTCGAGGGGAT	420				
QY	421	CTGGAGTCTCGTAGCCGTAGCAGATGCTGTTATTTCTACTCAACAGTCTGTACC	480				
DB	421	CTGGAGTCTCGTAGCCGTAGCAGATGCTGTTATTTCTACTCAACAGTCTGTACC	480				
QY	481	TGCGCCAGAACGCGCAAGAACAGCAGACGAGCTTCATATCTGTGTCATTTAAAC	540				
DB	481	TGCGCCAGAACGCGCAAGAACAGCAGACGAGCTTCATATCTGTGTCATTTAAAC	540				
QY	541	ATCTGTTGAAAGGGACAAACGAGCAAAAGTCAGCGCGATGCTCGGCTCGTAA	600				
DB	541	ATCTGTTGAAAGGGACAAACGAGCAAAAGTCAGCGCGATGCTCGGCTCGTAA	600				
QY	601	TTACAAATTCGTGATCCATGATGGCTTGAGAGATGGCTCAGGCTGCTTGGCAGC	660				
DB	601	TTACAAATTCGTGATCCATGATGGCTTGAGAGATGGCTCAGGCTGCTTGGCAGC	660				
QY	661	TCATGTTGGGAGCGCAAGACCTCGCCATAGTCTCGCAATCTTGGAACTCTTCTGGA	720				
DB	661	TCATGTTGGGAGCGCAAGACCTCGCCATAGTCTCGCAATCTTGGAACTCTTCTGGA	720				
QY	721	TTACCTTTGGGGTGGATTGTTGATGTTAACTCAACACTCCTAGTAGGCCCTGCT	780				
DB	721	TTACCTTTGGGGTGGATTGTTGATGTTAACTCAACACTCCTAGTAGGCCCTGCT	780				
QY	781	GGCAGGAGCGGTGCTTGCAGCAGTCTGCCAGATAGTACGCTTCTGGAGGATGGAGTCA	840				
DB	781	GGCAGGAGCGGTGCTTGCAGCAGTCTGCCAGATAGTACGCTTCTGGAGGATGGAGTCA	840				
QY	841	CTGGGCTACTGTTGGTTGCTGCTGCTTGTGGTATGCTGCTATCTTTGGCCCTG	900				
DB	841	CTGGGCTACTGTTGGTTGCTGCTGCTTGTGGTATGCTGCTATCTTTGGCCCTG	900				
QY	901	TCCCTGTAGTGGGCGCGGTCACCTGACCCAGACAAATACCACTCCTGACCAATTG	960				
DB	901	TCCCTGTAGTGGGCGCGGTCACCTGACCCAGACAAATACCACTCCTGACCAATTG	960				
QY	961	CTGCCAGGCTATCAGGTTATCTATGTTCTCCTTCCACTGCTACAGAGCTGGTTG	1020				
DB	961	CTGCCAGGCTATCAGGTTATCTATGTTCTCCTTCCACTGCTACAGAGCTGGTTG	1020				
QY	1021	TGTGATCTGTCCGACGAGTGTCTGGGTTCCGCGCAATCCGTACATCTCACACCTTCCAA	1080				
DB	1021	TGTGATCTGTCCGACGAGTGTCTGGGTTCCGCGCAATCCGTACATCTCACACCTTCCAA	1080				
QY	1081	TTGACTGGCAGGACACTCCTTCTTGGCTGACACATTTGATTTTGTATGGGCGCTCTGT	1140				
DB	1081	TTGACTGGCAGGACACTCCTTCTTGGCTGACACATTTGATTTTGTATGGGCGCTCTGT	1140				
QY	1141	GACCTGTGACGCCCTTGCATTTGTTGAGTGTGTGTCGTCGTGTATTAGTCGGTGACTG	1200				
DB	1141	GACCTGTGACGCCCTTGCATTTGTTGAGTGTGTGTCGTCGTGTATTAGTCGGTGACTG	1200				
QY	1201	GCTTGTCAAGCACTGGCTTATTTCATAGACCTCAATGAATACTGTATCTTGTACTCTGA	1260				
DB	1201	GCTTGTCAAGCACTGGCTTATTTCATAGACCTCAATGAATACTGTATCTTGTACTCTGA	1260				
QY	1261	AGTGGCCACTGGAATAGATCTCTGGTTCCTAGGTTTATCGGTGGATGGCGGCAAGGT	1320				
DB	1261	AGTGGCCACTGGAATAGATCTCTGGTTCCTAGGTTTATCGGTGGATGGCGGCAAGGT	1320				
QY	1321	CGAGCTGTCTATCTTTGACCAAACTGGCTTCAACGTACATACGCTATTGCGACTAT	1380				
DB	1321	CGAGCTGTCTATCTTTGACCAAACTGGCTTCAACGTACATACGCTATTGCGACTAT	1380				
QY	1381	GTTTAGCAGTGTACACTACCTGGCGTTGGCGCTCTGATCTACTATGCTCTCTCGGGCAA	1440				
DB	1381	GTTTAGCAGTGTACACTACCTGGCGTTGGCGCTCTGATCTACTATGCTCTCTCGGGCAA	1440				
QY	1441	GTGGTATCAGTTGCTCTAGCGCTTATGCTTTACATAGAGGACCTCTGGAACCCCAT	1500				
DB	1441	GTGGTATCAGTTGCTCTAGCGCTTATGCTTTACATAGAGGACCTCTGGAACCCCAT	1500				
QY	1501	CAGGTGCCACTGATGCTCAATAGCTGAGTTTGTCTCGCTTTGATGATACCATGTC	1560				
DB	1501	CAGGTGCCACTGATGCTCAATAGCTGAGTTTGTCTCGCTTTGATGATACCATGTC	1560				
QY	1561	TTGCCACTCTTATTTGAGTGAGATGTGTGAGAGTCAATTTGTTACAGTCCAAAGTGAC	1620				
DB	1561	TTGCCACTCTTATTTGAGTGAGATGTGTGAGAGTCAATTTGTTACAGTCCAAAGTGAC	1620				
QY	1621	CAGGCTATCATCTAGAGTATACAACTCCATATCTTTGGTACCCCTATACATCCCTGG	1680				
DB	1621	CAGGCTATCATCTAGAGTATACAACTCCATATCTTTGGTACCCCTATACATCCCTGG	1680				
QY	1681	TGCGAGGGGATGTATGTTTAAATTAACACATGCGGTTGCTGCGCTATTTCGCAA	1740				
DB	1681	TGCGAGGGGATGTATGTTTAAATTAACACATGCGGTTGCTGCGCTATTTCGCAA	1740				
QY	1741	TGTGCATCTGATCTGACACTATGGGCACTGATGAGTGTGGAAACGACACTCGCACTTA	1800				
DB	1741	TGTGCATCTGATCTGACACTATGGGCACTGATGAGTGTGGAAACGACACTCGCACTTA	1800				
QY	1801	CGAGCATGCGGTGTACACCATGGCTAAACCGCATGGCACAACGCTCAGCCCTGAA	1860				
DB	1801	CGAGCATGCGGTGTAAACCATGGCTAAACCGCATGGCACAACGCTCAGCCCTGAA	1860				
QY	1861	ATTGGCTATTTTACAAATACCTCGGTCTAAAGAAATGTTTAAACCTCATATTGGATGTC	1920				
DB	1861	ATTGGCTATTTTACAAATACCTCGGTCTAAAGAAATGTTTAAACCTCATATTGGATGTC	1920				
QY	1921	AGGCCATTTGATTTTGGAGGATCAGATACCCCTATAGTTTATCTTTATGACCCCTGTGAA	1980				
DB	1921	AGGCCATTTGATTTTGGAGGATCAGATACCCCTATAGTTTATCTTTATGACCCCTGTGAA	1980				
QY	1981	TTCCACTCTCTTACACCGGAGAGTGGGCTAGTGTGCCCGGTACCCCACTGTGGTAGC	2040				
DB	1981	TTCCACTCTCTTACACCGGAGAGTGGGCTAGTGTGCCCGGTACCCCACTGTGGTAGC	2040				
QY	2041	TGGTTCTTGGTTTACAGGTTTCGCAAGGTTTTCAGTGTATGTGAAAGACCTAGCCACAG	2100				
DB	2041	TGGTTCTTGGTTTACAGGTTTCGCAAGGTTTTCAGTGTATGTGAAAGACCTAGCCACAG	2100				
QY	2101	ATTGATCAACCAAGACAAAGCCCTGGAATAATTCAGGTCCTTATATTCGGCACCGGTGC	2160				

Db 2101 ATTGATACCAAGACAAAGCCTGGAAAAATTTATCAGGCTTATATCCGCCACCGGTGC 2160
Qy 2161 TTTGTCTCTTACGGGAGTTACCAACAAAGCCGTGGTAAATCTGTGTGGGGTTGTGTGG 2220
Db 2161 TTTGTCTCTTACGGGAGTTACCAACAAAGCCGTGGTAAATCTGTGTGGGGTTGTGTGG 2220
Qy 2221 CAGCAAGTATCTTATTTAGGCTACCTCTGTGTATCTGTGCCCTTTGTGTGGCGCGCTTC 2280
Db 2221 CAGCAAGTATCTTATTTAGGCTACCTCTGTGTATCTGTGCCCTTTGTGTGGCGCGCTTC 2280
Qy 2281 TGGTTACCCCTTTGGCGTCTGTGCTCCCATCCAGTCGTATCTCAAGCTGGCTGGGATGT 2340
Db 2281 TGGTTACCCCTTTGGCGTCTGTGCTCCCATCCAGTCGTATCTCAAGCTGGCTGGGATGT 2340
Qy 2341 TTTGTCTAAAGCTCAAGTAGCTCCCTTTTGTGCTTGAATTTCTTCACTGTGTCTATCTCCG 2400
Db 2341 TTTGTCTAAAGCTCAAGTAGCTCCCTTTTGTGCTTGAATTTCTTCACTGTGTCTATCTCCG 2400
Qy 2401 CTGCAAGCTACGTTATGCTGCCCTTTTAGAGTTTGTGCCCATGCTGGCGGCTTGCOCCT 2460
Db 2401 CTGCAAGCTACGTTATGCTGCCCTTTTAGAGTTTGTGCCCATGCTGGCGGCTTGCOCCT 2460
Qy 2461 AACTTTCTTTGTCAGCAGCTGCTGCCCAACCAAGATTATGACTGGTGGTGGCACTGCT 2520
Db 2461 AACTTTCTTTGTCAGCAGCTGCTGCCCAACCAAGATTATGACTGGTGGTGGCACTGCT 2520
Qy 2521 AGTGGCAGGGTAGTTTGTGGCGCGCGTAACCGTGCACCGCATAGCTCTGCTTGT 2580
Db 2521 AGTGGCAGGGTAGTTTGTGGCGCGCGTAACCGTGCACCGCATAGCTCTGCTTGT 2580
Qy 2581 AGGTCCTTGGCTCTGTGAGCGCTTTTAAACCTCTTGCAATTTGTAGCGCTGCTTACG 2640
Db 2581 AGGTCCTTGGCTCTGTGAGCGCTTTTAAACCTCTTGCAATTTGTAGCGCTGCTTACG 2640
Qy 2641 TTTTGTATCCAGATTAATTGAGGGCTGACAAATACCACCTGTAGTAGCAATTAGTGTCTAT 2700
Db 2641 TTTTGTATCCAGATTAATTGAGGGCTGACAAATACCACCTGTAGTAGCAATTAGTGTCTAT 2700
Qy 2701 GTCTCGTTTGGCTTCTTTGCTCACTTGTACCTCGCTGTGCTTTTGTAACTCCTATCT 2760
Db 2701 GTCTCGTTTGGCTTCTTTGCTCACTTGTACCTCGCTGTGCTTTTGTAACTCCTATCT 2760
Qy 2761 TTGGCAAGCTTGGAGAAATGGTTTGGAACTTACACTAAGACCGGAGAGGTTTTTCT 2820
Db 2761 TTGGCAAGCTTGGAGAAATGGTTTGGAACTTACACTAAGACCGGAGAGGTTTTTCT 2820
Qy 2821 TGTGCTGTTTGTTCGCCGTGGACATATGACCGCGTGTGACTTCTGTGTGTGCA 2880
Db 2821 TGTGCTGTTTGTTCGCCGTGGACATATGACCGCGTGTGACTTCTGTGTGTGCA 2880
Qy 2881 CGTAGCTCTTATGTTTAAATCCAGTGCAGCATCGTTCCTTGGGACTGACTCTAGGGT 2940
Db 2881 CGTAGCTCTTATGTTTAAATCCAGTGCAGCATCGTTCCTTGGGACTGACTCTAGGGT 2940
Qy 2941 TAGGGCCCATAGAAATGTTGGTGGCTTCGGAAAGTGTATGCTTGGTATTTCTCATTAATGT 3000
Db 2941 TAGGGCCCATAGAAATGTTGGTGGCTTCGGAAAGTGTATGCTTGGTATTTCTCATTAATGT 3000
Qy 3001 TCTTAAGTTTTTCTTCTAGTGTGTTGGTGGAGAAATGGTGTGTTTTCTATAAGACATTGCA 3060
Db 3001 TCTTAAGTTTTTCTTCTAGTGTGTTGGTGGAGAAATGGTGTGTTTTCTATAAGACATTGCA 3060
Qy 3061 TGGTGTGCTTGGCTTAATGATTTGGCTCGAACTACCATTTGCAAGAGCCATTTTTCCC 3120
Db 3061 TGGTGTGCTTGGCTTAATGATTTGGCTCGAACTACCATTTGCAAGAGCCATTTTTCCC 3120
Qy 3121 TTTTGAAGGCAAGGAGGCTATAGGAATCAAGGAAGACGCTTGGCGTGTGGGGACAC 3180
Db 3121 TTTTGAAGGCAAGGAGGCTATAGGAATCAAGGAAGACGCTTGGCGTGTGGGGACAC 3180
Qy 3181 GGTGTAGTGGTTGGCGTGTGGCGTCTGGCGACCTTGTGTTCGAGGGTTGGCTAT 3240

Db 3181 GGTGTAGTGGTTGGCGTGTGGCGTCTGGCGACCTTGTTCGACGGTTGGCTAT 3240
Qy 3241 GCCGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTCAGGTCTCTCTGAAACGTGG 3300
Db 3241 GCCGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTCAGGTCTCTCTGAAACGTGG 3300
Qy 3301 CACGCTGTACCGATGGCAGTGTCTAGCTGATGATAGACCCCGAACTTGGACTGGAAC 3360
Db 3301 CACGCTGTACCGATGGCAGTGTCTAGCTGATGATAGACCCCGAACTTGGACTGGAAC 3360
Qy 3361 TATCTTCAGATTTAGGATCTCTGGCCACTAGTACATGGGATTTGTGTGTGACAACTGTT 3420
Db 3361 TATCTTCAGATTTAGGATCTCTGGCCACTAGTACATGGGATTTGTGTGTGACAACTGTT 3420
Qy 3421 GTATACTGCTCACCATGGCAGCAAGGGCGCGGTGGCTCATCCACAGGCTCTATACA 3480
Db 3421 GTATACTGCTCACCATGGCAGCAAGGGCGCGGTGGCTCATCCACAGGCTCTATACA 3480
Qy 3481 CCCAATAACCGTTGACCGGCTAATGACCAAGGACATCTATCAACCACTGTGGAGCTGG 3540
Db 3481 CCCAATAACCGTTGACCGGCTAATGACCAAGGACATCTATCAACCACTGTGGAGCTGG 3540
Qy 3541 GTCCCTTACTCGGTGCTCTTGGGGGAGACCAAGGGTATCTGGTAACACGACTGGGTC 3600
Db 3541 GTCCCTTACTCGGTGCTCTTGGGGGAGACCAAGGGTATCTGGTAACACGACTGGGTC 3600
Qy 3601 ATTGGTTGAGGTCAACAAATCCGATGACCTTATTTGTGTGTGTGCGGGGCCCTTCCAT 3660
Db 3601 ATTGGTTGAGGTCAACAAATCCGATGACCTTATTTGTGTGTGTGCGGGGCCCTTCCAT 3660
Qy 3661 GGCTGTGCCAAGGGTCTTCAAGTGCCCGATCTGTGCTCTCCCGGGCATGTTATGG 3720
Db 3661 GGCTGTGCCAAGGGTCTTCAAGTGCCCGATCTGTGCTCTCCCGGGCATGTTATGG 3720
Qy 3721 GATGTTCAACCGCTGTAGAAATCTGCGGGTTCAGTCACTCAGATAGGTTAGGCTT 3780
Db 3721 GATGTTCAACCGCTGTAGAAATCTGCGGGTTCAGTCACTCAGATAGGTTAGGCTT 3780
Qy 3781 GGTGTGTGCTGGATACCATCCCACTACAGACACATGCCACTCTTGATACAAACCTTAC 3840
Db 3781 GGTGTGTGCTGGATACCATCCCACTACAGACACATGCCACTCTTGATACAAACCTTAC 3840
Qy 3841 TGTGCTTAAACGAGTATTCAGTGCAATTTTAAATTTGCCCCCACTGGCAGCGCAAGTCAAC 3900
Db 3841 TGTGCTTAAACGAGTATTCAGTGCAATTTTAAATTTGCCCCCACTGGCAGCGCAAGTCAAC 3900
Qy 3901 CAAATTAACCACTTTCTTACATGCAAGGAAAGTATGAGTCTTGTCTTAAATCCAGTGT 3960
Db 3901 CAAATTAACCACTTTCTTACATGCAAGGAAAGTATGAGTCTTGTCTTAAATCCAGTGT 3960
Qy 3961 GGCTTACAAACAGCATCAATGCCAAAGTACATGACGCGACGTACGCGGTGAATCCAAATTTG 4020
Db 3961 GGCTTACAAACAGCATCAATGCCAAAGTACATGACGCGACGTACGCGGTGAATCCAAATTTG 4020
Qy 4021 CTATTTTAAATGGCAAAATGTACCAACAGGGGCTTCACTTACGTACAGCACATATGGCAT 4080
Db 4021 CTATTTTAAATGGCAAAATGTACCAACAGGGGCTTCACTTACGTACAGCACATATGGCAT 4080
Qy 4081 GTACCTGACCGGAGCATGTTCCCGGAACTATGATGTAATCATTTGTGACGAAATGCCATGC 4140
Db 4081 GTACCTGACCGGAGCATGTTCCCGGAACTATGATGTAATCATTTGTGACGAAATGCCATGC 4140
Qy 4141 TACCGATGCAACCAACCGGCTTGGGCAATGGAAAGTCTTAAACCGAAGCTCCATCCAAAA 4200
Db 4141 TACCGATGCAACCAACCGGCTTGGGCAATGGAAAGTCTTAAACCGAAGCTCCATCCAAAA 4200
Qy 4201 TGTTAGGCTAGTGGTCTTGGCCACGGCTACCCCGCTGGAGTAATCCCTACACCATATGC 4260
Db 4201 TGTTAGGCTAGTGGTCTTGGCCACGGCTACCCCGCTGGAGTAATCCCTACACCATATGC 4260
Qy 4261 CACATTAACCTAGATTTCAATTAACCGATGAGGCACTATCCCTTTTCATGCAAAAAAGAT 4320
Db 4261 CACATTAACCTAGATTTCAATTAACCGATGAGGCACTATCCCTTTTCATGCAAAAAAGAT 4320

QY 4321 TAAAGGAGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG 4380
DB |||||
4321 TAAAGGAGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG 4380
QY 4381 TGATGAGCTTGCTAAAGAGTTAGCTGGAAGGGAATAACAGCTGTCTCTACTATAGGGG 4440
DB |||||
4381 TGAATGAGCTTGCTAAAGAGTTAGCTGGAAGGGAATAACAGCTGTCTCTACTATAGGGG 4440
QY 4441 ATGTGACATCTCAAAAATCCCTGAGGGGACGTCTAGTGTGCGACATGATGCGCTTGTG 4500
DB |||||
4441 ATGTGACATCTCAAAAATCCCTGAGGGGACGTCTAGTGTGCGACATGATGCGCTTGTG 4500
QY 4501 TACAGGGTACACTGGTGTACTTTGATTTCCGTGTATGACTGCGACCTCATGGTAGAGGCAC 4560
DB |||||
4501 TACAGGGTACACTGGTGTACTTTGATTTCCGTGTATGACTGCGACCTCATGGTAGAGGCAC 4560
QY 4561 ATGCCATGTTGACCTTGACCCCTACTTTTCAACATGCGGTGTGCTGTGCGGGGTTTCAGC 4620
DB |||||
4621 AATAGTTAAAGCCACAGCTGAGGGCCGACACAGCCGCTGGAGAGCTGGCATATACTACTA 4680
DB |||||
4621 AATAGTTAAAGCCACAGCTGAGGGCCGACAGCCGCTGGAGAGCTGGCATATACTACTA 4680
QY 4681 TGTAGACGGGAGTTGTACCCCTTCGGGTATGTTCTGAAATGCAACATTTGTTGAAAGCCCTT 4740
DB |||||
4681 TGTAGACGGGAGTTGTACCCCTTCGGGTATGTTCTGAAATGCAACATTTGTTGAAAGCCCTT 4740
QY 4741 CGACGAGCAAGGCAATGATATGTTTGTATCAACAGAGCTCAAACTATTCTCGACAC 4800
DB |||||
4741 CGACGAGCAAGGCAATGATATGTTTGTATCAACAGAGCTCAAACTATTCTCGACAC 4800
QY 4801 CTATCGCACCCAACTGGTACCTGCGATAGGACCAATTTGACGAGTGCGGTGATCT 4860
DB |||||
4801 CTATCGCACCCAACTGGTACCTGCGATAGGACCAATTTGACGAGTGCGGTGATCT 4860
QY 4861 CTTTTCCTATGTTCAACCCCGAACCTTCTTCTCAATACTGCAAAAAGAACTGCTGCAAA 4920
DB |||||
4861 CTTTTCCTATGTTCAACCCCGAACCTTCTTCTCAATACTGCAAAAAGAACTGCTGCAAA 4920
QY 4921 TTATGTTTTTTGACTGACGCCCAACTCAACATGTTGTCATGATGAGTATGCTGCTCC 4980
DB |||||
4921 TTATGTTTTTTGACTGACGCCCAACTCAACATGTTGTCATGATGAGTATGCTGCTCC 4980
QY 4981 CAATGACGCCACCGTGGCAGGGAGCCCGCTTGGGAAAAAACCTTGTGGGGTTCTGTG 5040
DB |||||
4981 CAATGACGCCACCGTGGCAGGGAGCCCGCTTGGGAAAAAACCTTGTGGGGTTCTGTG 5040
QY 5041 GCGCTTTGACGCGCTGACGCCCTGCTCGGCCACAGAGCCAGCGAGTGACCAATACCA 5100
DB |||||
5041 GCGCTTTGACGCGCTGACGCCCTGCTCGGCCACAGAGCCAGCGAGTGACCAATACCA 5100
QY 5101 AATGTCTTCACTGAAGTCAATCTTCTGGGACAGCGCACTCGCTGTTGGCGTTGGAGT 5160
DB |||||
5101 AATGTCTTCACTGAAGTCAATCTTCTGGGACAGCGCACTCGCTGTTGGCGTTGGAGT 5160
QY 5161 GGTATGCTTATCTAGCCATTTGACATTTTGGCGCCACTTGTGCGCGTTGCTGCTGTC 5220
DB |||||
5161 GGTATGCTTATCTAGCCATTTGACATTTTGGCGCCACTTGTGCGCGTTGCTGCTGTC 5220
QY 5221 TATTACATCAGTCCCTTACCGGTGCTACTGTCGCCCCAGTGGTTGACGAAGAAGAAATCGT 5280
DB |||||
5221 TATTACATCAGTCCCTTACCGGTGCTACTGTCGCCCCAGTGGTTGACGAAGAAGAAATCGT 5280
QY 5281 GGAGGAGTGTGCATCAATTCATTTCCCTTGGAGGCCATGTTGTGTCGAAATGACAGCTGAA 5340
DB |||||
5281 GGAGGAGTGTGCATCAATTCATTTCCCTTGGAGGCCATGTTGTGTCGAAATGACAGCTGAA 5340
QY 5341 GAGTACAAATCACCAACTAGTCCCTTTTCAATTTGGAAACCGCCCTTGA AAAACTTAAACAC 5400
DB |||||
5341 GAGTACAAATCACCAACTAGTCCCTTTTCAATTTGGAAACCGCCCTTGA AAAACTTAAACAC 5400

QY 5401 CTTTCTGGGCTCATGACAGCTACAACTCTTGCTATCATAGAGTATTTGCTGTGTTTGTAGT 5460
DB |||||
5401 CTTTCTGGGCTCATGACAGCTACAACTCTTGCTATCATAGAGTATTTGCTGTGTTTGTAGT 5460
QY 5461 CACTTTACTGACAAATCCCTTTGCTCATGCGTGTGCTTTTCAATTTGCGGTATTTACTTAC 5520
DB |||||
5461 CACTTTACTGACAAATCCCTTTGCTCATGCGTGTGCTTTTCAATTTGCGGTATTTACTTAC 5520
QY 5521 CCCACTACTCTCAAGAATCAAAATGTTCTCTGCTCATTTATTGAGAGCGCAATTTGCGTCCAA 5580
DB |||||
5521 CCCACTACTCTCAAGAATCAAAATGTTCTCTGCTCATTTATTGAGAGCGCAATTTGCGTCCAA 5580
QY 5581 GCTTACAGACGCTAGAGCGCACTGGCGTTTCAATGATGCGCGGCTGCGGAAACAGTCT 5640
DB |||||
5581 GCTTACAGACGCTAGAGCGCACTGGCGTTTCAATGATGCGCGGCTGCGGAAACAGTCT 5640
QY 5641 TGGTACATGGAACATCGGTGGGTTTTGCTTTTGACATGCTAGCGGCTATGCTGCGGCTC 5700
DB |||||
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DB |||||
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DB |||||
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DB |||||
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DB |||||
6001 CGTTGGCTTCCACACCCCGAGGAGTATGCGGCTCATTTGCTGGGCTCTAGAGAT 6060
QY 6061 TTGGCAGTATGTTGCAATTTCTTTGATTTGCTTTTAAATGCTTAAAGCTGGAGTTCA 6120
DB |||||
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DB |||||
6121 GAGCATGGTTAAACATTCCTGTTGCTTTCTACAGCTGCCAGAGGGGTACAAGGGCCC 6180
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DB |||||
6181 CTGGATTGGATCAGGTATGCTTCCAGACGCTGTCTCCATGCGGTGCTGAACTCATCTTTC 6240
QY 6241 TGTTCAGAAATGGTTTTCAGAACTTTTACAAAGGACCCAGAACTTCTTCAAATTAAGTGGAG 6300
DB |||||
6241 TGTTCAGAAATGGTTTTCAGAACTTTTACAAAGGACCCAGAACTTCTTCAAATTAAGTGGAG 6300
QY 6301 AGGGGCTGTTCCAGTCAACGCTAGGCTGTGGGTGCGGTAGACCGGACCCCACTGATG 6360
DB |||||
6301 AGGGGCTGTTCCAGTCAACGCTAGGCTGTGGGTGCGGTAGACCGGACCCCACTGATG 6360
QY 6361 GACTAGTCTTGTGCTCAATTTAGGGTTAGGGACTACTGTAAATATGAGAAATGGGAGA 6420
DB |||||
6361 GACTAGTCTTGTGCTCAATTTAGGGTTAGGGACTACTGTAAATATGAGAAATGGGAGA 6420
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Db 6481 CTTGAGAGCTCAGTGGCCGTGGACGGGTACAGGTTTCAGTGTATCTAGGTGAGCCCAA 6540
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Db 9361 TTCCAAGGGGAGGCAACCCCGCTTGGNAATTAANAAT 9399
FT
FT

RESULT 2
ADJ56732
ID ADJ56732 standard; cDNA; 9399 BP.
XX
AC ADJ56732;
XX
DT 06-MAY-2004 (first entry)
XX
DE Genome length hepatitis GB virus B cDNA SeqID 2.
XX
KW ss; GB virus B; GBV-B; HCV; flavivirus; hepatitis C virus; antiviral;
XX vaccine; virucidal; antiinflammatory.
XX
OS Hepatitis GB virus B.
XX
FH Key Location/Qualifiers
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FT stem_loop 29..61
FT FT /*tag= b
FT misc_binding 63..73
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WO2004005498-A1.
15-JAN-2004.
02-JUL-2003; 2003WO-US021002.
03-JUL-2002; 2002US-00189359.
(TEXA) UNIV TEXAS SYSTEM.
(INSP) INST PASTEUR.
Martin A, Sangar DV, Lemon SM, Rijnsbrand R;
WPI; 2004-091362/09.
New chimeric GBV-B polynucleotide, useful as a model for hepatitis C virus, for identifying compounds active against a viral infection, or for developing hepatitis C virus preventive and therapeutic treatments.
Example 22; SEQ ID NO 2; 108pp; English.
This invention relates to novel isolated chimeric GB virus B (GBV-B)/HCV polynucleotides. Specifically, it refers to using the hepatotropic flavivirus GBV-B that has a unique phylogenetic relationship to the human hepatitis C virus (HCV) and can serve as a surrogate virus in drug discovery efforts related to antiviral drug development. The present invention describes the construction of an infectious molecular clone

CC using the newly determined 3' terminal sequence of GBV-B. Furthermore,
CC the GBV-B/HCV chimeras exhibit liver-specific expression and express HCV
CC envelope proteins such that they can have utility as a vaccine immunogen
CC for hepatitis C. In addition, they can be used for screening compounds
CC active against viral infection, as well as for developing HCV
CC preventative and therapeutic treatments. Accordingly, these compositions
CC exhibit virucidal, antiinflammatory and hepatotropic activities. This
CC polynucleotide sequence is the GBV-B cDNA sequence of the invention.
XX

SQ Sequence 9399 BP; 2124 A; 2322 C; 2432 G; 2521 T; 0 U; 0 Other;

Query Match		99.9%;	Score 9386.2;	DB 12;	Length 9399;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 9391;		Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
QY	1	ACCAAAACACTCCAGTTTGTACACTCCGCTAGGAATGCTCTGGAGCACCCCTAG	60		
DB	1	ACCAAAACACTCCAGTTTGTACACTCCGCTAGGAATGCTCTGGAGCACCCCTAG	60		
QY	61	CAGGCGTGGGGATTTCCTCCCTGCCGCTCGAGAAGGGTGGAGCCAAACACCTTAGTAT	120		
DB	61	CAGGCGTGGGGATTTCCTCCCTGCCGCTCGAGAAGGGTGGAGCCAAACACCTTAGTAT	120		
QY	121	GTAGCGCGGGGACTCATGACGCTCGCGTGTGATGACAAGCGGCAAGCTTGATGGG	180		
DB	121	GTAGCGCGGGGACTCATGACGCTCGCGTGTGATGACAAGCGGCAAGCTTGATGGG	180		
QY	181	CCTGATGGCGTTTCATGGTTCGTTGGTGGCTTTAGCGAGCCTCCACGCCACCA	240		
DB	181	CCTGATGGCGTTTCATGGTTCGTTGGTGGCTTTAGCGAGCCTCCACGCCACCA	240		
QY	241	CCTCCAGATAGCGCGGCACTGTAGGGAAGACCGGGACCGGTCACTACCAAGGACG	300		
DB	241	CCTCCAGATAGCGCGGCACTGTAGGGAAGACCGGGACCGGTCACTACCAAGGACG	300		
QY	301	CAGACCTCTTTTGGATACAGCTCCGGAAGTAGTTGGGCAAGCCACCTATATGTGT	360		
DB	301	CAGACCTCTTTTGGATATCAAGCTCCGGAAGTAGTTGGGCAAGCCACCTATATGTGT	360		
QY	361	TGGGATGTTGGGTTAGCCATCATACCGTACTGCTGTAGGTCCTTCGGAGGGAT	420		
DB	361	TGGGATGTTGGGTTAGCCATCATACCGTACTGCTGTAGGTCCTTCGGAGGGAT	420		
QY	421	CTGGAGTCTCTGAGCGTAGCACATGCTGTTATTTCTACTCAAAACAAGTCTGTACC	480		
DB	421	CTGGAGTCTCTGAGCGTAGCACATGCTGTTATTTCTACTCAAAACAAGTCTGTACC	480		
QY	481	TGCGCCAGAAACGGCAAGAAACAAGCAGACGCGGCTTCATATCTGTGTCCATTA	540		
DB	481	TGCGCCAGAAACGGCAAGAAACAAGCAGACGCGGCTTCATATCTGTGTCCATTA	540		
QY	541	ATCTGTTGAAAGGGGACAAACGAGCAAGCGAAAGTCCAGCGCGATGCTCGGCTCGTAA	600		
DB	541	ATCTGTTGAAAGGGGACAAACGAGCAAGCGAAAGTCCAGCGCGATGCTCGGCTCGTAA	600		
QY	601	TTACAAAATTGCTGTATCCATGATGGCTTCGAGACATTTGGCTCAGGCTGCTTGGCCAGC	660		
DB	601	TTACAAAATTGCTGTATCCATGATGGCTTCGAGACATTTGGCTCAGGCTGCTTGGCCAGC	660		
QY	661	TCATGTTGGGGAACCCCAAGACCTTCGACATAGTCTCGCAATCTTGAATCTTCTGGA	720		
DB	661	TCATGTTGGGGAACCCCAAGACCTTCGACATAGTCTCGCAATCTTGAATCTTCTGGA	720		
QY	721	TTACCTTTGGGTTGGATGTTGATGTTACACTCACACCTCTAGTAGGCCCGCTGGT	780		
DB	721	TTACCTTTGGGTTGGATGTTGATGTTACACTCACACCTCTAGTAGGCCCGCTGGT	780		
QY	781	GGCAGGAGCGTCTGTCACAGCTCTGCAGATAGTACGCTTGCTGGAGGATGGAGTCAA	840		
DB	781	GGCAGGAGCGTCTGTCACAGCTCTGCAGATAGTACGCTTGCTGGAGGATGGAGTCAA	840		
QY	841	CTGGGCTACTGGTTCGTTGCTCCACCTTTTGTGGTATGTCCTGCTATCTTTGGGCTG	900		

DB	841	CTGGGCTACTGGTTCGTTGCTCCACCTTTTGTGGTATGTCGCTATCTTTGGGCTG	900		
QY	901	TCCCTGTAGTGGGCGGGTCACTGACCCAGACACAAATACCAATCTCTGACCAATTG	960		
DB	901	TCCCTGTAGTGGGCGGGTCACTGACCCAGACACAAATACCAATCTCTGACCAATTG	960		
QY	961	CTGCCAGGTAATCAGGTATCTATTGTTCTCTTCCACTTTCCTACAGAGCTGTTG	1020		
DB	961	CTGCCAGGTAATCAGGTATCTATTGTTCTCTTCCACTTTCCTACAGAGCTGTTG	1020		
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DB	1021	TGTGATCTGTGGGACGAGTCTGGGTTCCGCCAATCCGTCACATCTCACAACCTTCAA	1080		
QY	1081	TTGACTGGCACCGACTCTTCTTGGCTGACCAATGATTTTGTATGGCGCTCTTGT	1140		
DB	1081	TTGACTGGCACCGACTCTTCTTGGCTGACCAATGATTTTGTATGGCGCTCTTGT	1140		
QY	1141	GACCTGTGACGCGCTTGACATTTGGTGTGTTGTGGTGGTGTATTTAGTCGGTACTG	1200		
DB	1141	GACCTGTGACGCGCTTGACATTTGGTGTGTTGTGGTGGTGTATTTAGTCGGTACTG	1200		
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DB	1201	GCTTGTGAGGCACTGGCTTATTCATAGACCTCAATGAACTGGTACTTGTACCTGGA	1260		
QY	1261	AGTCCCACTGGAAATAGATCCTGGGTTCTAGGGTTTATCGGGTGGATGGCGGCAAGT	1320		
DB	1261	AGTCCCACTGGAAATAGATCCTGGGTTCTAGGGTTTATCGGGTGGATGGCGGCAAGT	1320		
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DB	1321	CGAGGCTGTCTATTCTTGTGACCAAACTGGCTTCAAGATACCAATGCGTATTTGCGACTAT	1380		
QY	1381	GTTTGTAGGCTGTACACTCTGGGTTGGGCTCTGATCTACTATGCTCTCGGGGCA	1440		
DB	1381	GTTTGTAGGCTGTACACTCTGGGTTGGGCTCTGATCTACTATGCTCTCGGGGCA	1440		
QY	1441	GTGGTATCAGTTGCTCCTAGCGCTTATGCTTTACATAGAGCGACCTCTGGAACCCCAT	1500		
DB	1441	GTGGTATCAGTTGCTCCTAGCGCTTATGCTTTACATAGAGCGACCTCTGGAACCCCAT	1500		
QY	1501	CAGGTCGCCACTGGATGCTCAATGATGCTTTTGTCTGCGCTTTGATGATACCATGTC	1560		
DB	1501	CAGGTCGCCACTGGATGCTCAATGATGCTTTTGTCTGCGCTTTGATGATACCATGTC	1560		
QY	1561	TTGCCACTTATTGTAGTGAGATGCTCAGAGTCAATTTGTACAGTCCAAAGTGGAC	1620		
DB	1561	TTGCCACTTATTGTAGTGAGATGCTCAGAGTCAATTTGTACAGTCCAAAGTGGAC	1620		
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QY	1681	TGCAGGGGATGTTATGTTTAAATTTCAAAAATAACAATGGGGTTGCTGCGCTATTCGCA	1740		
DB	1681	TGCAGGGGATGTTATGTTTAAATTTCAAAAATAACAATGGGGTTGCTGCGCTATTCGCA	1740		
QY	1741	TGTGCCATCTGATCTGCACTATGGGCACTGATGAGTGTGGNACGACACTCGCAACACTTA	1800		
DB	1741	TGTGCCATCTGATCTGCACTATGGGCACTGATGAGTGTGGNACGACACTCGCAACACTTA	1800		
QY	1801	CGAAGCATGGTGTAAACACCATGGCTAAACCGCATGGCACAACCGCTCAGGCCCTGAA	1860		
DB	1801	CGAAGTATGGTGTAAACACCATGGCTAAACCGCATGGCACAACCGCTCAGGCCCTGAA	1860		
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DB	1861	ATTGGCTATATTAACAATACCTTGGGCTCTAAAGAAATGTTTAAACCTCATATTTGGATGTC	1920		
QY	1921	AGGCCATTTGTATTTGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGGA	1980		
DB	1921	AGGCCATTTGTATTTGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGGA	1980		

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2101 ATTGATCACCAAGACAAAGCCCTGAAAAAATATCAGGTCCTTATATTCGGCCACGGGTGC 2160
2161 TTGTGCTCTTACGGGAGTTACCAACGAGCCCGTGGTGAATTCGTGTTGGGGTGTGTGG 2220
2161 TTGTGCTCTTACGGGAGTTACCAACGAGCCCGTGGTGAATTCGTGTTGGGGTGTGTGG 2220
2221 CAGCAAGTATCTTATTTAGGCTACCTCTGTGTTACCTGTTTACCTGTTTGGCGGCTTC 2280
2221 CAGCAAGTATCTTATTTAGGCTACCTCTGTTTACCTGTTTGGCGGCTTC 2280
2281 TGGTTACCTTTGGCTCTGTGCTCCATCCAGTCGTATCTCCAAGCTGGCTGGGATGT 2340
2281 TGGTTACCTTTGGCTCTGTGCTCCATCCAGTCGTATCTCCAAGCTGGCTGGGATGT 2340
2341 TTTGTCTAAAGCTCAAGTAGCTCCCTTTGCTTTGATTTTCTTCACTCTGTTGCTATCTCG 2400
2341 TTTGTCTAAAGCTCAAGTAGCTCCCTTTGCTTTGATTTTCTTCACTCTGTTGCTATCTCG 2400
2401 CTGAGGCTAGCTTATGCTGCCCTTTTAGGGTTTGTGCCATGGCTGGCGGCTTCCCTC 2460
2401 CTGAGGCTAGCTTATGCTGCCCTTTTAGGGTTTGTGCCATGGCTGGCGGCTTCCCTC 2460
2461 AACTTTCTTTGTTGAGAGCTGCTGCCCAACCAAGTATGACTGGTGGGTGGACTGCT 2520
2461 AACTTTCTTTGTTGAGAGCTGCTGCCCAACCAAGTATGACTGGTGGGTGGACTGCT 2520
2521 AGTGCAGGGTTAGTTTGTGGCGCGGCGTAACCGTGGTCAACCGATAGCTCTGCTTGT 2580
2521 AGTGCAGGGTTAGTTTGTGGCGCGGCGTAACCGTGGTCAACCGATAGCTCTGCTTGT 2580
2581 AGGTCCTTTGGCTCTGTTAGCGCTTTTAAACCTCTTGCAATTTGGTTACGCTGCTTACG 2640
2581 AGGTCCTTTGGCTCTGTTAGCGCTTTTAAACCTCTTGCAATTTGGTTACGCTGCTTACG 2640
2641 TTTTGATACCGAGATAATTGGAGGCTGACATACCACTGTAGTAGCATTTAGTTGTCTAT 2700
2641 TTTTGATACCGAGATAATTGGAGGCTGACATACCACTGTAGTAGCATTTAGTTGTCTAT 2700
2701 GTCTCGTTTGGCTTCTTTGCTCACTTGTACCTCGCTGCTGCTTTAGTTAACTCCTATCT 2760
2701 GTCTCGTTTGGCTTCTTTGCTCACTTGTACCTCGCTGCTGCTTTAGTTAACTCCTATCT 2760
2761 TTGGCAACGTTGGGAGAAATGGTTTTGGAAAGCTTACCTAAGACCGGAGAGTTTTTCT 2820
2761 TTGGCAACGTTGGGAGAAATGGTTTTGGAAAGCTTACCTAAGACCGGAGAGTTTTTCT 2820
2821 TGTGCTGTTGTTTTCCCGGTGGACATATACGCGCTGGTGACTTCTGTGTGTGTCA 2880
2821 TGTGCTGTTGTTTTCCCGGTGGACATATACGCGCTGGTGACTTCTGTGTGTGTCA 2880
2881 CGTAGCTCTCTTATGTTTTAACTTCAAGTGCAGATCTGTTCTTTGGAGCTGACTTAGGGT 2940
2881 CGTAGCTCTCTTATGTTTTAACTTCAAGTGCAGATCTGTTCTTTGGAGCTGACTTAGGGT 2940
2941 TAGGGCCCATAGAAATGTTGGTCGTCTCGGAAAGTGTCACTGCTGGTATTTCTATTATGT 3000
2941 TAGGGCCCATAGAAATGTTGGTCGTCTCGGAAAGTGTCACTGCTGGTATTTCTATTATGT 3000
3001 TCTTAAGTTTTTCCCTTAGTGTGTTGGTGAGATGGTGTGTTTTTCTATTAAGCACTTGA 3060
3001 TCTTAAGTTTTTCCCTTAGTGTGTTGGTGAGATGGTGTGTTTTTCTATTAAGCACTTGA 3060

3061 TGGTGATGCTTGGCTAATGATTTTGGCTCGAAACTACATTTGCAAGACCATTTTTCCC 3120
3061 TGGTGATGCTTGGCTAATGATTTTGGCTCGAAACTACATTTGCAAGACCATTTTTCCC 3120
3121 TTTTGAAGCAAGCAAGGCTCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGACAC 3180
3121 TTTTGAAGCAAGCAAGGCTCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGACAC 3180
3181 GGTTCATGTTTTTGGCGGTTGTCGGGCTCGGGACCTTCTTTTCGACAGGTTGGCTAT 3240
3181 GGTTCATGTTTTTGGCGGTTGTCGGGCTCGGGACCTTCTTTTCGACAGGTTGGCTAT 3240
3241 GCCGCAGATGGGTGGGCCATTACCGCACCTTTTACGCTGAGTGTCTCTCTGAACGTGG 3300
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3361 TATCTTCAGATTTAGGATCTCTGGGCCATAGCTACATGGGATTTGTTGTGACACGTTT 3420
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3421 GTATACTGCTCACCATGGCAGCGCGGTTGGCTCATCCACAGGCTCTATATA 3480
3421 GTATACTGCTCACCATGGCAGCGCGGTTGGCTCATCCACAGGCTCTATATA 3480
3481 CCCAATAACCGTTGACGGGCTAATGACAGAGACATCTATCAACCATGTGGAGCTGG 3540
3481 CCCAATAACCGTTGACGGGCTAATGACAGAGACATCTATCAACCATGTGGAGCTGG 3540
3541 GTCCCTTACTCGGTGCTCTCGGGGAGACCAAGGGTATCTGGTAAACAGACTGGGGTC 3600
3541 GTCCCTTACTCGGTGCTCTCGGGGAGACCAAGGGTATCTGGTAAACAGACTGGGGTC 3600
3601 ATTGGTTGAGGTCAACAAATCCGATGACCTTATTTGGTGTGTGTGCGGGGCCCTTCCC 3660
3601 ATTGGTTGAGGTCAACAAATCCGATGACCTTATTTGGTGTGTGTGCGGGGCCCTTCCC 3660
3661 GGCTGTTGCCAAGGGTCTTTCAGGTGCCCGAATCTGTGCTCTCCCGGGCATGTTATTGG 3720
3661 GGCTGTTGCCAAGGGTCTTTCAGGTGCCCGAATCTGTGCTCTCCCGGGCATGTTATTGG 3720
3721 GATGTTACCGCTCTAGAAATCTTGGCGGTTCACTGAGTCAGTACAGATTAGGGTTAGCCGTT 3780
3721 GATGTTACCGCTCTAGAAATCTTGGCGGTTCACTGAGTCAGTACAGATTAGGGTTAGCCGTT 3780
3781 GGTGTGCTGCTGGATACCAATCCCGAGTACACAGCATGCCACTCTTGTATACAAACCTAC 3840
3781 GGTGTGCTGCTGGATACCAATCCCGAGTACACAGCATGCCACTCTTGTATACAAACCTAC 3840
3841 TGTGCTAACCGAGTATTCAGTGCGAAAATTTTAAATTTGGCCCCACTGGCAGCGGCAAGTCAAC 3900
3841 TGTGCTAACCGAGTATTCAGTGCGAAAATTTTAAATTTGGCCCCACTGGCAGCGGCAAGTCAAC 3900
3901 CAATTTACCACTTCTTATACAGGAGAAATGATGAGGCTTGTGCTTAAATCCCAAGTGT 3960
3901 CAATTTACCACTTCTTATACAGGAGAAATGATGAGGCTTGTGCTTAAATCCCAAGTGT 3960
3961 GGCTACAAACAGCATCAATGCCCCAAGTATACGACGCGAGTACGGCGTGAATCCAAATTTG 4020
3961 GGCTACAAACAGCATCAATGCCCCAAGTATACGACGCGAGTACGGCGTGAATCCAAATTTG 4020
4021 CTATTTTAAATGGCAATGTACCAACAGGGGCTTCACTTACGTACAGACATATGGCAT 4080
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4081 GTACCTGACCGGAGCATCTTCCCGAACTATGATGTAATCATTTGTGACGAATGCCATGC 4140
4081 GTACCTGACCGGAGCATCTTCCCGAACTATGATGTAATCATTTGTGACGAATGCCATGC 4140
4141 TACCGATGCAACACCGGCTGTTGGGCAATTTGGAAAGGTCTTAAACCGAAGCTCCATCCAAAA 4200

4141	Db	 TACCGATGCAACCAACCGTGTGTGGGCATTGGAAAGGTCTTAACCGAAGCTCCATCTCCAAAAA	4200
4201	Qy	 TGTTTAGGCTAGTGTGTTCTTGCCACGGCTACCCCCCTTGGAGTAATCCTTACACCAATGC	4260
4201	Db	 TGTTTAGGCTAGTGTGTTCTTGCCACGGCTACCCCCCTTGGAGTAATCCTTACACCAATGC	4260
4261	Qy	 CAACATACTGAGATTCAATTAAACCGATGAAGGCACATATCCCCTTTCAATGAAAAAAGAT	4320
4261	Db	 CAACATACTGAGATTCAATTAAACCGATGAAGGCACATATCCCCTTTCAATGAAAAAAGAT	4320
4321	Qy	 TAAGGAGGAAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
4321	Db	 TAAGGAGGAAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
4381	Qy	 TGATGAGCTTGTCTAAACGAGTTAGTCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGG	4440
4381	Db	 TGATGAGCTTGTCTAAACGAGTTAGTCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGG	4440
4441	Qy	 ATGTGACATCTCAAAAAATCCCTGAGGCGGACCTGTGTAGTAGTTGCGCACTGATGCTTGTG	4500
4441	Db	 ATGTGACATCTCAAAAAATCCCTGAGGCGGACCTGTGTAGTAGTTGCGCACTGATGCTTGTG	4500
4501	Qy	 TACAGGGTACACTGGTGACCTTTGATTCCGTGTATGACTGCAGCCCTCATGTTAGAAAGCCAC	4560
4501	Db	 TACAGGGTACACTGGTGACCTTTGATTCCGTGTATGACTGCAGCCCTCATGTTAGAAAGCCAC	4560
4561	Qy	 ATGCCATGTTGACCTTCGACCTCACTTTCCACCATGGGTGTTCTGTGTGTGCGGGGTTTCAGC	4620
4561	Db	 ATGCCATGTTGACCTTCGACCTCACTTTCCACCATGGGTGTTCTGTGTGTGCGGGGTTTCAGC	4620
4621	Qy	 AATAGTTAAAGGCCAGCGTAGGGGCCGACAGAGCCGTGGGAGAGCTGGCATATACTACTA	4680
4621	Db	 AATAGTTAAAGGCCAGCGTAGGGGCCGACAGAGCCGTGGGAGAGCTGGCATATACTACTA	4680
4681	Qy	 TGTTAGACGGGAGTTGTACCCCTTCGGGTATGGTTCCTGAATGCAACATTTGTTGAAAGCTTT	4740
4681	Db	 TGTTAGACGGGAGTTGTACCCCTTCGGGTATGGTTCCTGAATGCAACATTTGTTGAAAGCTTT	4740
4741	Qy	 CGACGCAGCCAAAGCATGGTATGGTTGTTCATCAACAGAAAGCTCAAACCTATCTTGGACAC	4800
4741	Db	 CGACGCAGCCAAAGCATGGTATGGTTGTTCATCAACAGAAAGCTCAAACCTATCTTGGACAC	4800
4801	Qy	 CTATCGCACCCAAACCTGGGTTTACCTGCGATAGGAGCAAAATTTGACGAGTGGCTGATCT	4860
4801	Db	 CTATCGCACCCAAACCTGGGTTTACCTGCGATAGGAGCAAAATTTGACGAGTGGCTGATCT	4860
4861	Qy	 CTTTTCTATGTTCAACCCCGAACCTTCATTTGTCAATACTGTGCAAAAAAGAACTGCTGACAA	4920
4861	Db	 CTTTTCTATGTTCAACCCCGAACCTTCATTTGTCAATACTGTGCAAAAAAGAACTGCTGACAA	4920
4921	Qy	 TTATGTTTTGTTGACTCGAGCCCAACTACAACTGTCATCAGTATCGCTATGCTGCTCC	4980
4921	Db	 TTATGTTTTGTTGACTCGAGCCCAACTACAACTGTCATCAGTATCGCTATGCTGCTCC	4980
4981	Qy	 CAATGACGCACACGGGTGGCAGGAGCCCGGCTTTGGGAAAAAAACCTTTGGGGTTCCTGTG	5040
4981	Db	 CAATGACGCACACGGGTGGCAGGAGCCCGGCTTTGGGAAAAAAACCTTTGGGGTTCCTGTG	5040
5041	Qy	 GCGCTTGGACGGCGTGACCGCTGTCTTGCGCCAGAGCCCAAGCGAGTGACCAATACCA	5100
5041	Db	 GCGCTTGGACGGCGTGACCGCTGTCTTGCGCCAGAGCCCAAGCGAGTGACCAATACCA	5100
5101	Qy	 AATGTGCTTCACTGAATCAATATCTTGCGACACCGCACACTGCTGCTTGGCGTTGAGT	5160
5101	Db	 AATGTGCTTCACTGAATCAATATCTTGCGACACCGCACACTGCTGCTTGGCGTTGAGT	5160
5161	Qy	 GGCTATGGCTTATCTAGGCAATTGACATTTTGGCGCCACTTTGTGCGGGCTTGTCTGGTC	5220
5161	Db	 GGCTATGGCTTATCTAGGCAATTGACATTTTGGCGCCACTTTGTGCGGGCTTGTCTGGTC	5220
5221	Qy	 TATTACATCAGTCCCTACCGGTGCTACTGTGTCGCCCCCAAGTGAGTGAAGAAAGAAATCGT	5280

QY 6361 GACTAGTCTTGTGCGCAATTATGGCGTTAGGACTACTGTAAATATGAGAAATGGGAGA 6420
DB |||||
QY 6361 GACTAGTCTTGTGCGCAATTATGGCGTTAGGACTACTGTAAATATGAGAAATGGGAGA 6420
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QY 6421 TCACATTTTGTGACAGAGTATCTCTCCAAATGTCTGTTTACCCAGGTCGCCCCCAAC 6480
DB |||||
QY 6421 TCACATTTTGTGACAGAGTATCTCTCCAAATGTCTGTTTACCCAGGTCGCCCCCAAC 6480
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QY 6541 AACTCTCTGGACGACATCTGCTTGTCTGTACCGTCTCTGACGGTAAAGGTPAAACCTGTTAA 6600
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QY 7321 TCTGTCTGCAACTCGGGCCATCACTAGTGGTTTCTTCAAAAGAGATCACTGGTGTATGT 7380
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DB |||||
QY 7381 GACTGAGCGGGGATGCGGAGCTTAGAAAAAAGTCACTATTAATAGACAACTCT 7440

QY 7441 GTTCCCCCATATACCAAGAGTGAGATGGCTAAGGAAAAAGCTTCAAAAGTTGT 7500
DB |||||
QY 7441 GTTCCCCCATATACCAAGAGTGAGATGGCTAAGGAAAAAGCTTCAAAAGTTGT 7500
DB |||||
QY 7501 CGGTGTCATGTGGGACTATGATGAAGTAGAGCTCACACGCCCTCTAAGTCTGCTAAGTC 7560
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QY 7501 CGGTGTCATGTGGGACTATGATGAAGTAGAGCTCACACGCCCTCTAAGTCTGCTAAGTC 7560
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QY 8461 ATACAAACCCAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8520
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Db 8521 TAGCCGTGTGTGGCTGTCCTTTTATGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA 8580
Qy 8581 GACTGTGACCTTTGACTGTGATGGAAAAATATACGGTGTCTGTAGAGATCTGCCAG 8640
Db 8581 GACCGTGACCTTTGACTGTGATGGAAAAATATACGGTGTCTGTAGAGATCTGCCAG 8640
Qy 8641 CATCATTTGCTGTGTGCAAGGTATGAGGCTTTCTCGGTGTGCGCTACACCAACGCTGA 8700
Db 8641 CATCATTTGCTGTGTGCAAGGTATGAGGCTTTCTCGGTGTGCGCTACACCAACGCTGA 8700
Qy 8701 GATCCTCAGAGTTTCCCAATCACTAACAGACATGACCATGCCCTCGAGGCTGGCG 8760
Db 8701 GATCCTCAGAGTTTCCCAATCACTAACAGACATGACCATGCCCTCGAGGCTGGCG 8760
Qy 8761 AAGAAAGCCAGGGCGGTCTCGCAGGCCCAAGAGCGGTGGCGAGCACGCAAAATT 8820
Db 8761 AAGAAAGCCAGGGCGGTCTCGCAGGCCCAAGAGCGGTGGCGAGCACGCAAAATT 8820
Qy 8821 GGCTCGCTTCTTCTGTGGCATGCTACATCTAGACCTCTACAGATTGGATAAGACGAG 8880
Db 8821 GGCTCGCTTCTTCTGTGGCATGCTACATCTAGACCTCTACAGATTGGATAAGACGAG 8880
Qy 8881 CGTGGCTCGGTACACCACTTCAATTATTGTGATGTTTACTCCCGGAGGGGGATGTGT 8940
Db 8881 CGTGGCTCGGTACACCACTTCAATTATTGTGATGTTTACTCCCGGAGGGGGATGTGT 8940
Qy 8941 TATTACACACAGAGAGATGCGAGGTTCTCTGTGAAGTATTGGCTGTCATTGTTTT 9000
Db 8941 TATTACACACAGAGAGATGCGAGGTTCTCTGTGAAGTATTGGCTGTCATTGTTTT 9000
Qy 9001 TGCCCTAGGGCTCATTTGCTGTGGATAGCCATCAGCTGAAACCCCAAAATTCAAATTA 9060
Db 9001 TGCCCTAGGGCTCATTTGCTGTGGATAGCCATCAGCTGAAACCCCAAAATTCAAATTA 9060
Qy 9061 CTACAGTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGGCGAGCGGCAACAGGGGAGACCCCGGC 9120
Db 9061 CTACAGTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGGCGAGCGGCAACAGGGGAGACCCCGGC 9120
Qy 9121 TTAACGACCCCGCGATGTAGTTTGGCGACCATGGTGATCAGAACCGTTTTCGGGTGA 9180
Db 9121 TTAACGACCCCGCGATGTAGTTTGGCGACCATGGTGATCAGAACCGTTTTCGGGTGA 9180
Qy 9181 GCCATGTGCTGAAGGGGATGACGTCCTTCTGGCTCATCCACAAAAACCGTCTCGGGTGG 9240
Db 9181 GCCATGTGCTGAAGGGGATGACGTCCTTCTGGCTCATCCACAAAAACCGTCTCGGGTGG 9240
Qy 9241 GTGAGGAGTCTGCTGTGTGGGAAGCAGTCAGTATAATTCCCGTGTGTGTGTGACGC 9300
Db 9241 GTGAGGAGTCTGCTGTGTGGGAAGCAGTCAGTATAATTCCCGTGTGTGTGTGACGC 9300
Qy 9301 CTCACGAGTATTGTCCGCTGTGCAGAGCCTAGTACCAGGGCTGCACCCCGGTTTTTG 9360
Db 9301 CTCACGAGTATTGTCCGCTGTGCAGAGCCTAGTACCAGGGCTGCACCCCGGTTTTTG 9360
Qy 9361 TTCCAAGCGGAGGCAACCCCGCTTGGAAATTAATAACT 9399
Db 9361 TTCCAAGCGGAGGCAACCCCGCTTGGAAATTAATAACT 9399

RESULT 3
ID ADJ64244
XX ADJ64244 standard; DNA; 9399 BP.
AC ADJ64244;
XX
DT 20-MAY-2004 (first entry)
XX
DE GB virus B 3' terminal polynucleotide fragment seqid 2.
XX
KW antiinflammatory; hepatotropic; virucide; GB virus B; GBV-B;
XX hepatitis C virus; HCV; 3' terminal; ds.

OS Hepatitis GB virus B.
XX US2004039187-A1.
XX
PD 26-FEB-2004.
XX
PP 03-JUL-2002; 2002US-00189359.
XX
PR 04-JUN-1999; 99US-0137665P.
XX
PR 05-JUN-2000; 2000US-00587653.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (INSP) INST PASTEUR.
XX
PI Martin A, Sangar DV, Lemon SM, Rijnbrand R;
XX WPI; 2004-203294/19.
XX
PT New GB virus B and/or hepatitis C virus (HCV) sequences, useful in
PT diagnosing and in treating HCV and in investigating the mechanisms for
PT the different biological properties of the viruses.
XX
PS Claim 10; SEQ ID NO 2; 58pp; English.
XX
CC The invention describes a new isolated polynucleotide (1) encoding a 3'
CC sequence of the GB virus B (GBV-B) genome, or which comprises a chimeric
CC GBV-B genome, where at least part, but not all of a 5' nontranslated
CC region (NTR) sequence is derived from a hepatitis C virus (HCV) 5' NTR.
CC (1) is a GB virus B and/or hepatitis C virus polynucleotide comprising a
CC fully defined of 260 or 9399 bp (SEQ ID NOS: 1 or 2). The polynucleotides
CC or chimaeras are useful diagnosing or treating hepatitis C virus (HCV)
CC and in investigating the mechanisms for the different biological
CC properties of the viruses. This sequence represents a Hepatitis GB virus
CC B (GBV-B) 3' terminal polynucleotide.
XX
SQ Sequence 9399 BP; 2124 A; 2322 C; 2432 G; 2521 T; 0 U; 0 Other;

Query Match 99.9%; Score 9386.2; DB 12; Length 9399;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 9391; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 ACCAACAACACTCCAGTTTGTACACTCCGCTAGGAATGCTCTGGAGCACCCCTCTAG 60
Db 1 ACCAACAACACTCCAGTTTGTACACTCCGCTAGGAATGCTCTGGAGCACCCCTCTAG 60
Qy 61 CAGGGCGTGGGGGATTTCCCTGCGCTGTCAGAGGGTGGAGCCAACTTAGTAT 120
Db 61 CAGGGCGTGGGGGATTTCCCTGCGCTGTCAGAGGGTGGAGCCAACTTAGTAT 120
Qy 121 GTAGGCGGCGGACTCATGACGCTCGCGTGATGACAAAGCGCCAAAGCTTGA 180
Db 121 GTAGGCGGCGGACTCATGACGCTCGCGTGATGACAAAGCGCCAAAGCTTGA 180
Qy 181 CTGATGCGGGTTTCATGGGTTTGGTGTGGGCTTTTAGGAGCCTTCCAGCCACCA 240
Db 181 CTGATGCGGGTTTCATGGGTTTGGTGTGGGCTTTTAGGAGCCTTCCAGCCACCA 240
Qy 241 CCTCCAGATAGAGCGCGGCTGTAGGGAAGACCGGGACCGTCACTACCAAGGACG 300
Db 241 CCTCCAGATAGAGCGCGGCTGTAGGGAAGACCGGGACCGTCACTACCAAGGACG 300
Qy 301 CAGACCTCTTTTGTAGTATCACGCTTCCGGAAGTAGTTGGGCAAGCCACCTATATGT 360
Db 301 CAGACCTCTTTTGTAGTATCACGCTTCCGGAAGTAGTTGGGCAAGCCACCTATATGT 360
Qy 361 TGGGATGTTGGGTTAGCCATCCATACCTGCTGTAGGGTCTTCCGAGGGGAT 420
Db 361 TGGGATGTTGGGTTAGCCATCCATACCTGCTGTAGGGTCTTCCGAGGGGAT 420
Qy 421 CTGGGAGTCTCGTAGACCGTAGCACATGCTGTTATTTCTACTCAAAACAGTCTGTACC 480
Db 421 CTGGGAGTCTCGTAGACCGTAGCACATGCTGTTATTTCTACTCAAAACAGTCTGTACC 480

QY 481 TCGGCCAGAACCGCCAAAGAAACAAGCAGACGACGAGCTTCATATCTCTGTCTCATTTAAAC 540
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QY 541 ATCTGTTGAAGGGGACAAACGAGCAAGGGCAAGTCCAGCGCGATGCTCGGCCCTCGTAA 600
DB 541 ATCTGTTGAAGGGGACAAACGAGCAAGGGCAAGTCCAGCGCGATGCTCGGCCCTCGTAA 600
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DB 601 TTACAAAAATTGCTGTATCTCATGTATGGCTTGAGACATTTGGCTCAGGCTGCTTTGCCAGC 660
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QY 721 TTACCCCTTTGGGGTGGATTTGGTATGTTTACAACCTCACACACCTCTAGTAGGCCCGCTGGT 780
DB 721 TTACCCCTTTGGGGTGGATTTGGTATGTTTACAACCTCACACACCTCTAGTAGGCCCGCTGGT 780
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DB 781 GGCAGGAGCGGTCTGCAACAGTCTGCCAGATAGTACGCTTGCTGGAGGATGGAAGTCAA 840
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DB 841 CTGGGCTACTGGTGGTTCGGTCTCCACTTTTGTGGTATGCTGCTATCTTTGGCCCTG 900
QY 901 TCCCTGTAGTGGGGCGCGGTCACCTGACCCAGACACAAATACCAATCCTGACCAATTG 960
DB 901 TCCCTGTAGTGGGGCGCGGTCACCTGACCCAGACACAAATACCAATCCTGACCAATTG 960
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DB 1021 TGTGATCTGTGGGACGAGTGTGGTTCGCTTCCACTGCTACAGTCACTCACACCTTCCAA 1080
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QY 1141 GACCTGTACGCGCTTGACATTTGGTGTGGTGTGATTTAGTCCGTGACTG 1200
DB 1141 GACCTGTACGCGCTTGACATTTGGTGTGGTGTGATTTAGTCCGTGACTG 1200
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DB 1201 GCTTGTACGGCACTGGCTTTATCAATAGACCTCAATGAATCTGTTACTTGTACTCTGGA 1260
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DB 1321 CGAGGCTGTACTTCTTGAACCAACTGGCTTCAAGTACCATACGCTATTGCGACTAT 1380
QY 1381 GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCTCTCGGGGCA 1440
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DB 1501 CAGGTTGCCACTGGATGCTCAATAGCTGAGTTTTCGCTCGCCTTTGATGATACCATGTC 1560
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DB 1561 TTGCCACTCTTATTTAGTGAGAAATGTGTCAAGTCAATTTGTTACAGTCCAAAGTGGAC 1620
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DB 1621 CAGGCTATCACTCTAGAGTATAACACTCCATCTTTGGTACCCCTATACAAATCCCTGG 1680
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QY 1921 AGGCCATTTGTATTTTGAAGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAA 1980
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DB 2041 TGGTTCCTTGGTTACAGGTTCCGCAAGGTTTTTACAGTGATGTGAAAGACTTAGCCACAGG 2100
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DB 2101 ATTGATCAACAAAGCAAGCCTGGAAAAATTTATCAGGCTTTATTTCCGCCACGGGTGC 2160
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DB 2401 CTGAGGCTAGCTTATGTCGCCCTTTTAGGGTTTGTGCCATGGCTGGCGGCTTCCCTC 2460
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DB 2521 AGTGGCAGGGTTAGTTTGTGGCGCGGCTAAACCGTGGTCAACGCTCTCTCTTGT 2580
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Qy 9121 TTAAGGACCCCGC 9133
Db 9121 TTAAGGACCCCGC 9133
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RESULT 6
AAT00130
ID AAT00130 standard; DNA; 9143 BP.

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XX AAT00130;  
XX AC  
XX 27-AUG-2003 (revised)  
DT 02-JUL-1996 (first entry)  
XX  
XX Hepatitis GB virus (HGBV) clone GB contig B.  
DE  
XX Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine; reagents; non-A;  
KW non-B; non-C; non-D; non-E; clone; GB contig B; tamarin; infected plasma;  
KW lambda phage; cDNA library; ss.  
XX  
OS Hepatitis G virus.  
XX  
XX Key Location/Qualifiers  
FH 446..9040  
FT /*tag= a  
FT  
XX  
XX W09521922-A2.  
XX  
XX 17-AUG-1995.  
XX  
XX 14-FEB-1995; 95WO-US002118.  
XX  
XX 14-FEB-1994; 94US-00196030.  
PR 13-MAY-1994; 94US-00242654.  
PR 29-JUL-1994; 94US-00283314.  
PR 23-NOV-1994; 94US-00344185.  
PR 23-NOV-1994; 94US-00344190.  
PR 27-JAN-1995; 95US-00344557.  
XX  
XX (ABBO ) ABBOTT LAB.  
XX  
XX Simons JN, Pilot-Matias TJ, Dawson GJ, Schlauder GG, Desai SM;  
PI Leary TP, Muerhoff AS, Erker JC, Buljk SL, Mushahwar IK;  
XX  
XX WPI; 1995-293123/38.  
DR P-PSDB; AAR82072.  
XX  
XX Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful for  
diagnosis and therapy of hepatitis GB virus.  
XX  
XX Example 9; Page 434-447; 661pp; English.  
XX  
XX Double stranded hepatitis GB virus (HGBV) DNA obt'd. from HGBV infected  
CC tamarin plasma, using standard procedures, was used to prepare a lambda  
CC phage HGBV cDNA library. Clones were rescued from the lambda phage,  
CC searched against a sequence database and found to be unique HGBV  
CC sequences. The clones were then used to assemble the sequences  
CC AAT00129/30 (GB contig A and B) which encode the proteins AAR94345-47  
CC (the 3 possible coding strand reading frames) and AAR82072, respectively.  
CC Reagents which comprise the HGBV DNA, or its protein prods. can be used  
CC for the diagnosis, therapy or in a vaccine to prevent HGBV infection.  
CC (Updated on 27-AUG-2003 to correct OS field.)  
XX  
XX Sequence 9143 BP; 2071 A; 2266 C; 2349 G; 2457 T; 0 U; 0 Other;
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Query Match 96.4%; Score 9059.8; DB 2; Length 9143;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 9096; Conservative 0; Mismatches 37; Indels 4; Gaps 1;

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Db 1 ACCACAACAACTCCAGTTTGTACATCCGCTAGGAATGCTCTGGAGCACCCCCCTAG 60  
Qy 61 CAGGCGTGGGGATTTCCCTGCCCTCTGCAGAGGGTGGAGCCACCACTTAGTAT 120  
Db 61 CAGGCGTGGGGATTTCCCTGCCCTCTGCAGAGGGTGGAGCCACCACTTAGTAT 120  
Qy 121 GTAGCGCGGGACTCATGACGCTCGCTGATGACAGCGCAAGCTTGACTTGGATGGC 180  
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DB 421 CTGGAGTCTCTGATAGCCGTAGCA CATGCTGTTTATTTCTACTCAAAACAAGTCCTGTACC 480
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DB 481 TSCGCCAGAACGCCCAAGAACAGCAGACGAGGCTTCATATCCTGTGTCCATTTAAAC 540
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DB 541 ATCTGTTGAAAGGGGACAAACGAGCAAGCGCAAGTCCAGCGCGATGCTCGGCCCTCGTAA 600
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DB 661 TCATGTTGGGACGCCAAGACCTCGCCATAAGTCTCGCAATCTTGGAACTCTTCTCGA 720
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DB 1321 CGAGGCTGTCACTCTTTGACCAAACTGGCTTCAAACTGATACGATACGATATTCGACTAT 1380
QY 1381 GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCTCTCGGGGCAA 1440
DB 1381 GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCTCTCGGGGCAA 1440
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DB 1441 GTGGTATCAGTGTCTCTAGCGCTTATGCTTTTACATAGAAGCGACCTCTGGAACCCCAT 1500
QY 1501 CAGGGTGCCCACTGGATGCTCAATAGCTGAGTGTTCGCGCTTTGATGATACCAATGTCC 1560
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DB 1621 CAGGCTATCACTCTAGAGTATAA CAATCCATATCTTTGGTACCCCTATA CAATCCCTGG 1680
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DB 1741 TGTGCATCTGCTACTGCACTATGGGCACCTGATGCGAGTGGGAACGACACTCGCAACACTTA 1800
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QY 1921 AGGCCATTTGATTTTGTAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAA 1980
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Db 8401 CTACTTTTCAAGAGATCCTCGTATCCCTTTGGCAGGTGCTCTGCGAGGGTCTGG 8460
Qy 8461 ATACAAACCCAGTCTCGGTGGATGGGTATCTAATACATCACTACCCATGTTGTGGGT 8520
Db 8461 ATACAAACCCAGTCTCGGTGGATGGGTATCTAATACATCACTACCCATGTTGTGGGT 8520
Qy 8521 TAGCCGTGTGTTGGCTGCTCAATTCATGAGCAGATGCTCTTTCAGAGCAAACTTCCCGA 8580
Db 8521 TAGCCGTGTGTTGGCTGCTCAATTCATGAGCAGATGCTCTTTCAGAGCAAACTTCCCGA 8580
Qy 8581 GACTGTGACCTTTGACTGGTATGGGAAAAATTAACGGTGCCTGTAGAAGATCTGCCAG 8640
Db 8581 GACTGTGACCTTTGACTGGTATGGGAAAAATTAACGGTGCCTGTAGAAGATCTGCCAG 8640
Qy 8641 CATCATTTGCTGGTGTGACCGTATTAGGCTTTCTCGGTGGTGGCTACACCAAGCTGTA 8700
Db 8641 CATCATTTGCTGGTGTGACCGTATTAGGCTTTCTCGGTGGTGGCTACACCAAGCTGTA 8700
Qy 8701 GATCCTCAGAGTTTCCCAATCACATCAACAGATGATGATGCGGCTGGCGCTGGCG 8760
Db 8701 GATCCTCAGAGTTTCCCAATCACATCAACAGATGATGATGCGGCTGGCGCTGGCG 8760
Qy 8761 AAAGAAAGCCAGGCGGTCTCGCCAGCGGCGGCGGCGGCGGAGCACAACGAAAT 8820
Db 8761 AAAGAAAGCCAGGCGGTCTCGCCAGCGGCGGCGGCGGCGGAGCACAACGAAAT 8820
Qy 8821 GGCTGCTTCTGCTGGCATGCTACATAGACCTCTACAGATTTGGATAGACGAG 8880
Db 8821 GGCTGCTTCTGCTGGCATGCTACATAGACCTCTACAGATTTGGATAGACGAG 8880
Qy 8881 CGTGGCTCGGTACACACTTTCAATTTATGTTTACTTCCCGGAGGGGATGTTGT 8940
Db 8881 CGTGGCTCGGTACACACTTTCAATTTATGTTTACTTCCCGGAGGGGATGTTGT 8940

Sequence	9143 BP; 2071 A; 2266 C; 2349 G; 2457 T; 0 U; 0 Other;
Query Match	96.4%; Score 9059.8; DB 3; Length 9143;
Best Local Similarity	99.6%; Pred. No. 0;
Matches 9096; Conservative	0; Mismatches 37; Indels 4; Gaps 1;
Qy	1 ACCACAAACACTCCAGTTTGTTCACCTCCGCTAGGAATGCTCTCGAGCACCCCCCTAG 60
Db	
Qy	1 ACCACAACACTCCAGTTTGTTCACCTCCGCTAGGAATGCTCTCGAGCACCCCCCTAG 60
Db	
Qy	61 CAGGGCTGGGGGATTTCCCTCCGCTGCGAAGGGTGGAGCCAAACACCTTAGTAT 120
Db	
Qy	61 CAGGGCTGGGGGATTTCCCTCCGCTGCGAAGGGTGGAGCCAAACACCTTAGTAT 120
Db	
Qy	121 GTAGGCGCGGGACTCATGACGCTCGCGTGATGACAAAGCCCAAGCTTGACTTGGATGGC 180
Db	
Qy	121 GTAGGCGCGGGACTCATGACGCTCGCGTGATGACAAAGCCCAAGCTTGACTTGGATGGC 180
Db	
Qy	181 CTGTATGGGCGTTTATGGGTTTCGGTGGTGGTGGCTTTTAGGAGAGCTCTCACGCCCAACCA 240
Db	
Qy	181 CCTGATGGGCGTTTCATGGGTTTCGGTGGTGGTGGCTTTAGGAGAGCTCTCACGCCCAACCA 240
Db	
Qy	241 CCTCCCAGATAGAGCGCGGCACTGTAGGAAGACCGGGACCGGTCTACTTACCAAGGACG 300
Db	
Qy	241 CCTCCCAGATAGAGCGCGGCACTGTAGGAAGACCGGGACCGGTCTACTTACCAAGGACG 300
Db	
Qy	301 CAGACCTCTTTTGGAGTATCACGCCCTCCGGAAGTAGTTGGGCAAGCCACTATATGTGT 360
Db	
Qy	301 CAGACCTCTTTTGGAGTATCACGCCCTCCGGAAGTAGTTGGGCAAGCCACTATATGTGT 360
Db	
Qy	361 TGGGATGGTTGGGGTTAGCCATCATACCGTACTGCTGTATAGGGTCTTTCGAGGGGAT 420
Db	
Qy	361 TGGGATGGTTGGGGTTAGCCATCATACCGTACTGCTGTATAGGGTCTTTCGAGGGGAT 420
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Qy	421 CTGGGAGTCTCTGTAGACCGTAGCACATGCTCTGTATTTCTACTTCAACAAGTCTGTACC 480
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Qy	421 CTGGGAGTCTCTGTAGACCGTAGCACATGCTCTGTATTTCTACTTCAACAAGTCTGTACC 480
Db	
Qy	481 TGGCCCCAGAAACGCGCAAGAAACAGCAGACGCGAGGCTTCATATCTGTGTCTAAATAAC 540
Db	
Qy	481 TGGCCCCAGAAACGCGCAAGAAACAGCAGACGCGAGGCTTCATATCTGTGTCTAAATAAC 540
Db	
Qy	541 ATCTGTTGAAGGGGACAACGAGCAAGCCAAAGTCCAGCGCGATGCTCGGCTCTGTAA 600
Db	
Qy	541 ATCTGTTGAAGGGGACAACGAGCAAGCCAAAGTCCAGCGCGATGCTCGGCTCTGTAA 600
Db	
Qy	601 TTACAAAAATTCGTGGTATCCATGATGCTTTCGAGACATTTGGCTCAGGCTGCTTTCGACG 660
Db	
Qy	601 TTACAAAAATTCGTGGTATCCATGATGCTTTCGAGACATTTGGCTCAGGCTGCTTTCGACG 660
Db	
Qy	661 TCATGGTTGGGGACGCCAAGACCTCGCCATAAGTCTCGCAATCTTGGAAATCTCTTGGGA 720
Db	
Qy	661 TCATGGTTGGGGACGCCAAGACCTCGCCATAAGTCTCGCAATCTTGGAAATCTCTTGGGA 720
Db	
Qy	721 TTACCCCTTTGGGGTGGATTTGGTATTTACAACCTCACACACCTCTAGTAGGCGCGCTGGT 780
Db	
Qy	721 TTACCCCTTTGGGGTGGATTTGGTATTTACAACCTCACACACCTCTAGTAGGCGCGCTGGT 780
Db	
Qy	781 GGCAAGAGCGGTCGTTTCGACACGCTGTCGACAGATAGTACGCTTGCCTGAGGATGGAGTCAA 840
Db	
Qy	781 GGCAAGAGCGGTCGTTTCGACACGCTGTCGACAGATAGTACGCTTGCCTGAGGATGGAGTCAA 840
Db	
Qy	841 CTGGGCTACTGGTTGGTTTCGGTCCACCTTTTGTGGTATGTCGCTATCTTTGGGCTG 900
Db	
Qy	841 CTGGGCTACTGGTTGGTTTCGGTCCACCTTTTGTGGTATGTCGCTATCTTTGGGCTG 900
Db	
Qy	901 TCCCTGTAGTGGGGCGCGGTCAGTCAACCCAGACACAAATACCACAAATCTCGACCAATTG 960
Db	
Qy	901 TCCCTGTAGTGGGGCGCGGTCAGTCAACCCAGACACAAATACCACAAATCTCGACCAATTG 960
Db	
Qy	961 CTGCCAGCGTAATCAGGTTATCTATTGTTCTCTTCCACTTGGCTTACAGAGCCTGGTTG 1020
Db	
Qy	961 CTGCCAGCGTAATCAGGTTATCTATTGTTCTCTTCCACTTGGCTTACAGAGCCTGGTTG 1020
Db	

Qy	1021	TGTGATCTGTCCGACGAGTCTCGGTTCCGCAATCCGPA	1080
Db	1021	TGTGATCTGTCCGACGAGTCTCGGTTCCGCAATCCGPA	1080
Qy	1081	TTGGACTGGCAGCAGTCTCTTGGCTGACCAATTTGTT	1140
Db	1081	TTGGACTGGCAGCAGTCTCTTGGCTGACCAATTTGTT	1140
Qy	1141	GACCTGTGACCCCTTGA	1200
Db	1141	GACCTGTGACCCCTTGA	1200
Qy	1201	GCTTGTGAGGCACTGGCTTATTCATAGACCTCAATGA	1260
Db	1201	GCTTGTGAGGCACTGGCTTATTCATAGACCTCAATGA	1260
Qy	1261	AGTGCCCACTGGAATAGATCTGGGTTCCAGGCTTAT	1320
Db	1261	AGTGCCCACTGGAATAGATCTGGGTTCCAGGCTTAT	1320
Qy	1321	CGAGGCTGTCTATCTTTGACCAAACTGGCTTCA	1380
Db	1321	CGAGGCTGTCTATCTTTGACCAAACTGGCTTCA	1380
Qy	1381	GTTTGTAGCACTGACCTA	1440
Db	1381	GTTTGTAGCACTGACCTA	1440
Qy	1441	GTTGATACAGTGTCTCTAGGCTTATGCTTTATAG	1500
Db	1441	GTTGATACAGTGTCTCTAGGCTTATGCTTTATAG	1500
Qy	1501	CAGGCTGCCACTGGATGCTCAATAGCTAGTGTGCT	1560
Db	1501	CAGGCTGCCACTGGATGCTCAATAGCTAGTGTGCT	1560
Qy	1561	TTGCCACTCTTATTTGAGTGAAGTGTGAGAACTAT	1620
Db	1561	TTGCCACTCTTATTTGAGTGAAGTGTGAGAACTAT	1620
Qy	1621	CAGGCTTCACTCTAGAGTATACACTCAATCTAT	1680
Db	1621	CAGGCTTCACTCTAGAGTATACACTCAATCTAT	1680
Qy	1681	TGCAGGGGATGATGTTAAATCAAAATAACATG	1740
Db	1681	TGCAGGGGATGATGTTAAATCAAAATAACATG	1740
Qy	1741	TGTGCCATCTGCTGCACTATGGGCACTGATGCA	1800
Db	1741	TGTGCCATCTGCTGCACTATGGGCACTGATGCA	1800
Qy	1801	CGAAGCATGCGGTGTAACACCATGGCTTAAC	1860
Db	1801	CGAAGCATGCGGTGTAACACCATGGCTTAAC	1860
Qy	1861	ATTGGCTATATTAATAACCTGGCTTAAAGAAAT	1920
Db	1861	ATTGGCTATATTAATAACCTGGCTTAAAGAAAT	1920
Qy	1921	AGGCCATTTGATTTGAGGATCAGATACCCCTAT	1980
Db	1921	AGGCCATTTGATTTGAGGATCAGATACCCCTAT	1980
Qy	1981	TTCCACTCTCCTACACCGGAGGTGGCTAGGT	2040
Db	1981	TTCCACTCTCCTACACCGGAGGTGGCTAGGT	2040
Qy	2041	TGGTTCTTGGTTACAGGTTCCGCAAGGTTTTT	2100
Db	2041	TGGTTCTTGGTTACAGGTTCCGCAAGGTTTTT	2100

Qy	2101	ATTGATCACAAGACAAAGCCTGGAAAAATATCAG	2160
Db	2101	ATTGATCACAAGACAAAGCCTGGAAAAATATCAG	2160
Qy	2161	TTTGTCTCTTACGGAGTTACCAAGGCGTGTCTA	2220
Db	2161	TTTGTCTCTTACGGAGTTACCAAGGCGTGTCTA	2220
Qy	2221	CAGCAAGTATCTTATTTTACGCTACCTCTGT	2280
Db	2221	CAGCAAGTATCTTATTTTACGCTACCTCTGT	2280
Qy	2281	TGTTTACCTTTTGGTCTCTGCTCCCATCCAGT	2340
Db	2281	TGTTTACCTTTTGGTCTCTGCTCCCATCCAGT	2340
Qy	2341	TTTGTCTTAAAGCTCAAGTAGCTCTCTTTTGT	2400
Db	2341	TTTGTCTTAAAGCTCAAGTAGCTCTCTTTTGT	2400
Qy	2401	CTGCAGGCTACGTTATGCTGCCCTTTT	2460
Db	2401	CTGCAGGCTACGTTATGCTGCCCTTTT	2460
Qy	2461	AACCTTCTTTTGTGACAGCTGCTGCCCAAC	2520
Db	2461	AACCTTCTTTTGTGACAGCTGCTGCCCAAC	2520
Qy	2521	AGTGAGGCTTGTGTTTGTGGCGGCTTGTG	2580
Db	2521	AGTGAGGCTTGTGTTTGTGGCGGCTTGTG	2580
Qy	2581	AGTCTTGTGCTCTGCTAGCGCTTTTAA	2640
Db	2581	AGTCTTGTGCTCTGCTAGCGCTTTTAA	2640
Qy	2641	TTTTGTATACCGAGATAATGAGAGGCTG	2700
Db	2641	TTTTGTATACCGAGATAATGAGAGGCTG	2700
Qy	2701	GTCTCGTTTGTGGCTTCTTGTCTACCTG	2760
Db	2701	GTCTCGTTTGTGGCTTCTTGTCTACCTG	2760
Qy	2761	TTGGCAACGTTGGGAGAAATTTGGAACG	2820
Db	2761	TTGGCAACGTTGGGAGAAATTTGGAACG	2820
Qy	2821	TGTGCTGGTTTGTTCCTGGCTGCGCAT	2880
Db	2821	TGTGCTGGTTTGTTCCTGGCTGCGCAT	2880
Qy	2881	CGTAGCTCTTCTATGTTTAAACATCCAG	2940
Db	2881	CGTAGCTCTTCTATGTTTAAACATCCAG	2940
Qy	2941	TAGGGCCATAGAAATGTTGGTGGCTCT	3000
Db	2941	TAGGGCCATAGAAATGTTGGTGGCTCT	3000
Qy	3001	TCTTAAAGTCTTCTCTTGTAGTGTGTT	3060
Db	3001	TCTTAAAGTCTTCTCTTGTAGTGTGTT	3060
Qy	3061	TGTTGATGCTTGGCTTAAATGATTTTGC	3120
Db	3061	TGTTGATGCTTGGCTTAAATGATTTTGC	3120
Qy	3121	TTTTTGAAGGCAAGGAGGCTTATAGAA	3180
Db	3121	TTTTTGAAGGCAAGGAGGCTTATAGAA	3180
Qy	3181	GTTTGTGTTTGGCTTGTGTTGGCGCT	3240
Db	3181	GTTTGTGTTTGGCTTGTGTTGGCGCT	3240

Db 3181 GGTGATGGTTGCGGTTGTCGCGTCTGGGACCTTGTGTTTCGCGAGGTTAGCTAT 3240
QY 3241 GCCGCAGATGGGTGGGCCATTACCGCACTTTTACGCTGCGAGTGTCTCTCTGAACGTGG 3300
Db 3241 GCCGCAGATGGGTGGGCCATTACCGCACTTTTACGCTGCGAGTGTCTCTCTGAACGTGG 3300
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Db 3301 CACGCTGTACGGATGGCAGTGGTCACTGACTGGTATAGACCCCGGAACTTGGACTGGAAAC 3360
QY 3361 TATCTTTCAGATPAGGATCTCTGGCCCACTAGCTPACATGGGATTTGTTTGTGCAACGCTGT 3420
Db 3361 TATCTTTCAGATPAGGATCTCTGGCCCACTAGCTPACATGGGATTTGTTTGTGCAACGCTGT 3420
QY 3421 GTATCTGCTACCAATGCGCAGCAAGGGGGCGCGGTTGGCTCATCCACAGGCTCTATACA 3480
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Db 3601 ATTGGTTGAGTCAACAAATCCGATGACCCCTTATTTGGTGTGTGCGGGGCCCTTCCCAT 3660
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QY 3721 GATGTTTCAACCGCTGTAGAAATTTCTGGCGGTTTCACTGAGTCAAGTATAGGGTTAGGCCGTT 3780
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QY 3781 GGTGTGCTGTGATACCATCCCGAGTACACAGCACATGCGCACTCTTGATACAAAACCTAC 3840
Db 3781 GGTGTGCTGTGATACCATCCCGAGTACACAGCACATGCGCACTCTTGATACAAAACCTAC 3840
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QY 4021 CTATTTTAAATGCAATGTACCAACAGGGGCTTCACTAGTACAGCACATATGGCAT 4080
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QY 4081 GTACCTGACCGGAGCATGTTCCCGAACTATGATGAATCAATTTGTGACGAATGCCATGTC 4140
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QY 4141 TACCGATGCAACCGGTTGGGCAATTTGGAAGGCTCTTAACCGAAGCTCCATCCAAAA 4200
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QY 4201 TGTTAGGCTAGTGGTCTTTGCCACCGCTACCCCTGGAGTAATCCCTTACACCATGTC 4260
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QY 4261 CAACATAACTGAGATTCAATTAACCGATGAAGGCACTATCCCTTTTCATGGAATAAAGAT 4320

Db 4261 CAACATAACTGAGATTCAATTAACCGATGAAGGCACTATCCCTTTTCATGGAATAAAGAT 4320
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Db 4501 TACAGGGTACACTGTGACTTTTGATTCGCTGTATGACTGACGCTCATGTGTAAGAGGCAC 4560
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Db 4561 ATGCCATGTTGACCTTGAACCTTACTTTTCAACATGGGTGTTCTGTGTGCGGGGTTTCAGC 4620
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Db 4621 AATAGTTAAAGGCCACGCTAGGGGCGGCAAGGGCGGTGGAGAGCTGGCATATACTACTA 4680
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Db 4681 TGTAGACGGGAGTTGTACCCCTTCCGGGTATGTTTCTGAAATGCAACATTTGTTGAAGCCTT 4740
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Qy 6901 AGGAGTGTCTGCTGCAAGCGCTGCAACGAAGTGACCGTTAGAAGCTCTTCAAACT 6960
Db 6901 AGGAGTGTCTGCTGCAAGCGCTGCAACGAAGTGACCGTTAGAAGCTCTTCAAACT 6960
Qy 6961 CCCTCTTCCACCACTGTTCTACAGTTGGCCATGCGATGCCCCCTGTTGGAGCGGTTGA 7020
Db 6961 CCCTCTTCCACCACTGTTCTACAGTTGGCCATGCGATGCCCCCTGTTGGAGCGGTTGA 7020
Qy 7021 GTGTAAACCTTTTCACTGCAATTTGGATGTGCAATGACCGGAGGAGTGGTCAAC 7080
Db 7021 GTGTAAACCTTTTCACTGCAATTTGGATGTGCAATGACCGGAGGAGTGGTCAAC 7080
Qy 7081 TTTTACCAGTTTACCCTCCCAAAAGGAGTCTCTGNAATGGTCAGACGAAAGTTGTCGAC 7140
Db 7081 TTTTACCAGTTTACCCTCCCAAAAGGAGTCTCTGNAATGGTCAGACGAAAGTTGTCGAC 7140
Qy 7141 GGCTACAAACCGCTTCCAGCTACGTTACTGGCCCCCTGACCTTAAGATACGCGGAAAGGA 7200
Db 7141 GACTACAAACCGCTTCCAGCTACGTTACTGGCCCCCTGACCTTAAGATACGCGGAAAGGA 7200
Qy 7201 TTCCACTCAGTCAAGCCCCCGCAAAACGGCCCTACAAAAGAAAGTTGGGAAAGAGTGA 7260
Db 7201 TTCCACTCAGTCAAGCCCCCGCAAAACGGCCCTACAAAAGAAAGTTGGGAAAGAGTGA 7260
Qy 7261 TTCCGTGAGCATGAGCTACACCTGGACCGGCTGATTTAGCTTCAAACTGCTTCTAAAGT 7320
Db 7261 TTCCGTGAGCATGAGCTACACCTGGACCGGCTGATTTAGCTTCAAACTGCTTCTAAAGT 7320
Qy 7321 TCTGCTGCAACTCGGGCCATCACTAGTGGTTTCTCCTCAAAAGAAAGTCAATTTGGTGTATGT 7380
Db 7321 TCTGCTGCAACTCGGGCCATCACTAGTGGTTTCTCCTCAAAAGAAAGTCAATTTGGTGTATGT 7380
Qy 7381 GACTGAGCGCGGATCGGAGCTTAGAAAACAAAAGTCACTATTAATAGACAACTCT 7440
Db 7381 GACTGAGCGCGGATCGGAGCTTAGAAAACAAAAGTCACTATTAATAGACAACTCT 7440
Qy 7441 GTTCCCGCCCATCAACACAGCAAGTGAATGGCTTAAAGAAAAGTCTCAAAAGTTGT 7500
Db 7441 GTTCCCGCCCATCAACACAGCAAGTGAATGGCTTAAAGAAAAGTCTCAAAAGTTGT 7500
Qy 7501 CCGTGTCTATGTGGGACTATGATGAAGTAGCAGCTCACACGCTCTCTAAGTCTGCTAAGTC 7560
Db 7501 CCGTGTCTATGTGGGACTATGATGAAGTAGCAGCTCACACGCTCTCTAAGTCTGCTAAGTC 7560
Qy 7561 CCACATCACTGGGCTTCCGGGCACTGATGTTCTGGAGCAGCCCGCGGCTGTTCT 7620

Db 7561 CCACATCACTGGCCCTTCGGGGCACTGATGTTCTGAGCAGCCGCAAGGCTGTTCT 7620
 QY 7621 GGACTTGACAGAGTGTGTCGAGGAGGTGAGATACCGAGTCAATTCGGCAACTGCTGAT 7680
 Db 7621 GGACTTGACAGAGTGTGTCGAGGAGGTGAGATACCGAGTCAATTCGGCAACTGCTGAT 7680
 QY 7681 AGTTCCAAAGGAGGAGGTCTTCGTGAAGACCCCGAGAAACCAACAAAGAAACCCCAAG 7740
 Db 7681 AGTTCCAAAGGAGGAGGTCTTCGTGAAGACCCCGAGAAACCAACAAAGAAACCCCAAG 7740
 QY 7741 GCTTATCTCGTACCCCACTTGAATGAGATGTGTGAGAAAGATGTACTACGGTCAGGT 7800
 Db 7741 GCTTATCTCGTACCCCACTTGAATGAGATGTGTGAGAAAGATGTACTACGGTCAGGT 7800
 QY 7801 TGCTCTCAGCTAGTAAAGCTGTATGGGAGATCGGTACGGGTTTGTAGATCCAGCTAC 7860
 Db 7801 TGCTCTCAGCTAGTAAAGCTGTATGGGAGATCGGTACGGGTTTGTAGATCCAGCTAC 7860
 QY 7861 CCGTGTCAAGGCTCTGTTGTCCATGTGTGTCACCCGATGCGAGTCGAGCCACATGCGATAC 7920
 Db 7861 CCGTGTCAAGGCTCTGTTGTCCATGTGTGTCACCCGATGCGAGTCGAGCCACATGCGATAC 7920
 QY 7921 AGTGTGTTTGACAGTACCATCACACCCGAGGATATCATGTGAGAGACAGATCTACTC 7980
 Db 7921 AGTGTGTTTGACAGTACCATCACACCCGAGGATATCATGTGAGAGACAGATCTACTC 7980
 QY 7981 AGCAGCTAACTCAGTACCAACACCGAGCTGGCATTCACACCATTCGAGGAGCACTTATA 8040
 Db 7981 AGCAGCTAACTCAGTACCAACACCGAGCTGGCATTCACACCATTCGAGGAGCACTTATA 8040
 QY 8041 CGCTGGAGACCGATGATCGCTTATGATGGCCGAGAGATCGGATATCGTAGGTGATGTC 8100
 Db 8041 CGCTGGAGACCGATGATCGCTTATGATGGCCGAGAGATCGGATATCGTAGGTGATGTC 8100
 QY 8101 TTCGGCGCTATATCACTCAAGTTCACCAAGTTCACCAAGTTCGACCTGCTGCTGAAGGTAAATGC 8160
 Db 8101 TTCGGCGCTATATCACTCAAGTTCACCAAGTTCGACCTGCTGCTGAAGGTAAATGC 8160
 QY 8161 TGCAGCCGACAGGCTGGCATGAAGACCCCTGCTTCTTATTTGGGGCGATGATGCAC 8220
 Db 8161 TGCAGCCGACAGGCTGGCATGAAGACCCCTGCTTCTTATTTGGGGCGATGATGCAC 8220
 QY 8221 CGTAATTTTGGAGAGCGCGGAGCAGATGCAGACAAACAAAGCAATGCGTGTCTTTGCTAG 8280
 Db 8221 CGTAATTTTGGAGAGCGCGGAGCAGATGCAGACAAACAAAGCAATGCGTGTCTTTGCTAG 8280
 QY 8281 CTGGATGAAGGTGATGGGTGCAACCAAGATGTGTGCTCAACCCAAATACAGTTTGA 8340
 Db 8281 CTGGATGAAGGTGATGGGTGCAACCAAGATGTGTGCTCAACCCAAATACAGTTTGA 8340
 QY 8341 AGAATTAACATCATCTCATCAAAATGTTACCTCTGGAATTTACCAAAAGTGGCAAGCCTTA 8400
 Db 8341 AGAATTAACATCATCTCATCAAAATGTTACCTCTGGAATTTACCAAAAGTGGCAAGCCTTA 8400
 QY 8401 CTACTTTCTTACAGAGATCTCTGATCCCTTGGCAGGTGCTCTGCGAGGGTCTGGG 8460
 Db 8401 CTACTTTCTTACAGAGATCTCTGATCCCTTGGCAGGTGCTCTGCGAGGGTCTGGG 8460
 QY 8461 ATACAAACCCAGTGTGGGTGATGGGTATCTAATATACATCACTACCCATGTTTGGGT 8520
 Db 8461 ATACAAACCCAGTGTGGGTGATGGGTATCTAATATACATCACTACCCATGTTTGGGT 8520
 QY 8521 TAGCCGTGTGTGGGTGATGGGTATCTAATATACAGAGATGCTCTTTGAGGACAACTTCCGA 8580
 Db 8521 TAGCCGTGTGTGGGTGATGGGTATCTAATATACAGAGATGCTCTTTGAGGACAACTTCCGA 8580
 QY 8581 GACTGTGACTTTGATGTGATGGGAAATATACGGTGCCTGTAGAGATCTGCCAG 8640
 Db 8581 GACTGTGACTTTGATGTGATGGGAAATATACGGTGCCTGTAGAGATCTGCCAG 8640
 QY 8641 CATCATGCTGTGTGACAGTATTTGAGGCTTCTCGGTGTCGCTACCAACGCTGA 8700

Db 8641 CATCATGCTGTGTGACAGGTATTGAGGCTTTCTCGGTGTCGCTACACCAACGCTGA 8700
 QY 8701 GATCTCAGAGTTCCTCAATCACTAAACAGACATGACCATGCCCTGCGAGCTGCGG 8760
 Db 8701 GATCTCAGAGTTCCTCAATCACTAAACAGACATGACCATGCCCTGCGAGCTGCGG 8760
 QY 8761 AAAGAAAGCCAGGCGGTCTTCGCGAGCGCCAGAGGCGTGGCGAGCACACGCAAAAT 8820
 Db 8761 AAAGAAAGCCAGGCGGTCTTCGCGAGCGCCAGAGGCGTGGCGAGCACACGCAAAAT 8820
 QY 8821 GGCTCGCTTCTCTCTGGCATGCTACATCTAGACCTCTACAGATTTGGATAGACGAG 8880
 Db 8821 GGCTCGCTTCTCTCTGGCATGCTACATCTAGACCTCTACAGATTTGGATAGACGAG 8880
 QY 8881 CGTGGCTCGGTACACCACTTTCAATTTATGATGTTTACTCCCGAGGGGATGTGT 8940
 Db 8881 CGTGGCTCGGTACACCACTTTCAATTTATGATGTTTACTCCCGAGGGGATGTGT 8940
 QY 8941 TATTACACACAGAGAGATTGCAAGTTCCTTTGTGAAGTATTGCTGTCTCATTTGTTT 9000
 Db 8941 TATTACACACAGAGAGATTGCAAGTTCCTTTGTGAAGTATTGCTGTCTCATTTGTTT 9000
 QY 9001 TGCCCTAGGGCTCATTTGCTGTGGATTTAGCATCAGCTGAACCCCAATTCAAAATTA 9060
 Db 9001 TGCCCTAGGGCTCATTTGCTGTGGATTTAGCATCAGCTGAACCCCAATTCAAAATTA 9060
 QY 9061 CTAAACAG---TTTTTTTTTTTTTTTTTTTTTTTATGAGGCGGCAACAGGGGACACCC 9116
 Db 9061 CTAAACAGTTT-----TTTTTTTTTTTTTTTTTTTATGAGGCGGCAACAGGGGACACCC 9120
 QY 9117 GGGCTTAAACGACCCCGC 9133
 Db 9121 GGGCTTAAACGACCCCGC 9137

RESULT 8
 AAA55379
 ID AAA55379 standard; DNA; 9143 BP.
 XX
 AC AAA55379;
 XX
 DT 06-AUG-2003 (revised)
 DT 30-AUG-2000 (first entry)
 XX
 DE Hepatitis GB virus nucleotide sequence SEQ ID NO:393.
 XX
 KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
 KW detection; characterisation; hepatitis; ds.
 XX
 OS Hepatitis GB virus.
 XX
 PN US6051374-A.
 XX
 PD 18-APR-2000.
 XX
 PF 07-JUN-1995; 95US-00488445.
 XX
 PR 14-FEB-1994; 94US-00196030.
 PR 13-MAY-1994; 94US-00242654.
 PR 29-JUL-1994; 94US-00283314.
 PR 23-NOV-1994; 94US-00344185.
 PR 23-NOV-1994; 94US-00344190.
 PR 30-JAN-1995; 95US-00377557.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
 PI Mushawar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
 XX
 DR WPI; 2000-338307/29.
 XX
 PT Detecting target hepatitis GB virus nucleic acid in a test sample
 PT suspected of containing HGBV comprises reacting the test sample the HGBV

Db 1801 CGAAGCATGCGGTGTAACACCATGGCTAAACACCCATGGGCACAAACGGCTCAGCCCTGAA 1860
Qy 1861 ATTGGCTATATTACAAATACCCCTGGGTCTAAAGAAATGTTTAAACCTCATAAATTGGATGTC 1920
Db 1861 ATTGGCTATATTACAAATACCCCTGGGTCTAAAGAAATGTTTAAACCTCATAAATTGGATGTC 1920
Qy 1921 AGGCCATTGTAATTTGAGGGATCAGATACCCCTATAGTTACTTTTATGACCCCTGTGAA 1980
Db 1921 AGGCCATTGTAATTTGAGGGATCAGATACCCCTATAGTTACTTTTATGACCCCTGTGAA 1980
Qy 1981 TTCCACTCTCTACACCGGAGAGGTGGCTAGGTGGCCGGTACCCACCTGTGGTACG 2040
Db 1981 TTCCACTCTCTACACCGGAGAGGTGGCTAGGTGGCCGGTACCCACCTGTGGTACG 2040
Qy 2041 TGGTCTCTGGTTACAGGTTCCGCAAGGTTTTACAGTGATGTGAAGACCTAGGCACACAGG 2100
Db 2041 TGGTCTCTGGTTACAGGTTCCGCAAGGTTTTACAGTGATGTGAAGACCTAGGCACACAGG 2100
Qy 2101 ATTGATCACCAAGACAAAGCTCGAAATAATATCAGGTCTTATATCCGCCACGGGTGC 2160
Db 2101 ATTGATCACCAAGACAAAGCTCGAAATAATATCAGGTCTTATATCCGCCACGGGTGC 2160
Qy 2161 TTTGTCTCTTACGGAGATTACCAACAGCCGTGTGCTAATCTGTGGGTTGTGTGG 2220
Db 2161 TTTGTCTCTTACGGAGATTACCAACAGCCGTGTGCTAATCTGTGGGTTGTGTGG 2220
Qy 2221 CAGCAAGTATCTTATTTAGCCTACCTCTGTGTACTTGTCCCTTGTGTTTGGCGGCTTC 2280
Db 2221 CAGCAAGTATCTTATTTAGCCTACCTCTGTGTACTTGTGTTTGGCGGCTTC 2280
Qy 2281 TGGTTACCCCTTTGCGTCTGCTCCCATCCAGTCGTATCTCCAAGCTGGCTGGATGT 2340
Db 2281 TGGTTACCCCTTTGCGTCTGCTCCCATCCAGTCGTATCTCCAAGCTGGCTGGATGT 2340
Qy 2341 TTTGTCTTAAGCTCAAGTAGCTCTTTTGTCTTTGATTTTCTTCACTGTGCTATCTCG 2400
Db 2341 TTTGTCTTAAGCTCAAGTAGCTCTTTTGTCTTTGATTTTCTTCACTGTGCTATCTCG 2400
Qy 2401 CTGACGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCATGGCTGGCGGCTGCCCT 2460
Db 2401 CTGACGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCATGGCTGGCGGCTGCCCT 2460
Qy 2461 AACTTTCTTTGTGTCAGCAGCTGCTGCCCAACAGATTATGACTGGTGGTGCGACTGCT 2520
Db 2461 AACTTTCTTTGTGTCAGCAGCTGCTGCCCAACAGATTATGACTGGTGGTGCGACTGCT 2520
Qy 2521 AGTGCAGGGTTAGTTTGTGGGCGCGGCTAACCGTGTGTACCCGATAGCTCTGCTGT 2580
Db 2521 AGTGCAGGGTTAGTTTGTGGGCGCGGCTAACCGTGTGTACCCGATAGCTCTGCTGT 2580
Qy 2581 AGGTCTTTGGCCTCTGGTAGCGCTTTTAAACCTCTTGCAATTTGGTTAGCCTGCTCAGC 2640
Db 2581 AGGTCTTTGGCCTCTGGTAGCGCTTTTAAACCTCTTGCAATTTGGCTAGCGCTTTCAGC 2640
Qy 2641 TTTTGATACCGAGATAATTGAGGGCTGACATAACCACTGTAGTAGCATTTAGTTGTGAT 2700
Db 2641 TTTTGATACCGAGATAATTGAGGGCTGACATAACCACTGTAGTAGCATTTAGTTGTGAT 2700
Qy 2701 GTCTGTTTGGCTCTTTGCTCAGCTGTTACTCGCTGTGCTTTAGTTAACTCTATCT 2760
Db 2701 GTCTGTTTGGCTCTTTGCTCAGCTGTTACTCGCTGTGCTTTAGTTAACTCTATCT 2760
Qy 2761 TTGGCAACGTTGGGAGAAATTTGTTTGGAAACGTTACACTTAAGACCGGAGAGTTTCTCT 2820
Db 2761 TTGGCAACGTTGGGAGAAATTTGTTTGGAAACGTTTACACTTAAGACCGGAGAGTTTCTCT 2820
Qy 2821 TGTGCTGTTTGTCTTTCCCGGTGCGACATATGACCGCTGTGACTTTCTGTGTGTGCA 2880
Db 2821 TGTGCTGTTTGTCTTTCCCGGTGCGACATATGACCGCTGTGACTTTCTGTGTGTGCA 2880
Qy 2881 CGTAGCTCTTCTATGTTTAACTATCCAGTGACAGATGTTCTTTGGGACTGACTCTAGGGT 2940
Db 2881 CGTAGCTCTTCTATGTTTAACTATCCAGTGACAGATGTTCTTTTGGGACTGACTCTAGGGT 2940

Qy 2941 TAGGCCCATAGAAATGTTGGTGGCTCTCGGAAAGTGTCATGCTTGGTATTCTCATTTATGT 3000
Db 2941 TAGGCCCATAGAAATGTTGGTGGCTCTCGGAAAGTGTCATGCTTGGTATTCTCATTTATGT 3000
Qy 3001 TCTTAAAGTTTTTCTCTTAGTGGTTTGGTGAAGTGGTGTGTTTTTCTATAAGACACTTGCA 3060
Db 3001 TCTTAAAGTTTTTCTCTTAGTGGTTTGGTGAAGTGGTGTGTTTTTCTATAAGACACTTGCA 3060
Qy 3061 TGGTGATGTCCTTGAATTTTGGCTCGAAACTACCATTTGCAAGACCATTTTTCCTCC 3120
Db 3061 TGGTGATGTCCTTGAATTTTGGCTCGAAACTACCATTTGCAAGACCATTTTTCCTCC 3120
Qy 3121 TTTTGAAGCAAGCAAGGGTCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGGACAC 3180
Db 3121 TTTTGAAGCAAGCAAGGGTCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGGACAC 3180
Qy 3181 GGTGTAGTGGTTTGGCCGTTGTGGCGTCTCGGGACCTTGTGTTTTCGACAGGTTGGCTAT 3240
Db 3181 GGTGTAGTGGTTTGGCCGTTGTGGCGTCTCGGGACCTTGTGTTTTCGACAGGTTAGCTAT 3240
Qy 3241 GCCGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTGCAAGTGTCTCTGAAACGTGG 3300
Db 3241 GCCGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTGCAAGTGTCTCTGAAACGTGG 3300
Qy 3301 CACGCTGTACGCGATGGCAGTGGTCTATGACTGGTATAGACCCCGAACTTGGACTTGGAAAC 3360
Db 3301 CACGCTGTACGCGATGGCAGTGGTCTATGACTGGTATAGACCCCGAACTTGGACTTGGAAAC 3360
Qy 3361 TATCTTCAGATTAGGATCTCTGGCCACTAGTCTACATGGGATTTGTTTGTGACACAGTGT 3420
Db 3361 TATCTTCAGATTAGGATCTCTGGCCACTAGTCTACATGGGATTTGTTTGTGACACAGTGT 3420
Qy 3421 GTATACTGCTCACCATGCGCAGGAGGCGCGGTGCTCATCCACAGGCTCTATACA 3480
Db 3421 GTATACTGCTCACCATGCGCAGGAGGCGCGGTGCTCATCCACAGGCTCTATACA 3480
Qy 3481 CCCAATAACCCGTTGACGCGCTAATGACACAGGACATCTATCAACACCATGTGAGCTGG 3540
Db 3481 CCCAATAACCCGTTGACGCGCTAATGACACAGGACATCTATCAACACCATGTGAGCTGG 3540
Qy 3541 GTCCCTTACTCGGTGCTCTTGGGGGAGACCAAGGGGTATCTGTTAACACAGCTGGGTC 3600
Db 3541 GTCCCTTACTCGGTGCTCTTGGGGGAGACCAAGGGGTATCTGTTAACACAGCTGGGTC 3600
Qy 3601 ATTGGTTGAGGTCACAAATCCGATGACCTTATTGTTGTGTGCGGGGCTTCCCAT 3660
Db 3601 ATTGGTTGAGGTCACAAATCCGATGACCTTATTGTTGTGTGCGGGGCTTCCCAT 3660
Qy 3661 GGCTGTTGCCAAGGGTCTTTCAGGTGGCCCGATCTGTGCTCTCCCGGCGATGTTATTGG 3720
Db 3661 GGCTGTTGCCAAGGGTCTTTCAGGTGGCCCGATCTGTGCTCTCCCGGCGATGTTATTGG 3720
Qy 3721 GATGTTTCAACCGCTGTAGAAATCTGGCGGTTCACTAGTCAAGTATTAGGGTTAGGCGGTT 3780
Db 3721 GATGTTTCAACCGCTGTAGAAATCTGGCGGTTCACTAGTCAAGCAGATTAGGGTTAGGCGGTT 3780
Qy 3781 GGTGTGTGCTGATACCATCCAGTACACAGCAGTCCACTCTTGATACAAAACCTAC 3840
Db 3781 GGTGTGTGCTGATACCATCCAGTACACAGCAGTCCACTCTTGATACAAAACCTAC 3840
Qy 3841 TGTGCTTAAACGAGTATTTCAGTGCATAATTTTAAATTTGCCCCACTGGCAGCGGCAAGTCAAC 3900
Db 3841 TGTGCTTAAACGAGTATTTCAGTGCATAATTTTAAATTTGCCCCACTGGCAGCGGCAAGTCAAC 3900
Qy 3901 CAAATTACACTTCTTATACATGCGAGGAGATGAGGTCTTGGTCTTAAATCCAGTGT 3960
Db 3901 CAAATTACACTTCTTATACATGCGAGGAGATGAGGTCTTGGTCTTAAATCCAGTGT 3960
Qy 3961 GGTGTACACAGCATCAATGCCCCAAAGTACATGCAAGGAGTACGCGGTGAATCCAAATG 4020
Db 3961 GGTGTACACAGCATCAATGCCCCAAAGTACATGCAAGGAGTACGCGGTGAATCCAAATG 4020

Qy	4021	CTATTTTAATGGCAAAATGTATCCAAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT	4080
Db	4021	CTATTTTAATGGCAAAATGTATCCAAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT	4080
Qy	4081	GTACTCGACCGAGCATGTTCCCGAACTATGATGTAATCATTTTGTGAGCAATGCCATGC	4140
Db	4081	GTACTCGACCGAGCATGTTCCCGAACTATGAGCTATCATTTTGTGACGAATGCCATGC	4140
Qy	4141	TACCGATGCAACCAACCGTGTGGCATTTGGAAAGGTCCTTAACCGAAGCTCCATCCAAAA	4200
Db	4141	TACCGATGCAACCAACCGTGTGGCATTTGGAAAGGTTCTAACCGAAGCTCCATCCAAAA	4200
Qy	4201	TGTTAGGCTAGTGTCTTTCGCCAGGCTACCCGCCCTGGAGTAATCCCTACACACATGC	4260
Db	4201	TGTTAGGCTAGTGTCTTTCGCCAGGCTACCCGCCCTGGAGTAATCCCTACACACATGC	4260
Qy	4261	CAACATACTCAGATTCATTAACCGATGAAGGCACTATCCCTTTTCATGGAAAAAGAT	4320
Db	4261	CAACATACTCAGATTCATTAACCGATGAAGGCACTATCCCTTTTCATGGAAAAAGAT	4320
Qy	4321	TAAGGAGGAAATCTGAAGAAAGGAGACACTTATCTTTGAGGCTACCAAAAAACACTG	4380
Db	4321	TAAGGAGGAAATCTGAAGAAAGGAGACACTTATCTTTGAGGCTACCAAAAAACACTG	4380
Qy	4381	TGATGAGCTTGCCTAACCGAGTTAGCTCGAAAGGGAATTAACAGCTGTCTCTTACTATAGGG	4440
Db	4381	TGATGAGCTTGCCTAACCGAGTTAGCTCGAAAGGGAATTAACAGCTGTCTCTTACTATAGGG	4440
Qy	4441	ATGTGACATCTCAAAAATCCCTGAGGGGCACTGTGATAGTGTGCCACTGATGCTTGTG	4500
Db	4441	ATGTGACATCTCAAAAATCCCTGAGGGGCACTGTGATAGTGTGCCACTGATGCTTGTG	4500
Qy	4501	TACAGGGTACACTGGTGACTTTGATTCGGTGATGACTGCAAGCCTCATGTTAGAGGCAC	4560
Db	4501	TACAGGGTACACTGGTGACTTTGATTCGGTGATGACTGCAAGCCTCATGTTAGAGGCAC	4560
Qy	4561	ATGCCATGTTGACCTTGACCTACTTTCACCATGGGTGTTGCTGTGTGCGGGGTTTCAGC	4620
Db	4561	ATGCCATGTTGACCTTGACCTACTTTCACCATGGGTGTTGCTGTGTGCGGGGTTTCAGC	4620
Qy	4621	AATAGTTAAAGCCAGCGTAGGGCCGACAGAGCGGTGGAGAGCTGGCATATACTACTA	4680
Db	4621	AATAGTTAAAGCCAGCGTAGGGCCGACAGAGCGGTGGAGAGCTGGCATATACTACTA	4680
Qy	4681	TGTAGACGGAGTGTATCCCTTCGGGTATGGTTTCTGAAATGCAACATTTGTTGAAGCCTT	4740
Db	4681	TGTAGACGGAGTGTATCCCTTCGGGTATGGTTTCTGAAATGCAACATTTGTTGAAGCCTT	4740
Qy	4741	CGACGAGCCAAAGGATGGTATGTTTGTATCAACAGAAAGCTCAAACTATTTCTGGACAC	4800
Db	4741	CGACGAGCCAAAGGATGGTATGTTTGTATCAACAGAAAGCTCAAACTATTTCTGGACAC	4800
Qy	4801	CTATCGCACCAACTGGGTTTACCTCGATAGGAGCAAAATTTGCAGGTGGGCTGATCT	4860
Db	4801	CTATCGCACCAACTGGGTTTACCTCGATAGGAGCAAAATTTGCAGGTGGGCTGATCT	4860
Qy	4861	CTTTTCTATGTGTCAACCCGAACTTCAATTTGTCAATACTGCAAAAAAGAACTGCTGACAA	4920
Db	4861	CTTTTCTATGTGTCAACCCGAACTTCAATTTGTCAATACTGCAAAAAAGAACTGCTGACAA	4920
Qy	4921	TTATGTTTTGTGTGACTGAGCCCAACTACAATCTGTGTATCAGTATGGCTATGTCTCC	4980
Db	4921	TTATGTTTTGTGTGACTGAGCCCAACTACAATCTGTGTATCAGTATGGCTATGTCTCC	4980
Qy	4981	CAATGACGACCGGTGGAGGGAGCCCGCTTTGGGAAAAAACTTTGGGGTTCGTGTG	5040
Db	4981	CAATGACGACCAACCGGTGGAGGGAGCCCGCTTTGGGAAAAAACTTTGGGGTTCGTGTG	5040
Qy	5041	CGCGTTGGAACCGGCTGACGCTGTCTCGGCCAGAGCCGAGCGGTGACAGATACCA	5100
Db	5041	CGCGTTGGAACCGGCTGACGCTGTCTCGGCCAGAGCCGAGCGGTGACAGATACCA	5100
Qy	5101	AATGTGCTTCACTGAAGTCAATACTTCTGGGACAGCCGCACTCGCTGTGTGGCGTTGGAGT	5160

Db	5101	AATGTGCTTCACTGAAGTCAATACTTCTGGGACAGCCGCACTCGCTGTGTGGCGTTGGAGT	5160
Qy	5161	GGCTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACTTGTGTGGGGGTTCGTGCTGC	5220
Db	5161	GGCTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACTTGTGTGGGGGTTCGTGCTGC	5220
Qy	5221	TATTAATCATAGTCCCTAACCGGTGCTACTGCGGCCAGTGGTGTGACGAAGAAATCGT	5280
Db	5221	TATTAATCATAGTCCCTAACCGGTGCTACTGCGGCCAGTGGTGTGACGAAGAAATCGT	5280
Qy	5281	GGAGGAGTGTGCATTCATTCCTTGGAGGCCATGGTGTGCTGCAATTCGATTAAGCTGAA	5340
Db	5281	GGAGGAGTGTGCATTCATTCCTTGGAGGCCATGGTGTGCTGCAATTCGATTAAGCTGAA	5340
Qy	5341	GAGTACAAATCACCAAACTAGTCTTTTCAATTTGGAAACCGCCCTTGAAAAAACTTAACAC	5400
Db	5341	GAGTACAAATCACCAAACTAGTCTTTTCAATTTGGAAACCGCCCTTGAAAAAACTTAACAC	5400
Qy	5401	CTTTCTTTGGGCTCATGACGCTCAATCTCTTGCTATCATAGAGTATTTGCTGTGTTAGT	5460
Db	5401	CTTTCTTTGGGCTCATGACGCTCAATCTCTTGCTATCATAGAGTATTTGCTGTGTTAGT	5460
Qy	5461	CACCTTACCTGACAAATCCCTTTGCATCATCGGTGTTTCTTCAATTCGGGGTATTTACTAC	5520
Db	5461	CACCTTACCTGACAAATCCCTTTGCATCATCGGTGTTTCTTCAATTCGGGGTATTTACTAC	5520
Qy	5521	CCCACTACCTCACAAAGTCAAAATGTTCTGTCTATTTTGGAGGCGCAATTTGGCGTCCA	5580
Db	5521	CCCACTACCTCACAAAGTCAAAATGTTCTGTCTATTTTGGAGGCGCAATTTGGCGTCCA	5580
Qy	5581	GCTTACAGACGCTAGAGGCGCACCTGGCGTTCTATGATGCGCGGGCTCGGGAAACAGCTCT	5640
Db	5581	GCTTACAGACGCTAGAGGCGCACCTGGCGTTCTATGATGCGCGGGCTCGGGAAACAGCTCT	5640
Qy	5641	TGCTACATGACATCGGTGGGTTTGTCTTTGACATGCTAGGCGGCTATGCTCGCGGCTC	5700
Db	5641	TGCTACATGACATCGGTGGGTTTGTCTTTGACATGCTAGGCGGCTATGCTCGCGGCTC	5700
Qy	5701	ATCCACTGCTTGTGTGACATTTAAATGCTTGAATGGGTGAGTGGCCCACTATGGATCAGCT	5760
Db	5701	ATCCACTGCTTGTGTGACATTTAAATGCTTGAATGGGTGAGTGGCCCACTATGGATCAGCT	5760
Qy	5761	TGCTGGTTTATGCTACTCCGCGTTCAATCGGCGCAGGAGTGTGTGGCGCTTGTGTCAGC	5820
Db	5761	TGCTGGTTTATGCTACTCCGCGTTCAATCGGCGCAGGAGTGTGTGGCGCTTGTGTCAGC	5820
Qy	5821	TGTTGCAATGTTTGTGTTGACAGAGGCGCCAGATCACTGGGCCCAACAGACTTCTTAC	5880
Db	5821	TGTTGCAATGTTTGTGTTGACAGAGGCGCCAGATCACTGGGCCCAACAGACTTCTTAC	5880
Qy	5881	TATGCTTGTAGGAGCAACACTGTATGTAATGAGTACTTTTATTTGCCACTCGTGACATCCG	5940
Db	5881	TATGCTTGTAGGAGCAACACTGTATGTAATGAGTACTTTTATTTGCCACTCGTGACATCCG	5940
Qy	5941	CAGGAAGATATCTGGGCAATCTGAGGCGCATCTACCCCTGGAGTGTATATCAGCTTGAT	6000
Db	5941	CAGGAAGATATCTGGGCAATCTGAGGCGCATCTACCCCTGGAGTGTATATCAGCTTGAT	6000
Qy	6001	CGTTGGCTCCACACCCCGAGCGAGGATGATGGGCTCATTTGCTTTGGGGTCTAGAGAT	6060
Db	6001	CGTTGGCTCCACACCCCGAGCGAGGATGATGGGCTCATTTGCTTTGGGGTCTAGAGAT	6060
Qy	6061	TTGGCAGTATGTGTGCAATTTCTTTGTGATTTGCTTTAAATGCTTAAAGCTGGAGTTCA	6120
Db	6061	TTGGCAGTATGTGTGCAATTTCTTTGTGATTTGCTTTAAATGCTTAAAGCTGGAGTTCA	6120
Qy	6121	GAGCATGTTTAAACATTCCTGTTGTCTTCTACAGCTGCCAGAAAGGGGTACAAGGGGCC	6180
Db	6121	GAGCATGTTTAAACATTCCTGTTGTCTTCTACAGCTGCCAGAAAGGGGTACAAGGGGCC	6180
Qy	6181	CTGATTTGGATCAGGTATGCTCCAGCACGCTGTCTCATGGGTGCTGAACTCATCTTTTC	6240

Db 6181 CTGGATTGGATCAGGTATGCTCCAAAGCACGCTGTCCATGCGGTGCTGAACCTCATCTTTTC 6240
Qy TGTTCAGAAATGTTTTGCAAACTTTTACAAAGAGCCCAAGACTCTCTCAAAATTACTGGAG 6300
Db TGTTCAGAAATGTTTTGCAAACTTTTACAAAGAGCCCAAGACTCTCTCAAAATTACTGGAG 6300
Qy AGGGCTGCTTCCAGTCAACGCTAGGCTGTGTGGGTGCGGTAGACCGGAGCCCAACTGATTG 6360
Db AGGGCTGCTTCCAGTCAACGCTAGGCTGTGTGGGTGCGGTAGACCGGAGCCCAACTGATTG 6360
Qy GACTAGTCTTGTGCGTCAATATTATGGCGTTAGGACCTACTCTGTAATAATGAGAAATGGGAGA 6420
Db GACTAGTCTTGTGCGTCAATATTATGGCGTTAGGACCTACTCTGTAATAATGAGAAATGGGAGA 6420
Qy TCACATTTTGTGTACAGCAGTATCTCTCCAAATGCTCTGTTTCAACCCAGGTGCCCCCAAC 6480
Db TCACATTTTGTGTACAGCAGTATCTCTCCAAATGCTCTGTTTCAACCCAGGTGCCCCCAAC 6480
Qy CTTTGAGAGCTGCAGTGGCGGTGGAGCGGGGTACAGGTTTCAAGTGTATCTAGGTGAGCCCAA 6540
Db CTTTGAGAGCTGCAGTGGCGGTGGAGCGGGGTACAGGTTTCAAGTGTATCTAGGTGAGCCCAA 6540
Qy AACTCTTTGGACGACATCTGTCTGTGTTACCGTCTCTGACCGTAAAGGTAAACTGTTAA 6600
Db AACTCTTTGGACGACATCTGTCTGTGTTACCGTCTCTGACCGTAAAGGTAAACTGTTAA 6600
Qy GCTTCCCTTCCGCGTTGACGGTACACACCTGGTGTGGCGATGCAACTTAATTTCCGTGA 6660
Db GCTTCCCTTCCGCGTTGACGGTACACACCTGGTGTGGCGATGCAACTTAATTTCCGTGA 6660
Qy TGCACCTTGAGACAAATGACTGTAATTTCCAAACAACTCTCTAGTGTAGAGCCCAAGT 6720
Db TGCACCTTGAGACAAATGACTGTAATTTCCAAACAACTCTCTAGTGTAGAGCCCAAGT 6720
Qy GTCCGCTCTTGTGTTTCAAACAGAGTTGCGGCGTACAAACCAATTTCTTGAGGCAATTTTC 6780
Db GTCCGCTCTTGTGTTTCAAACAGAGTTGCGGCGTACAAACCAATTTCTTGAGGCAATTTTC 6780
Qy AGCTGGCGTTGACACCAACCTGCCAGCCCTCCATCGAAGAGTGTAGTGAAGAA 6840
Db AGCTGGCGTTGACACCAACCTGCCAGCCCTCCATCGAAGAGTGTAGTGAAGAA 6840
Qy GCGCCAGTTCCGGGCAAGAACTGGTTGCTTACCTTGCCTCCCGCTCCGAGATCCGTCCTC 6900
Db GCGCCAGTTCCGGGCAAGAACTGGTTGCTTACCTTGCCTCCCGCTCCGAGATCCGTCCTC 6900
Qy AGGAGTGCAATGCTCTGAAAAGCCTGCAACGAAGTGACCCGTTAGAAAGTCTCTCAAACT 6960
Db AGGAGTGCAATGCTCTGAAAAGCCTGCAACGAAGTGACCCGTTAGAAAGTCTCTCAAACT 6960
Qy CCCTCTTCAACACCTGTTCTACAGTTGGCCATGCGGATGCCCTGTTGGGAGCGGTTGA 7020
Db CCCTCTTCAACACCTGTTCTACAGTTGGCCATGCGGATGCCCTGTTGGGAGCGGTTGA 7020
Qy GTGTAACTCTTCACTGCAATTTGGATGTGCAATGACCGAAACAGCGGAGGCCCTGATGA 7080
Db GTGTAACTCTTCACTGCAATTTGGATGTGCAATGACCGAAACAGCGGAGGCCCTGATGA 7080
Qy TTTTACCCAGTTACCTTCCAAAAGGAGGTCTCTGAATGGTTCAGACGAAAGTTGTCGAC 7140
Db TTTTACCCAGTTACCTTCCAAAAGGAGGTCTCTGAATGGTTCAGACGAAAGTTGTCGAC 7140
Qy GGCTACACCGCTTCCAGCTAGCTTACTGGCCCCCGGTACCTTAAGATACGGGGAAGGA 7200
Db GGCTACACCGCTTCCAGCTAGCTTACTGGCCCCCGGTACCTTAAGATACGGGGAAGGA 7200
Qy TTCCACTCAGTCAGCCCCCGCCCAACGGCTTACAAAAGAGTTGGGAAAGAGTGAGTT 7260
Db TTCCACTCAGTCAGCCCCCGCCCAACGGCTTACAAAAGAGTTGGGAAAGAGTGAGTT 7260
Qy TTCGTGCAAGCATGAGCTACCTTGGACCGACGTGATTTAGCTTCAAAACTGCTTCTAAAGT 7320
Db TTCGTGCAAGCATGAGCTACCTTGGACCGACGTGATTTAGCTTCAAAACTGCTTCTAAAGT 7320

Qy TCTGTCTGCAACTCGGGCCATCATCTAGTGGTTTCTCTCAAAACAAGATCATTTGGTGTATGT 7321
Db TCTGTCTGCAACTCGGGCCATCATCTAGTGGTTTCTCTCAAAACAAGATCATTTGGTGTATGT 7380
Qy GACTGAGCCGCGGATCGGAGCTTTAGAAAAAAGTCTACTATTAAATAGACAACCTCT 7440
Db GACTGAGCCGCGGATCGGAGCTTTAGAAAAAAGTCTACTATTAAATAGACAACCTCT 7440
Qy GTTCCCCCATCATACCAAGCAAGTGAGATTGGCTAAGGAAAAAGCTTCAAAAGTTGT 7500
Db GTTCCCCCATCATACCAAGCAAGTGAGATTGGCTAAGGAAAAAGCTTCAAAAGTTGT 7500
Qy CGGTGTCTATGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTTAAGTCTGCTAAGTC 7560
Db CGGTGTCTATGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTTAAGTCTGCTAAGTC 7560
Qy CCACATCACTGGCCCTTCCGGGCACTGATTTGTTCTGGAGCAGCCCGCAAGGCTGTTCT 7620
Db CCACATCACTGGCCCTTCCGGGCACTGATTTGTTCTGGAGCAGCCCGCAAGGCTGTTCT 7620
Qy GGACTTGCAAGAGTGTCTGAGGCAAGTGAGATACCGAGTCACTTATCGGCAACTGTGTAT 7680
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Qy AGTTCCAAAGGAGGAGTCTTCTGTGAAGACCCCGCAGAAAAACAACAAAGAAAAACCCCAAG 7740
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Qy GCTTATCTCTGTAACCCCACTTGAAGTGTGTTGAGAAAGTGTACTACGGTCAAGT 7800
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Qy TGCTCTCTGACGTAGTTAAAGCTGTCACTGGGAGATGCGTACCGGTTTGTAGATCCACGTAC 7860
Db TGCTCTCTGACGTAGTTAAAGCTGTCACTGGGAGATGCGTACCGGTTTGTAGATCCACGTAC 7860
Qy CCGTGTCAAGGCTCTGTTGTGTCAGTCCGATCCGATCGAGTCGAGGCCACATGCGATAC 7920
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Qy AGTGTGTTTTGACAGTACCATCACACCCGAGGATATCATGTGGAGACAGACATCTACTC 7980
Db AGTGTGTTTTGACAGTACCATCACACCCGAGGATATCATGTGGAGACAGACATCTACTC 7980
Qy AGCAGCTAACTCAGTGAACCAACCCGAGCTGGCATTCACACCATTTGCGAGGCACTTATA 8040
Db AGCAGCTAACTCAGTGAACCAACCCGAGCTGGCATTCACACCATTTGCGAGGCACTTATA 8040
Qy CGCTGGAGGACCGATGATCGCTTATGATGGCCGAGAGATCGATATCGTAGGTGTAGGTC 8100
Db CGCTGGAGGACCGATGATCGCTTATGATGGCCGAGAGATCGATATCGTAGGTGTAGGTC 8100
Qy TTCCGGCGTCTATACTACTCTCAAGTTCCAAACAGTTTGAACCTGCTGGCTGAAGGTAAATGC 8160
Db TTCCGGCGTCTATACTACTCTCAAGTTCCAAACAGTTTGAACCTGCTGGCTGAAGGTAAATGC 8160
Qy TGCAGCCGAAACAGGCTGGCATGAAAGAACCTCTGCTTCTCTTATTTGCGGCGATGATGAC 8220
Db TGCAGCCGAAACAGGCTGGCATGAAAGAACCTCTGCTTCTCTTATTTGCGGCGATGATGAC 8220
Qy CGTAAATTTGGAAGAGCGCGGAGCAGATGCAGAAAAACAAGCAATGCTGCTTTGCTAG 8280
Db CGTAAATTTGGAAGAGCGCGGAGCAGATGCAGAAAAACAAGCAATGCTGCTTTGCTAG 8280
Qy CTGGATGAAGTGTAGGTGCAACCAAGATTGTGTGCTCAACCCAAATACAGTTTGA 8340
Db CTGGATGAAGTGTAGGTGCAACCAAGATTGTGTGCTCAACCCAAATACAGTTTGA 8340
Qy AGAATTAACATCATGCTCATCAAAATGTTACCTCTGGAATTTACCAAGTGGCAGCCCTTA 8400
Db AGAATTAACATCATGCTCATCAAAATGTTACCTCTGGAATTTACCAAGTGGCAGCCCTTA 8400

Db	421	CTGGAGTCTCGTAGACCGTAGACATGCTGTATTCTTACTCAAAACAAGTCTCTGTACC	480
Qy	481	TGGCCCCAGAACCGCAAGCAACAGCAGACGCAAGCTTCATATCTCTGTGTCCATATAAAC	540
Db	481	TGGCCCCAGAACCGCAAGCAACAGCAGACGCAAGCTTCATATCTCTGTGTCCATATAAAC	540
Qy	541	ATCTGTTGAAAGGGGACAAACGAGCAAAAGCGCAAAGTCCAGCGCGATGCTCGGCGCTCGTAA	600
Db	541	ATCTGTTGAAAGGGGACAAACGAGCAAAAGCGCAAAGTCCAGCGCGATGCTCGGCGCTCGTAA	600
Qy	601	TTACAAAATTGCTCGGTATCCATGATGCTTTCAGACATTTGGCTCAGGCTGCTTTGGCAGC	660
Db	601	TTACAAAATTGCTCGGTATCCATGATGCTTTCAGACATTTGGCTCAGGCTGCTTTGGCAGC	660
Qy	661	TCATGCTTGGGACCGCAAGACCCCTGCCCATAGTCTCGCAATCTTCGGAATCTCTTCGGA	720
Db	661	TCATGCTTGGGACCGCAAGACCCCTGCCCATAGTCTCGCAATCTTCGGAATCTCTTCGGA	720
Qy	721	TTACCCCTTTGGGGTGGATTGGTGATGTTACAACCTCACACCTCTAGTAGGCCCGCTGGT	780
Db	721	TTACCCCTTTGGGGTGGATTGGTGATGTTACAACCTCACACCTCTAGTAGGCCCGCTGGT	780
Qy	781	GGCAGGACGGTCTGTCGACGCTGCCAGATAGTAGCGTTGCTGGAGGATGAGTCAA	840
Db	781	GGCAGGACGGTCTGTCGACGCTGCCAGATAGTAGCGTTGCTGGAGGATGAGTCAA	840
Qy	841	CTGGGCTACTGGTTGGTTCCGGTGCCACCTTTTGTGCTATGCTGCTATCTTTGGCCTG	900
Db	841	CTGGGCTACTGGTTGGTTCCGGTGCCACCTTTTGTGCTATGCTGCTATCTTTGGCCTG	900
Qy	901	TCCCTGTAGTGGGCGCGGGTCACTGACCCAGACAAATACCAACATCTGACCAATTG	960
Db	901	TCCCTGTAGTGGGCGCGGGTCACTGACCCAGACAAATACCAACATCTGACCAATTG	960
Qy	961	CTGCCACGGTAATCAGGTTATCTAATGTTCTCTTCACCTTGCTCACAGGCTGGTTG	1020
Db	961	CTGCCACGGTAATCAGGTTATCTAATGTTCTCTTCACCTTGCTCACAGGCTGGTTG	1020
Qy	1021	TGTGATCTGTGCCGACGAGTGCTGGGTTCCGCCCAATCCGTACATCTCACACCTTCCAA	1080
Db	1021	TGTGATCTGTGCCGACGAGTGCTGGGTTCCGCCCAATCCGTACATCTCACACCTTCCAA	1080
Qy	1081	TTGACTTGGCACGGACTCCCTCTTTGGGCTGACCAATGATTTGTATTGGCGCTCTTGT	1140
Db	1081	TTGACTTGGCACGGACTCCCTCTTTGGGCTGACCAATGATTTGTATTGGCGCTCTTGT	1140
Qy	1141	GACCTGTGACGCCCTTGACATTTGGTAGTTGTGTGGTCCGTGTATTTAGTCGGTGAATG	1200
Db	1141	GACCTGTGACGCCCTTGACATTTGGTAGTTGTGTGGTCCGTGTATTTAGTCGGTGAATG	1200
Qy	1201	GCTTGTGAGGCACTGGCTTATTCATAGACCTCAATGAAACTGGTACTTTGTACCTGGA	1260
Db	1201	GCTTGTGAGGCACTGGCTTATTCATAGACCTCAATGAAACTGGTACTTTGTACCTGGA	1260
Qy	1261	AGTGCCCACTGGAATAGATCTGGGTTCTTAGGGTTTATCGGGTGGATGCGCGCAAGT	1320
Db	1261	AGTGCCCACTGGAATAGATCTGGGTTCTTAGGGTTTATCGGGTGGATGCGCGCAAGT	1320
Qy	1321	CGAGGCTGTCACTTCTTTGACCAAACTGGCTTCAAGTAGTACCATCGCTATTGCGACTAT	1380
Db	1321	CGAGGCTGTCACTTCTTTGACCAAACTGGCTTCAAGTAGTACCATCGCTATTGCGACTAT	1380
Qy	1381	GTTTATGAGTGATCACTACCTGGGGTTGGGCTCTGATCTATGCTCTCGGGGCAA	1440
Db	1381	GTTTATGAGTGATCACTACCTGGGGTTGGGCTCTGATCTATGCTCTCGGGGCAA	1440
Qy	1441	GTGGTATCAGTTGCTCTAGGCTTATGCTTTACATAGACGCACTCTGGAACCCCAT	1500
Db	1441	GTGGTATCAGTTGCTCTAGGCTTATGCTTTACATAGACGCACTCTGGAACCCCAT	1500
Qy	1501	CAGGGTGCCCACTGGATGCTCAATAGCTAGTTTTGTCTCGGCTTTGATGATCACCATGTC	1560

Qy	2641	TTTTGATACCGAGATAAATTGGAGGGCTGACAATACCACCTGTAGTAGCAATTAGTGTGCAT	2700
Dd	2641	TTTTGATACCGAGATAAATTGGAGGGCTGACAATACCACCTGTAGTAGCAATTAGTGTGCAT	2700
Qy	2701	GTCTCGTTTGGCTTCTTTGCTCACTTGTGTACCTCGCTGCTGCTTTAGTTAACTGCTATCT	2760
Dd	2701	GTCTCGTTTGGCTTCTTTGCTCACTTGTGTACCTCGCTGCTGCTTTAGTTAACTGCTATCT	2760
Qy	2761	TTGGCAACGTTGGGAGAAATCGTTTGGAAAGTTTACACTAAGACCGGAGAGGTTTTCCT	2820
Dd	2761	TTGGCAACGTTGGGAGAAATCGTTTGGAAAGTTTACACTAAGACCGGAGAGGTTTTCCT	2820
Qy	2821	TGTGCTGCTTTGTTTCCCGGTGGACATATGACGCGCTGGTGACTTTCTGTGTGTGCA	2880
Dd	2821	TGTGCTGCTTTGTTTCCCGGTGGACATATGACACGCTGGTGACTTTCTGTGTGTGCA	2880
Qy	2881	CGTAGCTTCTATGTTTAAACATCCAGTGCAGCATCGTTCTTGGGACTGACTCTAGGGT	2940
Dd	2881	CGTAGCTTCTATGTTTAAACATCCAGTGCAGCATCGTTCTTGGGACTGACTCTAGGGT	2940
Qy	2941	TAGGSCCAATAGAAATGTTGGTGGCTCTCGAAAGTGTCAATGCTTGGTATCTCATTAATGT	3000
Dd	2941	TAGGSCCAATAGAAATGTTGGTGGCTCTCGAAAGTGTCAATGCTTGGTATCTCATTAATGT	3000
Qy	3001	TCTTAAAGTTTTCTCTTAGTGTGTTGGTGAATGGTGTGTTTCTATAAGCACTTGCA	3060
Dd	3001	TCTTAAAGTTTTCTCTTAGTGTGTTGGTGAATGGTGTGTTTCTATAAGCACTTGCA	3060
Qy	3061	TGGTGATGCTTGCCTAATGATTTTGGCTCGAAACTACCATGTCGAAAGCAATTTTCCC	3120
Dd	3061	TGGTGATGCTTGCCTAATGATTTTGGCTCGAAACTACCATGTCGAAAGCAATTTTCCC	3120
Qy	3121	TTTTGAAGCGAAGCAAGGCTCTATAGGAATGAAGGAAGACGTTGGCGTGTGGGACAC	3180
Dd	3121	TTTTGAAGCGAAGCAAGGCTCTATAGGAATGAAGGAAGACGTTGGCGTGTGGGACAC	3180
Qy	3181	GGTTGATGGTTTGGCCGTTGTTGGCGTCTCGGGACCTTGTTTTCGACAGGTTGGCTAT	3240
Dd	3181	GGTTGATGGTTTGGCCGTTGTTGGCGTCTCGGGACCTTGTTTTCGACAGGTTAGCTAT	3240
Qy	3241	CGCGCAGATGGGTGGGCCATTAACGGACCTTTTACGCTGCAGTGTCTCTCTGACAGTGG	3300
Dd	3241	CGCGCAGATGGGTGGGCCATTAACGGACCTTTTACGCTGCAGTGTCTCTCTGACAGTGG	3300
Qy	3301	CACGCTGCAGCGATGGCAGTGTGATGACCTGTTATAGACCCCGAACTCGGACTGGAAC	3360
Dd	3301	CACGCTGCAGCGATGGCAGTGTGATGACCTGTTATAGACCCCGAACTTGGACTGGAAC	3360
Qy	3361	TATCTTCAGATTAGGATCTCTGGCCACTAGCTACATGGGAATTTGTTGTGACAAACGTTT	3420
Dd	3361	TATCTTCAGATTAGGATCTCTGGCCACTAGCTACATGGGAATTTGTTGTGACAAACGTTT	3420
Qy	3421	GTATCTGCTACCATGACAGAGGGCGCGGTGCTCATCCACAGGCTCTATACA	3480
Dd	3421	GTATCTGCTACCATGACAGAGGGCGCGGTGCTCATCCACAGGCTCCATACA	3480
Qy	3481	CCCAATAACCGTTGACGCGGTAAATGACAGGACATCTATCAACACCATCTGGAGCTGG	3540
Dd	3481	CCCAATAACCGTTGACGCGGTAAATGACAGGACATCTATCAACACCATCTGGAGCTGG	3540
Qy	3541	GTCCCTTACTCGGTGCTCTTGGGGGAGACCAAGGGGTATCTGGTAAACAGACTGGGGTC	3600
Dd	3541	GTCCCTTACTCGGTGCTCTTGGGGGAGACCAAGGGGTATCTGGTAAACAGACTGGGGTC	3600
Qy	3601	ATTGTTGAGGTCAACAAATCCGATGACCTTTAATGGTGTGTGTGCGGGGCCCTTCCCAT	3660
Dd	3601	ATTGTTGAGGTCAACAAATCCGATGACCTTTAATGGTGTGTGTGCGGGGCCCTTCCCAT	3660
Qy	3661	GGCTGTGCGAAGGGTCTTCAGGTGGCCCGATCTGTGCTCCCTCCGGGCAATGTTATGG	3720
Dd	3661	GGCTGTGCGAAGGGTCTTCAGGTGGCCCGATCTGTGCTCCCTCCGGGCAATGTTATGG	3720

Qy	3721	GATGTTCAACGCTGCTAGAAATTTCTGGCGGTTCAAGTCAGTCAGATTAAGGTTAGGCCGTT	3780
Dd	3721	GATGTTCAACGCTGCTAGAAATTTCTGGCGGTTCAAGTCAGTCAGTCAGATTAAGGTTAGGCCGTT	3780
Qy	3781	GGTGTGCTGGATACCATCCAGTACACAGACATGCCACTCTTGATACAAAACCTAC	3840
Dd	3781	GGTGTGCTGGATACCATCCAGTACACAGACATGCCACTCTTGATACAAAACCTAC	3840
Qy	3841	TGTGCTTAAACGAGTATTTAGTGCAGAAATTTAAATTTGCCCCCACTGGCAGCGCAAGTCAAC	3900
Dd	3841	TGTGCTTAAACGAGTATTTAGTGCAGAAATTTAAATTTGCCCCCACTGGCAGCGCAAGTCAAC	3900
Qy	3901	CAAAATACACACTTTCTTACATGACGAGAGATGAGGTCCTTGCTCTTAATATCCAGTGT	3960
Dd	3901	CAAAATACCACTTTCTTACATGACGAGAGATGAGGTCCTTGCTCTTAATATCCAGTGT	3960
Qy	3961	GGCTACAAACAGCATCAATGCGCAAGTACATGACGCGAGCTACGCGCTGAATCAAAATTG	4020
Dd	3961	GGCTACAAACAGCATCAATGCGCAAGTACATGACGCGAGCTACGCGCTGAATCAAAATTG	4020
Qy	4021	CTATTTTAAATGGCAAAATGTATACCAACACAGGGGCTTCACTTACGTACAGCACATATGCGAT	4080
Dd	4021	CTATTTTAAATGGCAAAATGTATACCAACACAGGGGCTTCACTTACGTACAGCACATATGCGAT	4080
Qy	4081	GTACTGACCGGAGCATGTTCCCGAACTATGACGTCAATCAATTTGTGACGAATGCCATGC	4140
Dd	4081	GTACTGACCGGAGCATGTTCCCGAACTATGACGTCAATCAATTTGTGACGAATGCCATGC	4140
Qy	4141	TACCGATGACACACCGTGTGGGCAATGGAAAGGCTCTAACCGAAGCTCCATCCAAAA	4200
Dd	4141	TACCGATGACACACCGTGTGGGCAATGGAAAGGCTCTAACCGAAGCTCCATCCAAAA	4200
Qy	4201	TGTTAGGCTAGTGGTTCTTGCCACGGCTACCCCCCTGGAGTAATCCCTACACACATGC	4260
Dd	4201	TGTTAGGCTAGTGGTTCTTGCCACGGCTACCCCCCTGGAGTAATCCCTACACACATGC	4260
Qy	4261	CAACATACTGAGATTCAATTAACCGATGAAGGCACTATCCCTTTCATGGAAGAAAGAT	4320
Dd	4261	CAACATACTGAGATTCAATTAACCGATGAAGGCACTATCCCTTTCATGGAAGAAAGAT	4320
Qy	4321	TAGGAGGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACATG	4380
Dd	4321	TAGGAGGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACATG	4380
Qy	4381	TGATGAGCTTGTCTAAACGAGTTAGCTCGAAAGGGAATAACAGCTCTCTCTTACTATAGGG	4440
Dd	4381	TGATGAGCTTGTCTAAACGAGTTAGCTCGAAAGGGAATAACAGCTCTCTCTTACTATAGGG	4440
Qy	4441	ATGTGACATCTCAAAAATCCCTGAGGGGACTGTGTAGTAGTTGCCACTGATGCCCTTGTG	4500
Dd	4441	ATGTGACATCTCAAAAATCCCTGAGGGGACTGTGTAGTAGTTGCCACTGATGCCCTTGTG	4500
Qy	4501	TACAGGCTACACTGCTGACCTTGAATTCGGTGTATGACTGACGAGCTCATGTTAGAGGCAC	4560
Dd	4501	TACAGGCTACACTGCTGACCTTGAATTCGGTGTATGACTGACGAGCTCATGTTAGAGGCAC	4560
Qy	4561	ATGCGATGTTGACCTTCAACCTACTTTTACCATTGGGTTTCGTGTGTGCGGGGTTTACG	4620
Dd	4561	ATGCGATGTTGACCTTCAACCTACTTTTACCATTGGGTTTCGTGTGTGCGGGGTTTACG	4620
Qy	4621	AATAGTTAAAGGCCAGCGTAGGGGCCACAGGCGTGGGAGAGCTGGCATATATACTA	4680
Dd	4621	AATAGTTAAAGGCCAGCGTAGGGGCCACAGGCGTGGGAGAGCTGGCATATATACTA	4680
Qy	4681	TGTAGACGGGAGTTGTACCCCTTCCGGGTATGGTTCTGTAATGCAACATTTGTTGAGCCCT	4740
Dd	4681	TGTAGACGGGAGTTGTACCCCTTCCGGGTATGGTTCTGTAATGCAACATTTGTTGAGCCCT	4740
Qy	4741	CGAGCAGCCAAAGGCATGTTGTTGTCTCATCAACAGAGCTCAAACTATTCTTGGACAC	4800
Dd	4741	CGAGCAGCCAAAGGCATGTTGTTGTCTCATCAACAGAGCTCAAACTATTCTTGGACAC	4800
Qy	4801	CTATCGCAACCAACCTGGGTTTACCTGCGATAGGAGCAAAATTTGGACGAGTGGGCTGATCT	4860

|||||
4801 CTATCGCAACCCAACTGGGTACCTGCGATAGGAGCAAAATTTGGACGAGTGGGCTGATCT 4860
QY |||||
4861 CTTTCTTATGTTCAACCCGACCTTCAATTTGTCATTAAGTCAAAAGAACTGCTGACAA 4920
Db |||||
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QY |||||
4921 TTATGTTTTTGTGACTGACGCCCAACTCAAACTGTGTCAATAGTATGGCTATGCTGCTCC 4980
Db |||||
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QY |||||
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QY |||||
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QY |||||
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QY |||||
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Db |||||
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QY |||||
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QY |||||
5461 CACTTTACCTGCAATCCCTTTGCACTCATGCGTGTGTTGCTTCAATTTGCGGGTATTACTAC 5520
Db |||||
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Db |||||
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QY |||||
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Db |||||

Db |||||
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Db |||||
6001 CCGTTGGCTCCACACCCCGACGGAGGATGATTTGGCGGCTCATTTGCTTGGGGTCTAGAGAT 6060
QY |||||
6061 TTGGCAGTATGCTGCAATTTCTTTGTGATTTGCTTTAATGCTTTAAAGCTGGAGTTCA 6120
Db |||||
6061 TTGGCAGTATGCTGCAATTTCTTTGTGATTTGCTTTAATGCTTTAAAGCTGGAGTTCA 6120
QY |||||
6121 GAGCATGCTTAAACATTCCTGGTGTCTTTCTACAGCTGCCAGAGGGGTACAAGGGGCC 6180
Db |||||
6121 GAGCATGCTTAAACATTCCTGGTGTCTTTCTACAGCTGCCAGAGGGGTACAAGGGGCC 6180
QY |||||
6181 CTGGAATTGGATCAGGTATGCTCCAAAGCACGCTGCTCATGCGGTGCTGAACCTCATCTTTTC 6240
Db |||||
6181 CTGGAATTGGATCAGGTATGCTCCAAAGCACGCTGCTCATGCGGTGCTGAACCTCATCTTTTC 6240
QY |||||
6241 TGTGAGAAATGGTTTGGCAAACTTTTACAAAGGACCCAGAACTTGTTCANAAATTAACGGAG 6300
Db |||||
6241 TGTGAGAAATGGTTTGGCAAACTTTTACAAAGGACCCAGAACTTGTTCANAAATTAACGGAG 6300
QY |||||
6301 AGGGCTGTTCAGTCAACGCTAGGCTGTGTGGGTGCGGTAGACCGGACCCCAACTGATTTG 6360
Db |||||
6301 AGGGCTGTTCAGTCAACGCTAGGCTGTGTGGGTGCGGTAGACCGGACCCCAACTGATTTG 6360
QY |||||
6361 GACTAGTCTTGTGCTCAATTTATGCGGTTAGGAGCTACTGTAAATATGAGAAATTTGGGAGA 6420
Db |||||
6361 GACTAGTCTTGTGCTCAATTTATGCGGTTAGGAGCTACTGTAAATATGAGAAATTTGGGAGA 6420
QY |||||
6421 TCACATTTTGTGTTACAGCAGTATCTCTCCAAATGCTGTTTCCAAATGCTGTTTACCCAGGTCGCCCCCAAC 6480
Db |||||
6421 TCACATTTTGTGTTACAGCAGTATCTCTCTCCAAATGCTGTTTCCAAATGCTGTTTACCCAGGTCGCCCCCAAC 6480
QY |||||
6481 CTTGAGAGCTGCGTGGCGGTGCGGTAGAGGTTACAGGTTTCAAGTGTATCTAGGTGAGCCCA 6540
Db |||||
6481 CTTGAGAGCTGCGTGGCGGTGCGGTAGAGGTTACAGGTTTCAAGTGTATCTAGGTGAGCCCA 6540
QY |||||
6541 AACTCCTTTGGACGACATCTGCTTGTGTTAGCGTCCGACCGGTAAAGGTTAAACTGTTAA 6600
Db |||||
6541 AACTCCTTTGGACGACATCTGCTTGTGTTAGCGTCCGACCGGTAAAGGTTAAACTGTTAA 6600
QY |||||
6601 GCTTCCCTTCCGCTTGAAGGCTCACACCTGCTGCGCATGCAACTTAATTTTCGCTGA 6660
Db |||||
6601 GCTTCCCTTCCGCTTGAAGGCTCACACCTGCTGCGCATGCAACTTAATTTTCGCTGA 6660
QY |||||
6661 TGCACCTTGAGACAAATGACTGTAAATTTCCACAAACAACTCTCTAGTGTAGAGCCGCACT 6720
Db |||||
6661 TGCACCTTGAGACAAATGACTGTAAATTTCCACAAACAACTCTCTAGTGTAGAGCCGCACT 6720
QY |||||
6721 GTCGCTCTTGTGTTTCAAAACAGGAGTTCGCGGTACAAACCAATTTGCTTGAAGCAATTTTC 6780
Db |||||
6721 GTCGCTCTTGTGTTTCAAAACAGGAGTTCGCGGTACAAACCAATTTGCTTGAAGCAATTTTC 6780
QY |||||
6781 AGCTGGGCTTGACACCAACAACTGCGAGCCCTCCATCGAAGAGGTAGTGGTAAGAAA 6840
Db |||||
6781 AGCTGGGCTTGACACCAACAACTGCGAGCCCTCCATCGAAGAGGTAGTGGTAAGAAA 6840
QY |||||
6841 GCGCCAGTTCGCGGCAAGAACTGGTTTCGTTTACCTTGTGCTCCCTCCGAGATCCGTCCTCC 6900
Db |||||
6841 GCGCCAGTTCGCGGCAAGAACTGGTTTCGTTTACCTTGTGCTCCCTCCGAGATCCGTCCTCC 6900
QY |||||
6901 AGGAGTGTCTGTCTGTAAGGCTGCAACGAAAGTGAACCGGTTAGAAAGTCTTCAAACT 6960
Db |||||
6901 AGGAGTGTCTGTCTGTAAGGCTGCAACGAAAGTGAACCGGTTAGAAAGTCTTCAAACT 6960
QY |||||
6961 CCCTCTTTCACCACTGTTTCTACAGTTGGCCATGCGGATGCCCTGTTGGGAGCGGTTGA 7020
Db |||||
6961 CCCTCTTTCACCACTGTTTCTACAGTTGGCCATGCGGATGCCCTGTTGGGAGCGGTTGA 7020


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RESULT 10
AAA55280
ID AAA55280 standard; DNA; 8912 BP.
XX
AC AAA55280;
XX
DT 06-AUG-2003 (revised)
DT 30-AUG-2000 (first entry)
XX
DE Hepatitis GB virus B nucleotide sequence SEQ ID NO:11.
XX
KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
KW detection; characterisation; hepatitis; ss.
XX
OS Hepatitis GB virus.
XX
PN US6051374-A.
XX
PD 18-APR-2000.
XX
PF 07-JUN-1995; 95US-00488445.
XX
PR 14-FEB-1994; 94US-00196030.
PR 13-MAY-1994; 94US-00242654.
PR 29-JUL-1994; 94US-00283314.
PR 23-NOV-1994; 94US-00344185.
PR 23-NOV-1994; 94US-00344190.
PR 30-JAN-1995; 95US-00377557.
XX
PA (ABBO ) ABBOTT LAB.
XX
PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
PI Mushahwar IK, Simons JN, Deesai SM, Erker JC, Schlauder GG;
XX
DR WPI; 2000-338307/29.
XX
PT Detecting target hepatitis GB virus nucleic acid in a test sample
PT suspected of containing HGBV comprises reacting the test sample the HGBV
PT polynucleotide probe and detecting the complex that contains target HGBV.
XX
PS Example 4; Col 131-140; 369pp; English.
XX
The present invention describe a method for detecting target hepatitis GB
virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of
containing HGBV. The method involves reacting (T) with a HGBV
polynucleotide probe (I) containing 15 contiguous nucleotides, and which
selectively hybridises to the HGBV genome or its full complement, and
detecting the complex that contains THN, indicating the presence of
target HGBV. The method is used for detecting target HGBV nucleic acid in
the test sample suspected of containing HGBV and for characterisation of
newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
-E hepatitis causing agents collectively termed as hepatitis GB virus.
CC AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and
CC protein sequences used in the exemplification of the present invention.
XX (Updated on 06-AUG-2003 to correct OS field.)
SQ Sequence 8912 BP; 2019 A; 2169 C; 2265 G; 2400 T; 0 U; 59 Other;

Query Match 92.5%; Score 8692.6; DB 3; Length 8912;
Beat Local Similarity 98.7%; Pred. No. 0;
Matches 8781; Conservative 56; Mismatches 52; Indels 10; Gaps 8;

QY 196 TGGGTTCCGTTGGTGGCGCTTTAGGCGAGCCCTCCACGCCACCCACCTCCAGATAGAGC 255
DB |||||||
DB 11 TGGGTTCCGTTGGTGGCGCTTTAGGCGAGCCCTCCACGCCACCCACCTCCAGATAGAGC 70
QY 256 GCGCGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACGAGACCTCTTTTGA 315
DB |||||||
DB 71 GCGCGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACGAGACCTCTTTTGA 130
QY 316 GTATCAGCGCTCCGGAAGTAGTTGGGCAAGCCACTATATGTGTGGGATGTTGGGT 375
DB |||||||
DB 131 GTATCAGCGCTCCGGAAGTAGTTGGGCAAGCCACTATATGTGTGGGATGTTGGGT 190
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QY 376 TAGCATCCATACCGTACTGCTGATAGGGTCCCTTGCGAGGGGATCTCGGAGTCTCGTAG 435
DB |||||||
DB 191 TAGCATCCATACCGTACTGCTGATAGGGTCCCTTGCGAGGGGATCTCGGAGTCTCGTAG 250
QY 436 ACCGTAGCATGCTGCTGTTATTTCTACTCAAAACAAGTCTGTACTGTGCGCCGAGAACGG 495
DB |||||||
DB 251 ACCGTAGCATGCTGCTGTTATTTCTACTCAAAACAAGTCTGTACTGTGCGCCGAGAACGG 310
QY 496 CAAGAACAGCAGACGCGAGGCTTCATATCTGTGTCCATTAAACATCTGTGTGAAGGG 555
DB |||||||
DB 311 CAAGAACAGCAGACGCGAGGCTTCATATCTGTGTCCATTAAACATCTGTGTGAAGGG 370
QY 556 ACAAGGAGCAAGCGCAAGTCCAGCGGATGCTCGGCTCGTAAATTAACAAATTCGCTGG 615
DB |||||||
DB 371 ACAAGGAGCAAGCGCAAGTCCAGCGGATGCTCGGCTCGTAAATTAACAAATTCGCTGG 430
QY 616 TATCATGATGCTTGCAGACATTTGGCTCAGGCTGCTTTCAGCTCATGTGTGGGACG 675
DB |||||||
DB 431 TATCATGATGCTTGCAGACATTTGGCTCAGGCTGCTTTRCAGCTCATGTGTGGGACG 490
QY 676 CCAAGACCTCGCATAGTCTCGCAATCTTGGAACTCTTCTGGATTACCTTTGGGGTG 735
DB |||||||
DB 491 CCAAGACCTCGCATAGTCTCGCAATCTTGGAACTCTTCTGGATTACCTTTGGGGTG 550
QY 736 GATTGGTGTATGTTAACTCACAACCTCTAGTAGGCCCGCTGGTGGCAGGACGGTGGT 795
DB |||||||
DB 551 GATTGGTGTATGTTAACTCACAACCTCTAGTAGGCCCGCTGGTGGCAGGACGGTGGT 610
QY 796 TCGACAGTCTGCGAGATAGTACGCTTGTCTCGAGATGGAGTCAACTGGGCTACTGGTTG 855
DB |||||||
DB 611 TCGACAGTCTGCGAGATAGTACGCTTGTCTCGAGATGGAGTCAACTGGGCTACTGGTTG 670
QY 856 GTTCGGTGTCCACCTTTTGGTATGCTGCTATCTTTGGCCTGCTCCTGTAGTGGGGC 915
DB |||||||
DB 671 GTTCGGTGTCCACCTTTTGGTATGCTGCTATCTTTGGCCTGCTCCTGTAGTGGGGC 730
QY 916 CGGGTCACTGACCCAGACACAAATACCAATCTGACCAATTTGCTGCCACGCGTAATCA 975
DB |||||||
DB 731 CGGGTCACTGACCCAGACACAAATACCAATCTGACCAATTTGCTGCCACGCGTAATCA 790
QY 976 GGTATATCTATTTGTTCTCCTCACTACAGAGCTGGTGTGTGTGATCTGTCGGA 1035
DB |||||||
DB 791 GGTATATCTATTTGTTCTCCTCACTACAGAGCTGGTGTGTGTGATCTGTCGGA 850
QY 1036 CGAGTGTGGGTTCCCGCAATCGGTACATCTCACACCTTCCAATTCGATTCGACCGCA 1095
DB |||||||
DB 851 CGAGTGTGGGTTCCCGCAATCGGTACATCTCACACCTTCCAATTCGATTCGACCGCA 910
QY 1096 CTCTTCTTGGTCAACCAATTTGTTTATGGGCGCTCTTGTGACCTGTGACGCGCT 1155
DB |||||||
DB 911 CTCTTCTTGGTCAACCAATTTGTTTATGGGCGCTCTTGTGACCTGTGACGCGCT 970
QY 1156 TGACATTCGTTGAGTGTGTGTGTGTGTATAGTCCGTTGATGCTGGTGTGTCAGGACTG 1215
DB |||||||
DB 971 TGACATTCGTTGAGTGTGTGTGTGTATAGTCCGTTGATGCTGGCTGTGTCAGGACTG 1030
QY 1216 GCTTATTCATAGACCTCAATGAACTGGTACTTGTACTTGGAGTGGCCACTGGAA 1275
DB |||||||
DB 1031 GCTTATTCATAGACCTCAATGAACTGGTACTTGTACTTGGAGTGGCCACTGGAA 1090
QY 1276 AGATCCTGGGTTCTTAGGGTTTATCGGGTGGATGGCCGCAAGGTCGAGGGCTGTCTATCT 1335
DB |||||||
DB 1091 AGATCCTGGGTTCTTAGGGTTTATCGGGTGGATGGCCGCAAGGTCGAGGGCTGTCTATCT 1150
QY 1336 CTTGACCAAACTGGCTTCAAGTACCATAGCGTATTCGACTATGTTTAGCAGTGTACA 1395
DB |||||||
DB 1151 CTTGACCAAACTGGCTTCAAGTACCATAGCGTATTCGACTATGTTTAGCAGTGTACA 1210
QY 1396 CTACTCGGGGTTGGCGCTCTGATCTACTATGCCCTCTCGGGCAAGTGGTATCAGTGTCT 1455
DB |||||||
DB 1211 CTACTCGGGGTTGGCGCTCTGATCTACTATAGCCCTCTCGGGCAAGTGGTATCAGTGTCT 1270
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QY 1456 CCTAGCGCTTATGCTTTACATAGAAAGCAACCTCTGGAAACCCCATCAGGGTGCCCACTGG 1515
Db CCTAGCGCTTATGCTTTACATAGAAAGCAACCTCTGGAAACCCCATCAGGGTGCCCACTGG 1330
QY 1516 ATGCTCAATAGCTAGTGTTCCTCGCCCTTTCATGATACCAATGCTCTTGCACACTCTTATTT 1575
Db ATGCTCAATAGCTAGTGTTCCTCGCCCTTTCATGATACCAATGCTCTTGCACACTCTTATTT 1390
QY 1576 GAGTGAGAAATGTGTCAGAAAGTCATTGTTTACAGTCCAAAGTGGACAGGCCCTATCACTCT 1635
Db GAGTGAGAAATGTGTCAGAAAGTCATTGTTTACAGTCCAAAGTGGACAGGCCCTATCACTCT 1450
QY 1636 AGAGTATAAACAACTCATCTTGTGTACCCCTATACAAATCCCTGGTGGAGGGAGTGTAT 1695
Db AGAGTATAAACAACTCATCTTGTGTACCCCTATACAAATCCCTGGTGGAGGGAGTGTAT 1510
QY 1696 GGTAAATTTCAAATAACACATGGGGTGTGCGGTATTCGCAATTCGCAATGCGCATGCTACTG 1755
Db GGTAAATTTCAAATAACACATGGGGTGTGCGGTATTCGCAATTCGCAATGCGCATGCTACTG 1569
QY 1756 CACTATGGGCACTGATGCAGTGTGGAAACGACATCGCAACACTTACGAAGCATGCGGTGT 1815
Db CACTATGGGCACTGATGCAGTGTGGAAACGATCGCAACACTTACGAAGCATGCGGTGT 1629
QY 1816 AACACCATGGCTAACACCGCATGGCAACACGGCTCAGCCCTGAAATTTGGCTATATTACA 1875
Db AACACCATGGCTAACACCGCATGGCAACACGGCTCAGCCCTGAAATTTGGCTATATTACA 1689
QY 1876 ATACCTGGGTCTAAAGAAATGTTTAAACCTCATAAATTTGGATGTCAGGCCATTTGTATTT 1935
Db ATACCTGGGTCTAAAGAAATGTTTAAACCTCATAAATTTGGATGTCAGGCCATTTGTATTT 1749
QY 1936 TGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAATTCACCTCCTTACC 1995
Db TGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAATTCACCTCCTTACC 1809
QY 1996 ACCGAGAGTGGGTAGGTTGCCGGTACCCCACTGTGTGTACGTGTCTTGTGTTTACA 2055
Db ACCGAGAGTGGGTAGGTTGCCGGTACCCCACTGTGTGTACGTGTCTTGTGTTTACA 1869
QY 2056 GGTTCGCAAGGGTTTTACGTGATGTGAAGACCTAGCCACAGATGATCACCAGA 2115
Db GGTTCGCAAGGGTTTTACGTGATGTGAAGACCTAGCCACAGATGATCACCAGA 1928
QY 2116 CAAGCCCTGGAAAAATATCAGGTCTTATATTTCCGCAACGGGTGCTTTGTCTTACGGG 2175
Db CAAGCCCTGGAAAAATATCAGYCTTATATTTCCGCAACGGGTGCTTTGTCTTACGGG 1988
QY 2176 AGTTACCAACAGGCCGTGGTCTAAATCTGTGGGGTTGTGTGGCAGCAAGTATCTTAT 2235
Db AGTTACCAACAGGCCGTGGTCTAAATCTGTGGGGTTGTGTGGCAGCAAGTATCTTAT 2048
QY 2236 TTTAGCCTACCTGTGTTACTTGTCCCTTTGTTGGGCGCGCTTCTGGTTACCCCTTTCG 2295
Db TTTAGCCTACCTGTGTTACTTGTCCCTTTGTTGGGCGCGCTTCTGGTTACCCCTTTCG 2108
QY 2296 TCCTGTGCTCCCATCCAGTCTGTCTCAAGCTGGCTGGGATGTTTTGTCTAAAGCTCA 2355
Db TCCTGTGCTCCCATCCAGTCTGTCTCAAGCTGGCTGGGATGTTTTGTCTAAAGCTCA 2168
QY 2356 AGTAGCTCTTTTGTGATTTTCTCATCTGTTGTATCTCCGCTGCAGGCTACGTTA 2415
Db AGTAGCTCTTTTGTGATTTTCTCATCTGTTGTATCTCCGCTGCAGGCTACGTTA 2228
QY 2416 TGCTGCCCTTTTAGGGTTTGGCCATGGCTGCGGGCTTGGCCCTTAACCTTTCTTTGTTC 2475
Db TGCTGCCCTTTTAGGGTTTGGCCATGGCTGCGGGCTTGGCCCTTAACCTTTCTTTGTTC 2288
QY 2476 AGCAGCTCTGCCAAACAGATTTATGACTGTGGGTGGACTGTGTAGTGGCAGGGTGTAGT 2535
Db AGCAGCTCTGCCAAACAGATTTATGACTGTGGGTGGCACTGTGTAGTGGCAGGGTGTAGT 2348
QY 2536 TTTGTGGGCGGCCGTAAACCGTGGTACCCGATAGCTCTGCTTGTGTAGGTCTCTGGCCTCT 2595

Db 2349 TTTGTGGGCGGCCGTACCCGTGTGTCACGATAGCTCTGCTTGTAGGTCTCTTGGCCCTCT 2407
QY 2596 GGTAGCCCTTTTAAACCTCTTTCATTTGGTTAGCCTGCTTACGCTTTTTCATACCCGAGA 2654
Db GGTAGCCCTTTTAAACCTCTTTCATTTSTKACGCCCTGCTT-AGCTTTTGCACCCGAGA 2466
QY 2655 TAAATTGAGGGCTGCAATAACCACTGTAGTACATTTAGTTGTTCATGTCCTGTTTGGCT 2714
Db TAAATTGAGGGCTGCAATAACCACTGTAGTACATTTAGTTGTTCATGTCCTGTTTGGCT 2526
QY 2715 TCTTTGCTCACTTGTTCCTCGCTGCTTTAGTTTAACTCTATCTTTTGGCAAGTTCGG 2774
Db TCTTTGCTCACTTGTTCCTCGCTGCTTTAGTTTAACTCTATCTTTTGGCAAGTTCGG 2586
QY 2775 AGAATTGGTTTGGAAAGTTACATAAGACCGGAGAGGTTTTTCTTGTGCTGGTTTCTT 2834
Db AGAATTGGTTTGGAAAGTTACATAAGACCGGAGAGGTTTTCTCTTGTGCTGGTTTCTT 2646
QY 2835 TCCCGGTGGCAATATGACGCGCTGTGACTTTTCTGTGTGTGTCACTAGCTCTTCTAT 2894
Db TCCCGGTGGCAATATGACGCTGTGCTGTGACTTTTCTGTGTGTGTCACTAGCTCTTCTAT 2706
QY 2895 GTTTAAACATCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGTTAGGGCCCATAGAA 2954
Db GTTTAAACATCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGTTAGGGCCCATAGAA 2766
QY 2955 TGTGTGTGCTCTCGGAAAGTGTCACTGCTGGTATTTCTCATATGTTCTTAAAGTTTTTCC 3014
Db TGTGTGTGCTCTCGGAAAGTGTCACTGCTGGTATTTCTCATATGTTCTTAAAGTTTTTCC 2826
QY 3015 TCTTGTGTTTGGTGTGAGATGGTGTGTTTTCTATAAGCACTTGCATGGTGTATGCTTTC 3074
Db TCTTGTGTTTGGTGTGAGATGGTGTGTTTTCTATAAGCACTTGCATGGTGTATGCTTTC 2886
QY 3075 CTAATGATTTTGCCTCGAAACTACCATTTGCAAGAGCCATTTTCCCTTTTGAAGCAAGG 3134
Db CTAATGATTTTGCCTCGAAACTACCATTTGCAAGAGCCATTTTCCCTTTTGAAGCAAGG 2946
QY 3135 CAAGGGTCTATAGGAATGAAAGAGACGCTTGGGCTGTGGGACACGGTTGATGTTTTC 3194
Db CAAGGGTCTATAGGAATGAAAGAGACGCTTGGGCTGTGGGACACGGTTGATGTTTTC 3006
QY 3195 CCGTTGTGCGCTCTCGGCGACCTTGTGTTTTCGAGGGTTGGCTATGCGCCAGATGGT 3254
Db CCGTTGTGCGCTCTCGGCGACCTTGTGTTTTCGAGGGTTAGCTATGCGCCAGATGGT 3066
QY 3255 GGGCCATTAACGCACTTTTACGCTGAGTGTCTCTGAAAGCTGGCAAGCTGTGAGCGA 3314
Db GGGCCATTAACGCACTTTTACGCTGAGTGTCTCTGAAAGCTGGCAAGCTGTGAGCGA 3126
QY 3315 TGGCAGTGGTCACTGCTGATAGACCCCGAAGCTTGGAGCTTGGAACTATCTTTCAGATTAG 3374
Db TGGCAGTGGTCACTGCTGATAGACCCCGAAGCTTGGAGCTTGGAACTATCTTTCAGATTAG 3186
QY 3375 GATCTCTGGCCACTAGCTACATGGGATTTGTTGTGCAACGTTGTATATCTGCTACC 3434
Db GATCTCTGGCCACTAGCTACATGGGATTTGTTGTGCAACGTTGTATATCTGCTACC 3246
QY 3435 ATGGCAGAAAGGGCGCGGTGGCTCATCCACAGGCTCTATACACCAATTAACCGTTG 3494
Db ATGGCAGAAAGGGCGCGGTGGCTCATCCACAGGCTCTATACACCAATTAACCGTTG 3306
QY 3495 ACGGGCTAATGACAGGACATCTATCAACACCATGTGGAGCTGGGTCCCTTACTCCGT 3554
Db ACGGGCTAATGACAGGACATCTATCAACACCATGTGGAGCTGGGTCCCTTACTCCGT 3366
QY 3555 GCTCTTGGGGGAGACCAAGGGGTATCTGTGTAAACACGCTGGGGTCAITGGTTGAGGTCA 3614
Db GCTCTTGGGGGAGACCAAGGGGTATCTGTGTAAACACGCTGGGGTCAITGGTTGAGGTCA 3426
QY 3615 ACAATTCGATGACCTTATTTGTGTGTGGGGGCGCTTCCCATGGCTGTGCGCAAGG 3674

Db 3427 ACAATCCGATGACCCCTATTATGGTGTGTGTGCGGGCCCTTCCCATGGCTGTGTGCCAAGG 3486
Qy 3675 GTTCTTCAAGTGCCCGGATCTCTGCTCCTCCGCGCATGTATTATGGGATGTTTCAACCGCTG 3734
Db 3487 GTTCTTCAAGTGCCCGGATCTCTGCTCCTCCGCGCATGTATTATGGGATGTTTCAACCGCTG 3546
Qy 3735 CTAGAAATTTCTGGCGGTTCAAGTCAGTCAGATPAGGTTAGGCGGTTAGGCTGTGTGTCTGGAT 3794
Db 3547 CTAGAAATTTCTGGCGGTTCAAGTCAGTCAGTCAGATPAGGTTAGGCGGTTAGGCTGTGTGTCTGGAT 3606
Qy 3795 ACCATCCCAGTACACAGCAGATGCGACTCTCTGTGATACAAAACCTACTGTGCTCAAGAGT 3854
Db 3607 ACCATCCCAGTACACAGCAGATGCGACTCTCTGTGATACAAAACCTACTGTGCTCAAGAGT 3666
Qy 3855 ATTCAAGTCGAAATTTTAAATTTGCCCCCAGCTGGCAGCGCGCAAGTCAACCAAAATPACCACTTT 3914
Db 3667 ATTCAAGTCGAAATTTTAAATTTGCCCCCAGCTGGCAGCGCGCAAGTCAACCAAAATPACCACTTT 3726
Qy 3915 CTTACATCGAGGAGATGATGAGTCTTGGTCTTAAATCCCAAGTGTGCTACAAACAGAT 3974
Db 3727 CTTACATCGAGGAGATGATGAGTCTTGGTCTTAAATCCCAAGTGTGCTACAAACAGAT 3786
Qy 3975 CAATGCCAAAGTACATGACCGCAGCTAGCGGCTGAATCCCAAAATGCTATTATTAATGGA 4034
Db 3787 CAATGCCAAAGTACATGACCGCAGCTAGCGGCTGAATCCCAAAATGCTATTATTAATGGA 3846
Qy 4035 AATGTACCACACACAGGGGCTTCACCTTACGTACAGCACATATGGCATGTACCTGACCGGAG 4094
Db 3847 AATGTACCACACACAGGGGCTTCACCTTACGTACAGCACATATGGCATGTACCTGACCGGAG 3906
Qy 4095 CATGTTCCCGGAACTATGATGTAATCATTTGTGACGAATGCCATGCTACCGATGCAACCA 4154
Db 3907 CATGTTCCCGGAACTATGATGTAATCATTTGTGACGAATGCCATGCTACCGATGCAACCA 3966
Qy 4155 CGGTGTTGGGCATTTGGAAAGTCTTAACCGAAGCTCCATCCGAAATGTTAGGCTAGTGG 4214
Db 3967 CGGTGTTGGGCATTTGGAAAGTCTTAACCGAAGCTCCATCCGAAATGTTAGGCTAGTGG 4026
Qy 4215 TTCTTGCCACAGGCTACCCCGCTGGAGTAATCCCTACACCAATGCCAATCAACTGAGA 4274
Db 4027 TTCTTGCCACAGGCTACCCCGCTGGAGTAATCCCTACACCAATGCCAATCAACTGAGA 4086
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Db 4087 TTCAATTAACCGATGAAGGCACTATCCCTTTTATGAAAAAAGATTAAGGAGGAAAAATC 4146
Qy 4335 TGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACATGTGATGAGCTTGCTA 4394
Db 4147 TGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACATGTGATGAGCTTGCTA 4206
Qy 4395 ACGAGTTAGTTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGGATGTGACATCTCAA 4454
Db 4207 ACGAGTTAGTTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGGATGTGACATCTCAA 4266
Qy 4455 AAATCCCTGAGGGCGACTGTGTAGTAGTTGGCACTGATGCTCTTGTGTACAGGGTACACTG 4514
Db 4267 AAATCCCTGAGGGCGACTGTGTAGTAGTTGGCACTGATGCTCTTGTGTACAGGGTACACTG 4326
Qy 4515 GTGACTTTGATTCGGTGTATGACTGAGGCTCATGGTAGAAGGCACATGCCATGTTGACC 4574
Db 4327 GTGACTTTGATTCGGTGTATGACTGAGGCTCATGGTAGAAGGCACATGCCATGTTGACC 4386
Qy 4575 TTGACCCCTACTTTACCATGGGTGTGTGTGTGCGGGGTTTTCAGCAATAGTTTAAAGGCC 4634
Db 4387 TTGACCCCTACTTTACCATGGGTGTGTGTGTGCGGGGTTTTCAGCAATAGTTTAAAGGCC 4446
Qy 4635 AGCGTAGGGGCGGCACAGCCGCTGGGAGAGCTGGCATATACTACTATGTAGACGGGAGTT 4694
Db 4447 AGCGTAGGGGCGGCACAGCCGCTGGGAGAGCTGGCATATACTACTATGTAGACGGGAGTT 4506
Qy 4695 GTACCCCTTCGGGTATGGTTCCTGTAATGCCAAATTTGTAAGCCCTTCGACGAGCCAAAGG 4754
Db 4507 GTACCCCTTCGGGTATGGTTCCTGTAATGCCAAATTTGTAAGCCCTTCGACGAGCCAAAGG 4566

Qy 4755 CATGATATGGTTTGTTCATCAACAGAGCTCAAACCTATTCTCGACACCTTATCGCAACCCAAC 4814
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Qy 4815 CTGGGTTACCTTCGATAGGAGCAAAATTTGGACGAGTGGGCTGATCTCTTTCTATATGGTCA 4874
Db 4627 CTGGGTTACCTTCGATAGGAGCAAAATTTGGACGAGTGGGCTGATCTCTTTCTATATGGTCA 4686
Qy 4875 ACCCGAACCTTTCAATTTGTCAATACTGCAAAAGAACCTGTGACAAATATGTTTTGTTGA 4934
Db 4687 ACCCGAACCTTTCAATTTGTCAATACTGCAAAAGAACCTGTGACAAATATGTTTTGTTGA 4746
Qy 4935 CTGACAGCCCAACTCAACTGTGTCTCATCATGATATGGCTATGCTCTCCCAATGACGACCAAC 4994
Db 4747 CTGACAGCCCAACTCAACTGTGTCTCATCATGATATGGCTATGCTCTCCCAATGACGACCAAC 4806
Qy 4995 GGTGGCAGGAGCCCGGCTTGGGAAAAAAACCTTTGTGGGGTCTGTGGGCTTGGAGCGGG 5054
Db 4807 GGTGGCAGGAGCCCGGCTTGGGAAAAAAACCTTTGTGGGGTCTGTGGGCTTGGAGCGGCT 4866
Qy 5055 CTGACGCTGTCTGGGCCAGAGCCCGAGAGTGACAGATACCAAAATGTCTTCACTG 5114
Db 4867 GTGACGCTGTCTGGGCCAGAGCCCGAGAGTGACAGATACCAAAATGTCTTCACTG 4926
Qy 5115 AAGTCAATACTTCTGGGACAGCCGCACTCGCTGTGTGGGCTTGGAGTGGCTATGGCTTATC 5174
Db 4927 AAGTCAATACTTCTGGGACAGCCGCACTCGCTGTGTGGGCTTGGAGTGGCTATGGCTTATC 4986
Qy 5175 TAGCCATTGACACTTTTGGCGCCACTTGTGTGGCGGCTTGTGTCTATATTACATCAGTCC 5234
Db 4987 TAGCCATTGACACTTTTGGCGCCACTTGTGTGGCGGCTTGTGTCTATATTACATCAGTCC 5046
Qy 5235 CTACGGGTCTACTGTGCGCCAGTGTGTGACGAAGAAGAAATCGTGAGGAGTGTGAT 5294
Db 5047 CTACGGGTCTACTGTGCGCCAGTGTGTGACGAAGAAGAAATCGTGAGGAGTGTGAT 5106
Qy 5295 CATTCATTTCCCTTGAGGCGCATGTTGTGCAATTTGACAAGCTGAAGAGTACAATCACC 5354
Db 5107 CATTCATTTCCCTTGAGGCGCATGTTGTGCAATTTGACAAGCTGAAGAGTACAATCACC 5166
Qy 5355 CAACATGCTCTTTTACATGGAACCCGCCCTTGAAAAAATTAACACCTTTCTTGGGCGCTC 5414
Db 5167 CAACATGCTCTTTTACATGGAACCCGCCCTTGAAAAAATTAACACCTTTCTTGGGCGCTC 5226
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Qy 5595 GAGGCGCATGCGGCTTCAATGATGCGCGGCTGCGGGAACAGCTCTTGTGATCATGAGAT 5654
Db 5407 GAGGCGCATGCGGCTTCAATGATGCGCGGCTGCGGGAACAGCTCTTGTGATCATGAGAT 5466
Qy 5655 CGGTGGGTTTTGTCTTTTGACATGCTTAGGCGGCTATGCTGCGCGCTCATCCACTGCTTGTCT 5714
Db 5467 CGGTGGGTTTTGTCTTTTGACATGCTTAGGCGGCTATGCTGCGCGCTCATCCACTGCTTGTCT 5526
Qy 5715 TGACATTTAAATGCTGTGATGGGTGAGTGGCCCACTATATGGATCAGCTTGTGCTGTTAGTCT 5774
Db 5527 TGACATTTAAATGCTGTGATGGGTGAGTGGCCCACTATATGGATCAGCTTGTGCTGTTAGTCT 5586
Qy 5775 ACTCCGCTTCAATCCGCGCGCAGAGTTGTGGGCGTCTTGTACGCTTGTGCAATGTTTGG 5834
Db 5587 ACTCCGCTTCAATCCGCGCGCAGAGTTGTGGGCGTCTTGTACGCTTGTGCAATGTTTGG 5646

QY 5835 CTTTGAACAAGCGGCCAGATCACTGGGCCAAACAGACTTCTTACTATGCTTCTAGGA 5894
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QY 5895 GCAACACTGATGTAATGAGTACTTTATTTGCCACTCGTGACATCGCGAGGAGTACTGG 5954
DB GCAACACTGATGTAATGAGTACTTTATTTGCCACTCGTGACATCGCGAGGAGTACTGG 5766
QY 5955 GCATTTCTGGAGGCATCTACCCCTCGGAGTGTCTATATCAGCTTGCATCCGTTGGCTCCACA 6014
DB GCATTTCTGGAGGCATCTACCCCTCGGAGTGTCTATATCAGCTTGCATCCGTTGGCTCCACA 5826
QY 6015 CCCGACGGAGGATGATTTGGGCGCTCATTTGCTGGGCTCTAGAGATTTGGCAGTATGTT 6074
DB CCCGACGGAGGATGATTTGGGCGCTCATTTGCTGGGCTCTAGAGATTTGGCAGTATGTT 5886
QY 6075 GCAATTTCTTTGCTGATTTGCTTTTAAATGCTTAAAGCTGGAGTTTCAGAGCATGTTAAACA 6134
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QY 6135 TTCCTGGTGTCTTCTACAGCTGCCAGAAAGGGGTACAAAGGCGCCCTTGGATTTGGATCAG 6194
DB TTCCTGGTGTCTTCTACAGCTGCCAGAAAGGGGTACAAAGGCGCCCTTGGATTTGGATCAG 6006
QY 6195 GTATGCTTCAAAGCAGCTGTCCATCGGTGCTGAACCTCATCTTTCTGTTGAGAAATGTT 6254
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QY 6255 TTGCANAACCTTTACAAAGGACCCAGACTTGTTCANAATTACTGAGAGGGGCTGTTCCAG 6314
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QY 6315 TCAACGCTTAGGCTGTGTGGGTGCGGTAGACCGGACCCCAACTGATTTGGAAGTCTGTTCG 6374
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QY 6375 TCAATTAATGCGGTAGGACCTACTGTAAATATGAGAAATGGGAGATCACATTTTGTGTA 6434
DB TCAATTAATGCGGTAGGACCTACTGTAAATATGAGAAATGGGAGATCACATTTTGTGTA 6246
QY 6435 CAGCAGTATCTCTCCAAATGCTGTGTTTACCCAGGTGCCCCCAACTTTGAGAGCTGCG 6494
DB CAGCAGTATCTCTCCAAATGCTGTGTTTACCCAGGTGCCCCCAACTTTGAGAGCTGCG 6306
QY 6495 TGGCGGTGAGCGGCTACAGGTTTCAAGTGTATCTAGGTGAGCCCAAACTCTTTGGACGA 6554
DB TGGCGGTGAGCGGCTACAGGTTTCAAGTGTATCTAGGTGAGCCCAAACTCTTTGGACGA 6366
QY 6555 CATCTGCTTGTGTTACGGTCTGACCGGTAAAGGTAAAACTGTTTAAAGCTTCCCTTCCGCG 6614
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QY 6615 TTGAGCGGTACACACCTGGTGGCGATGCAACTTAATTTTGGGTGATGCACTTGAGACNA 6674
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QY 6675 ATGACTGTAAATTCACAAAACAACTCTCTAGTGTATGAAAGCGCAGTGTCCGCTCTTGT 6734
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QY 6735 TCAAAAGGAGTTGGCGGTACAAACCAATTTGCTTGAAGGCAATTTACAGTGGCGTTGACA 6794
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QY 6795 CCACCAACTGCGACCCCTCC---ATCGAAGAGGTAGTGGTAAGAAAGCGCAGTTCC 6851
DB CCACCAACTGCGACCCCTCC---ATCGAAGAGGTAGTGGTAAGAAAGCGCAGTTCC 6666
QY 6852 GGGCAAGAACTGGTTTGGCTTACCTTGGCTCCCGCTCCGAGATCCGTTCCAGAGGTGTCAT 6911
DB GGGCAAGAACTGGTTTGGCTTACCTTGGCTCCCGCTCCGAGATCCGTTCCAGAGGTGTCAT 6726
QY 6912 GTCCTGAAAGCCTGCAACGAAAGTGACCCGTTTGAAGGTCCTTCAAACCTCCCTCCTTCCAC 6971

DB 6727 GTCCTGAAAGCCTGCAACGAAAGTGACCCGTTAGAAGGTCCTTCAAMCCTCCTCTTCCAC 6786
QY 6972 CACCTGTTTACAGTTTGGCCATGCCGATGCCCTGTTGGAGCGGTGAGTGAACCCCTT 7031
DB CACCTGTTTACAGTTTGGCCATGCCGATGCCCTGTTGGAGCGAGTGAAGTGAACCCCTT 6846
QY 7032 TCACTGCAATTGGATGTGCAATGACCGAAACAGCGGAGGCCCTTGATGATTTTACCCAGTT 7091
DB TCACTGCAATTGGATGTGCAATGACCGAAACAGCGGAGGCCCTTGATGATTTTACCCAGTT 6906
QY 7092 ACCCTCCAAAAGAGGAGTCTCTGAATGCTCAGACGAAAGTTGGTCCAGCGCTACACCG 7151
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QY 7152 CTTCCAGCTAGTGTACTGGGCCCCCGCTACCTTAAGATACGGGGAAAGGATTTCCACTCAGT 7211
DB CTTCCAGCTAGTGTACTGGGCCCCCGCTACCTTAAGATACGGGGAAAGGATTTCCACTCAGT 7026
QY 7212 CAGCCCCCGCAACCGCCTACAAAAGAGTTGGAAAGAGTGAGTTTCTGTCGACGA 7271
DB CAGCCACCGCAACCGCCTACAAAAGAGTTGGAAAGAGTGAGTTTCTGTCGTCGACGA 7086
QY 7272 TGAGCTACACTGAGACCGAGTGTATTAGCTTCAAACCTGCTTCTAAAGTTCTGTCGCA 7331
DB TGAGCTACACTGAGACCGAGTGTATTAGCTTCAAACCTGCTTCTAAAGTTCTGTCGCA 7146
QY 7332 CTCGGGCGATCAGTGTGTTTCTCTCAACCAAGATCAATTGGTGTATGTCAGTCAGCGCG 7391
DB CTCGGGCGATCAGTGTGTTTCTCTCAACCAAGATCAATTGGTGTATGTCAGTCAGCGCG 7206
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DB GGGATGCGGAGCTTTAGAAAAACAAAAGTCACTATTATAGACAACTCTGTTTCCCCCAT 7266
QY 7452 CATACCAACAGCAAGTGAGATTGCTAAGGAAAAAGCTTCAAAGTTGTGCGGTGTCATGT 7511
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QY 7572 GCCTTCGGGCGACTGATGTTCTGTTCTGGAGCAGCCCGCAAGGCTGTTCTGGAATTCGACA 7631
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QY 7692 AGGAGGTCTTCTGTAAGACCCCGCAGAAACCAACAAAGAAACCCCAAGGCTTATCTCGT 7751
DB AGGAGGTCTTCTGTAAGACCCCGCAGAAACCAACAAAGAAACCCCAAGGCTTATCTCGT 7566
QY 7752 ACCCCACCTTGAATGAGATGTTTGGAGAGATGTACTACGGTCAGGTCAGTCTCCTGACG 7811
DB ACCCCACCTTGAATGAGATGTTTGGAGAGATGTACTACGGTCAGGTCAGTCTCCTGACG 7626
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QY 7872 GTCCTGTTGTGATGTCGCTCAGTCAGTCAGTCGAGCCACATGCGATACAGTGTGTTTGT 7931
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QY 7932 ACAGTACCATCACACCCGAGGATATCATGTGGAGACAGACATCTACTCAGCAGCTAAAC 7991
DB ACAGTACCATCACACCCGAGGATATCATGTGGAGACAGACATCTACTCAGCAGCTAAAC 7806
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Db 7807 TCAGTGACCAACCGAGCTGGCATTACACCAATTCGAGGCGAGTATCACGCTGGAGGAC 7866
Qy 8052 CGATGATCGCTTATGATCGCGAGAGATCGGATATCGTAGGTGTAGGCTTCCTCCGCGCTCT 8111
Db 7867 CGATGATCGCTTATGATCGCGAGAGATCGGATATCGTAGGTGTAGGCTTCCTCCGCGCTCT 7926
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Db 7927 ATACTACCTCAAGTTCCAAAGTTTTCGACCTGCTGGCTGAAGGTAAATGCTGCAGCCGAAC 7986
Qy 8172 AGGCTGGGATGAAGAACCTTCCTCTTATTTGGGGGATGATTCGACCGTAATTTGGA 8231
Db 7987 AGGCTGGGATGAAGAACCTTCCTCTTATTTGGGGGATGATTCGACCGTAATTTGGA 8046
Qy 8232 AGAGCGCGGAGCAGATGACAGAAACAAAGCAATCGCTGCTTTCCTAGCTAGCTGATGAAGG 8291
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Qy 8412 CAAGAGATCCTCGTATCCCTTGGCAGGTGCTCTGCCGAGGCTCTGGGATACAAACCCCA 8471
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Qy 8472 GTGCTCGCTGGATTTGGGTATCTAATACATCACTACCCATGTTTGTGGTGTAGCCGTGTGT 8531
Db 8287 GKGCKGCTGGATTTGGGTATCTAATACATCACTACCCATGTTTGTGGTGTAGCCGTGTGT 8346
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Db 8407 TTGACTGTGTGGGAAAATATACGCTGCTGTAGAGATCTGCCAGACTCATTTGCTG 8466
Qy 8652 GTGTGACGGTATTAGGCTTTCTCGGTGGTGGCTACACCAAGCTGAGATCTCTCAGAG 8711
Db 8467 GTGTGACGGTATTAGGCTTTCTCGGTGGTGGCTACACCAAGCTGAGATCTCTCAGAG 8526
Qy 8712 TTTCCCAATCACTACAGACATGACATGCCCTTGGAGCCTTGGGAGGAAAGAGCA 8771
Db 8527 TTTCCCAATCACTACAGACATGACATGCCCTTGGAGCCTTGGGAGGAAAGAGCA 8586
Qy 8772 GGGCGGTCTCGCCAGCGCAAGAGCGTGGCGGAGCACACGCAAAATTTGGCTCGCTTCC 8831
Db 8587 GGGCGGTCTCGCCAGCGCAAGAGCGTGGCGGAGCACACG -AAATTTGGCTCGCTTCC 8645
Qy 8832 TTCTCTGCGATGCTACATCTAGACCTCTACACAGATTTGGATAAGACGAGCGTGGCTCGGT 8891
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Db 8706 ACACCACTTCAATTTATGTGATGTTTACT -CCCSGAGGGGATGTTTATTATACACAC 8764
Qy 8952 AGAGAAGATTGAGAAAGTTCTTTGTAAGTATTTGGCTGCTCAATTTTGGCTTAGGCG 9011
Db 8765 AGAGAAGATTGAGAAAGTTTCTTTGTAAGTATTTGGCTGCTCAATTTTGGCTTAGGCG 8824
Qy 9012 TCATTGCTGTTGGATTAGCCATCAGCTGAACCCCAAAATTCAAAATTAACACAGTTTT 9071
Db 8825 TCATTGCTGTTGGACTAGCCATCAGCTGAACCCCAAAATTCAAAATTAACACAGTTTT 8884
Qy 9072 TTTTTTTTTTTTTTTTTTT 9090
Db 8885 TTTTTTTTTTTTTTTTTTT 8903

RESULT 11
AAT00040
ID AAT00040 standard; DNA; 8912 BP.
XX
AC AAT00040;
XX
DT 27-AUG-2003 (revised)
DT 02-JUL-1996 (first entry)
XX
DE Hepatitis GB virus (HGBV-B) DNA.
XX
KW Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine; reagents; non-A;
KW non-B; non-C; non-D; non-E; HGBV-B; tamarin; infected plasma;
KW lambda phage; cDNA library; ss.
XX
OS Hepatitis G virus.
XX
FH Key Location/Qualifiers
FT mat_peptide 4524..4751
FT /*tag= a
FT /note= "Clone 48-1A1.1 protein prod."
FT mat_peptide 6450..6731
FT /*tag= b
FT /transl_except= pos:6474..6476, aa:Ala
FT /transl_except= pos:6630..6632, aa:Deleted
FT /note= "Clone 70-3A1.37 protein prod."
FT misc_difference 6772
FT /*tag= d
FT /note= "given as j in specification, may be Stanford
FT Ambiguity Code for C or A"
FT mat_peptide 6834..7457
FT /*tag= C
FT /note= "Clone 4-3B1.1 protein prod."
XX
PN W09521922-A2.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-US002118.
XX
PR 14-FEB-1994; 94US-00196030.
PR 13-MAY-1994; 94US-00242654.
PR 29-JUL-1994; 94US-00283314.
PR 23-NOV-1994; 94US-00344185.
PR 23-NOV-1994; 94US-00344190.
PR 27-JAN-1995; 95US-00344557.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Simons JN, Pilot-Matias TJ, Dawson GJ, Schlauder GG, Deesai SM;
PI Leary TP, Muernhoff AS, Erker JC, Buijk SL, Mushahwar IK;
XX
XX WPI; 1995-293123/38.
DR P-PSDB; AAR81402, AAR81403, AAR81404.
XX
PT Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful for
PT diagnosis and therapy of hepatitis GB virus.
XX
PS Example 4; Page 179-184; 661pp; English.
XX
CC Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV infected
CC tamarin plasma, using standard procedures, was used to prepare a lambda
CC phage HGBV cDNA library. cDNA clones (which encode the proteins AAR81402-
CC 04) rescued from the lambda phage, were found to have nearly 100%
CC sequence homology with the HGBV-B DNA sequence AAT00040. Reagents which
CC comprise the HGBV DNA, or its protein prods. can be used for the
CC diagnosis, therapy or in a vaccine to prevent HGBV infection. (Updated on
CC 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 8912 BP; 2019 A; 2169 C; 2265 G; 2400 T; 0 U; 59 Other;

Query Match	92.5%	Score 8691.4	DB 2	Length 8912
Best Local Similarity	98.7%	Pred. No. 0		
Matches 8781	Conservative 54	Mismatches 54	Indels 10	Gaps 8
Qy	196	TGGGTTTCGGTGTGGTGTGGCGCTTTAGGACGAGCTCCAGCCGACCTCCAGATAGAGC	255	
Db	11	TGGGTTTCGGTGTGGTGTGGCGCTTTAGGACGAGCTCCAGCCGACCTCCAGATAGAGC	70	
Qy	256	GGCGGCACCTGTAGGGAAGACGGGGACCGGTCCTACTACCAAGGACGACAGCTCTTTTGA	315	
Db	71	GGCGGCACCTGTAGGGAAGACGGGGACCGGTCCTACTACCAAGGACGACAGCTCTTTTGA	130	
Qy	316	GTATACGCGCTCCGAAGTAGTTGGGCAAGCCACCTATATGTGTGGGATGGTTGGGCT	375	
Db	131	GTATACGCGCTCCGAAGTAGTTGGGCAAGCCACCTATATGTGTGGGATGGTTGGGCT	190	
Qy	376	TAGCATCCATACCGTACTGCTCATAGGGTCCTTGGAGGGGATCTGGAGTCTCGTAG	435	
Db	191	TAGCATCCATACCGTACTGCTCATAGGGTCCTTGGAGGGGATCTGGAGTCTCGTAG	250	
Qy	436	ACCGTAGCACATGCTGTATTTCTACTCAAACAAGTCCTGTACCTCGCCAGAACGCG	495	
Db	251	ACCGTAGCACATGCTGTATTTCTACTCAAACAAGTCCTGTACCTCGCCAGAACGCG	310	
Qy	496	CAAGAACAGCAGACGCGGCTTCATATCTGTGTCCATTAAACATCTGTTGAAAGGGG	555	
Db	311	CAAGAACAGCAGACGCGGCTTCATATCTGTGTCCATTAAACATCTGTTGAAAGGGG	370	
Qy	556	ACACGAGCAAGCGCAAGTCACAGCGGATGCTCGGCGCTGTAATTTACAAAATTCGCTG	615	
Db	371	ACACGAGCAAGCGCAAGTCACAGCGGATGCTCGGCGCTGTAATTTACAAAATTCGCTG	430	
Qy	616	TATCCATGATGGCTTGCAGACATTTGGCTCAGGCTGCTTGGCAGCTCATGTTGGGACG	675	
Db	431	TATCCATGATGGCTTGCAGACATTTGGCTCAGGCTGCTTTRCCAGCTCATGTTGGGACG	490	
Qy	676	CCAAGACCTCGCATTAAGTCTCGAATCTTTGGAAATCCTTCTGGAATTAACCTTTGGGGT	735	
Db	491	CCAAGACCTCGCATTAAGTCTCGAATCTTTGGAAATCCTTCTGGAATTAACCTTTGGGGT	550	
Qy	736	GATTTGGTATGTTACACTACACACTACACACTCTAGTAGGGCCGCTGCTGGCAGGAGCGT	795	
Db	551	GATTTGGTATGTTACACTACACACTCTAGTAGGGCCGCTGCTGGCAGGAGCGT	610	
Qy	796	TCGACCACTCTGCCAGATAGTACGCTTGTCTGGAGATGGAGTCAACTGGGCTACTGGTTG	855	
Db	611	TCGACCACTCTGCCAGATAGTACGCTTGTCTGGAGATGGAGTCAACTGGGCTACTGGTTG	670	
Qy	856	GTTTCGGTGTCCACCTTTTGTGTGATGTCTGCTATCTTTGGGCTGTCCCTGTAGTGGGG	915	
Db	671	GTTTCGGTGTCCACCTTTTGTGTGATGTCTGCTATYTTTGGGCTGTCCCTGTAGTGGGG	730	
Qy	916	GGGGTCACTGACCCAGACAAATACCAACATCCTGACCAATTTGCTCCAGCGTATCA	975	
Db	731	GGGGTCACTGACCCAGACAAATACCAACATCCTGACCAATTTGCTCCAGCGTATCA	790	
Qy	976	GGTTATCTATTTGTTCTCCTTCCACTTGGCTACAGAGCCTGGTTGTGTGATCTGTGGGA	1035	
Db	791	GGTTATCTATTTGTTCTCCTTCCACTTGGCTACAGAGCCTGGTTGTGTGATCTGTGGA	850	
Qy	1036	CGAGTGTGGGTTCCCGCAATCCGTACATCTCAACAACCTTTCCAAATGGAGTGGCA	1095	
Db	851	CGAGTGTGGGTTCCCGCAATCCGTACATCTCAACAACCTTTCCAAATGGAGTGGCA	910	
Qy	1096	CTCCTTCTTGCTGACCAATTTGATTTGTTATGGGCGCTCTTGTGACCTGTGACGCGCT	1155	
Db	911	CTCCTTCTTGCTGACCAATTTGATTTGTTATGGGCGCTCTTGTGACCTGTGACGCGCT	970	
Qy	1156	TGACATTTGGTGTGTGTGTGTATTTAGTCTGGTCACTGGCTTGTTCAGGCACTG	1215	
Db	971	TGACATTTGGTGTGTGTGTGTATTTAGTCTGGTCACTGGCTTGTTCAGGCACTG	1030	
Qy	1216	GCTTATTTACATAGACCTCAATGAACCTGGTACTTTGTACCTGGAAGTGCCCACTGGAAT	1275	

1031	Db	GCTTATTTCATAGACCTCAATGAAACTGGTACTTGTTACTCTGGAANKTGCTACTGGAAT	1099
1276	Qy	AGATCCTCGGGTCTCCTAGGGTTTATTCGGGTGGATGGCGCGGAAGGTGAGGCTGTGCATCTTT	1335
1091	Db	AGATCCTCGGGTCTCCTAGGGTTTATTCGGGTGGATGGCGCGGAAGGTGAGGCTGTGCATCTTT	1150
1336	Qy	CTTGACCAAACTGGCTTTCACAAGTACCATACGCTATATGCGACTATATTTTACGACAGTGATACA	1395
1151	Db	CTTGACCAAACTGGCTTTCACAAGTACCATACGCTATATGCGACTATATTTTACGACAGTGATACA	1210
1396	Qy	CTACTCGCGCTTGGCGCTCTGATCTACTATGCTCTCTCGGGGCAAGTGGTATCAGTTGGCT	1455
1211	Db	CTACTCGCGCTTGGCGCTCTGATCTACTATGCTCTCTCGGGGCAAGTGGTATCAGTTGGCT	1270
1456	Qy	CCTAGCGCTTATGCTTTTACATAGAACGCACTCTCTGGAAACCCCATCAGGGTGCCCACTGG	1515
1271	Db	CCTAGCGCTTATGCTTTTACATAGAACGCACTCTCTGGAAACCCCATCAGGGTGCCCACTGG	1330
1516	Qy	ATGCTCAATAGCTGAGTTTTGCTCGCTTTGATGATACCAATGTCCTTGGCCACTCTTATTTT	1575
1331	Db	ATGCTCAATAGCTGAGTTTTGCTCGCTTTGATGATACCAATGTCCTTGGCCACTCTTATTTT	1390
1576	Qy	GAGTGAAATGTGTGAGAAGTCATTTGTTACAGTCCAAAGTGGACAGGCGCTATCACTCT	1635
1391	Db	GAGTGAAATGTGTGAGAAGTCATTTGTTACAGTCCAAAGTGGACAGGCGCTATCACTCT	1450
1636	Qy	AGAGTAAACAACCTCCATATCTTGGTACCCTCATACAATCCCTGGTCGAGGGGATGTAT	1695
1451	Db	AGAGTAAABAACCTCCATATCTTGGTACCCTCATACAATCCCTGGTCGAGGGGATGTAT	1510
1696	Qy	GGTTAAATTCAAAAATAACACATGGGGTGTCTGCGGTATTCGCAATGTGCCATCGTACTG	1755
1511	Db	GGTTAAATTCAAAAATAACACATGGGGTGTCTGCGG-WMTGCGAAATGCGCATCGTACTG	1569
1756	Qy	CACATATGGGCACCTGATGTCAGTGTGGAAASSACAGTCGCAACACTTACGAACATCGCGGT	1815
1570	Db	CACATATGGGCACCTGATGTCAGTGTGGAAASSACAGTCGCAACACTTACGAACATCGCGGT	1629
1816	Qy	AACACCATGGCTAACAAACCCGATGGCAACAGGCTCAGCCCTGAAATTTGGCTATATTACA	1875
1630	Db	AACACCATGGCTAACAAACCCGATGGCAACAGGCTCAGCCCTGAAATTTGGCTATATTACA	1689
1876	Qy	ATACCTCGGCTTAAAGAAATGTTTAAACCTCATATATGATGTGAGGCCAATTTGATATTT	1935
1690	Db	ATACCTCGGCTTAAAGAAATGTTTAAACCTCATATATGATGTGAGGCCAATTTGATATTT	1749
1936	Qy	TGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAAATTCCACTCTCCCTACC	1995
1750	Db	TGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAAATTCCACTCTCCCTACC	1809
1996	Qy	ACCGAGAGGTGGGCTAGGTTGGCCGGTACCCACCTGTGGTACGTGGTCTTTGGTTTACA	2055
1810	Db	ACCGAGAGGTGGGCTAGGTTGGCCGGTACCCACCTGTGGTACGTGGTCTTTGGTTTACA	1869
2056	Qy	GGTTCCGCAAGGGTTTTACAGTGAATGAAAGACCTAGCCACAGGATTGATACCAAAAGA	2115
1870	Db	GGTTCCGCAA-GGTTTTACAGTGAATGAAAGACCTAGCCACAGGATTGATACCAAAAGA	1928
2116	Qy	CAAAAGCCTGGAAAAATTTATCAGGTCTTATATTTCCGCCACGGGTGCTTTGCTCTTACGGG	2175
1929	Db	CAAAAGCCTGGAAAAATTTATCAGGTCTTATATTTCCGCCACGGGTGCTTTGCTCTTACGGG	1988
2176	Qy	AGTTTACCACCAAGGCGGTGTCTAAATTCGTTGGGGTGTGTGGGACAGCAAGATCTTAT	2235
1989	Db	AGTTTACCACCAAGGCGGTGTCTAAATTCGTTGGGGTGTGTGGGACAGCAAGATCTTAT	2048
2236	Qy	TTTTAGCCTACCTCTGTTACTTGTGCCCTTTGTTTTGGGCGGCTCTCGGTTACCCCTTTCG	2295
2049	Db	TTTTAGCCTACCTCTGTTACTTGTGCCCTTTGTTTTGGGCGGCTCTCGGTTACMCCTTTCG	2108
2296	Qy	TCCTGTGCTCCATCCCAAGTCGTATCTCCAAGCTGGCTGGGATGTTTTGTCTAAAGCTCA	2355

Db 2109 TCCTGTGCTCCCATCCAGTCGTATCTCCAAAGCTGGCTGGGATGTTTTGTCTAAAGCTCA 2168
QY 2356 AGTAGCTCCTTTTGGCTTTGATTTTCTCATCTGTTGCTATCTCCGCTCAGGCTACGTTA 2415
Db 2169 AGTAGCTCMTTTTGGCTTTGATTTTCTCATCTGTTGCTATCTCCGCTCGAGGCTACGTTA 2228
QY 2416 TGCTGCCCTTTTAGGGTTTGTGCCCATGGCTCGGGCTTGGCCCTTAACCTTTCTTTGTTGC 2475
Db 2229 TGCTGCCCTTTTAGGGTTTGTGCCCATGGCTCGGGCTTGGCCCTTAACCTTTCTTTGTTGC 2288
QY 2476 AGCAGCTGCTGCCCAACAGATTATGACTGTGGGTGCGACTGTGCTAGTGCGAGGTTAGT 2535
Db 2289 AGCAGCTGCTGCCCAACAGATTATGACTGTGGGTGCGACTGTGCTAGTGCGAGGTTAGT 2348
QY 2536 TTTTGGGCGGCGCTAACCGTGTACCGCATAGCTCTGCTGTAGGTCCCTTGGCCCTCT 2595
Db 2349 TTTTGGGCGGCGCTGACCGTGGTCA - CGCATAGCTCTGCTGTAGGTCCCTTGGCCCTCT 2407
QY 2596 GGTAGCGCTTT - TAAACCTCTTTGCAATTTGGTTACGCCCTGCTTCAGCTTTTGTATACCGAGA 2654
Db 2408 GGTAGCGCTTTTAAACCTCTTTGCAATTTSSTKACGCCCTGCTT - AGCTTTTGACACCGAGA 2466
QY 2655 TAAATTGGAGGGCTGACAATACCACTGTAGTAGCAATTAGTTGTGCTATGTCTCGTTTGGCT 2714
Db 2467 TAAATTGGAGGGCTGACAATACCACTGTAGTAGCAATTAGTTGTGCTATGTCTCGTTTGGCT 2526
QY 2715 TCTTTGCTCACTGTTTACCTCGCTGCTTTAGTTTAACTCCTATCTTTGGCAACGTTGGG 2774
Db 2527 TCTTTGCTCACTGTTTACCTCGCTGCTTTAGTTTAACTCCTATCTTTGGCAACGTTGGG 2586
QY 2775 AGAATTGGTTTTTGGAAACGTTTACACTAAGACCGGAGAGGTTTTTCTGCTGCTGTTTTGTT 2834
Db 2587 AGAATTGGTTTTTGGAAACGTTTACACTAAGACCGGAGAGGTTTTTCTGCTGCTGTTTTGTT 2646
QY 2835 TCCCGGCTGCGACATATGACCGGCTGGTGACTTCTGTGTGTGTCAGCTAGCTCTTCTAT 2894
Db 2647 TCCCGGCTGCGACATATGACCGTGTGGTGACWTTTCTGTGTGTGTCAGCTAGCTCTTCTAT 2706
QY 2895 GTTTAAACATCCAGTCCAGCTGTTCTTTGGGACTGACTTAGGGTTAGGGCCCATAGAA 2954
Db 2707 GTTTAAACATCCAGTCCAGCAAGTTCTTTGGGACTGACTTAGGGTTAGGGCCCATAGAA 2766
QY 2955 TGTGTGCTGCTCTCGGAAAGTGTCTATGCTTGGTATTTCTCATTTATGTTCTTAAGTTTTTCC 3014
Db 2767 TGTGTGCTGCTCTCGGAAAGTGTCTATGCTTGGTATTTCTCATTTATGTTCTTAAGTTTTTCC 2826
QY 3015 TCTTAGTGTGTTGGTGAAGTGTGTTTTTCTATAAGCACTGTGCATGGTGATGCTTGC 3074
Db 2827 TCTTAGTGTGTTGGTGAAGTGTGTTTTTCTAKAAGCACTTGCATGGTGATGCTTGC 2886
QY 3075 CTAATGATTTTGGCTCGAAACTACCATTGCAAGAGCCATTTTTTCCCTTTTGAAGGCAAGG 3134
Db 2887 CTAATGATTTTGGCTCGAAACTACCATTGCAAGAGCCATTTTTTCCCTTTTGAAGGCAAGG 2946
QY 3135 CAAGGCTCTATAGGAATGAAGGAAGACGCTTGGCTGTGGGACACGGTTGATGTTTGC 3194
Db 2947 CAAGGCTCTATAGGAATGAAGGAAGACGCTTGGSKGTGGGACACGGTTGATGTTGS 3006
QY 3195 CCGTTGTTGGGCTCTCGGCGACCTTTGTTTCGAGGGTTGGCTATGCCCGCAGATGGGT 3254
Db 3007 SCGTTGTBGGCGCTCTCGGCGACCTTTGTTTTCGACGGGTTAGCTATGCGCGCCAGATGGGT 3066
QY 3255 GGGCCATTACCGCACCTTTTACGCTGCAGTGCTCTCTGAACGTGGCAGCGCTGCAGCGA 3314
Db 3067 GGGCCATTACCGCACCTTTTACGCTGCAGTGCTCTCTGAACGTGGCAGCGCTGCAGCGA 3126
QY 3315 TGGCAGTGGTCTATGACTGATAGACCCCGCACTTGGACTGGAACCTATCTTCAGATTAG 3374
Db 3127 TGGCAGTGGTCTATGACTGATAGACCCCGCACTTGGACTGGAACCTATCTTCAGATTAG 3186
QY 3375 GATCTCTGGCCACTAGCTACATGGGATTTGTTGTGACAACTGTTGTATACGTCTCACC 3434
Db 3187 GATCTCTGGCCACTAGCTACATGGGATTTGTTGTGACAACTGTTGTGAATACTGCTCACC 3246

QY 3435 ATGCAGCAAGGGCGCGGTTGGCTCATCCACAGGCTCTATACACCAATAAACCGTTG 3494
Db 3247 ATGCAGCAAGGGCGCGGTTGGCTCATCCCAAGGCTCCATACACCAATAAACCGTTG 3306
QY 3495 ACGCGGCTAATGACCAAGACATCTATCAACACCATGTGGAGCTGGGTCCTTACTCGGT 3554
Db 3307 ACGCGGCTAATGACCAAGACATCTATCAACACCATGTGGAGCTGGGTCCTTACTCGGT 3366
QY 3555 GCTCTTGGGGGAGACCAAGGGGTATCTGGTAAACAGCATGGGGTCATTTGGTTGAGGTCA 3614
Db 3367 GCTCTTGGGGGAGACCAAGGGGTATCTGGTAAACAGCATGGGGTCATTTGGTTGAGGTCA 3426
QY 3615 ACAAATCCGATGACCTTTATTGGTGTGTGCGGGGCCCTTTCCCATGGCTGTGTCGAAGG 3674
Db 3427 ACAATCCGATGACCTTTATTGGTGTGTGCGGGGCCCTTTCCCATGGCTGTGTCGAAGG 3486
QY 3675 GTTCTTCAAGTGCCTCCGATCTGTGCTCTCCCGGCACTGTTATTGGGATGTTCAACCGTG 3734
Db 3487 GTTCTTCAAGTGCCTCCGATCTGTGCTCTCCCGGCACTGTTATTGGGATGTTCAACCGTG 3546
QY 3735 CTAGAAATTTCTGGCGGTTTCACTCAGTCAGATTAGGTTAGGCCGTTGGTGTGCTGGAT 3794
Db 3547 CTAGAAATTTCTGGCGGTTTCACTCAGTCCGCCAGATTAGGGTTAGGCCGTTGGTGTGCTGGAT 3606
QY 3795 ACCATCCCGAGTACACAGCATGCTCTTGTATACAAAACCTACTGTGCTTAACGAGT 3854
Db 3607 ACCATCCCGAGTACACAGCATGCTCTTGTATACAAAACCTACTGTGCTTAACGAGT 3666
QY 3855 ATTCAAGTCAAAATTTTAAATGCCCCCACTGCGAGCGGCAAGTCAACCAAAATTAACACTTT 3914
Db 3667 ATTCAAGTCAAAATTTTAAATGCCCCCACTGCGAGCGGCAAGTCAACCAAAATTAACACTTT 3726
QY 3915 CTTATGTCAGAGAAATGATGAGTCTTGGTCTTAAATCCAGTGTGCTACACAGAT 3974
Db 3727 CTTATGTCAGAGAAATGATGAGTCTTGGTCTTAAATCCAGTGTGCTACACAGAT 3786
QY 3975 CAATGCCAAAGTACATGCAACGCGTACGCGGTGAATCCAAATTTGCTATTATTAATGCA 4034
Db 3787 CAATGCCAAAGTACATGCAACGCGTACGCGGTGAATCCAAATTTGCTATTATTAATGCA 3846
QY 4035 AATGTACAAACACAGGGGCTTCACTACGTACAGCAATATGGCATGTACCTGACCGGAG 4094
Db 3847 AATGTACAAACACAGGGGCTTCACTACGTACAGCAATATGGCATGTACCTGACCGGAG 3906
QY 4095 CATGTTCCCGAACTATGATGTAATCATTTGTGACGATGCCATGCTACCGATGCAACA 4154
Db 3907 GATGTTCCCGAACTATGATGTAATCATTTGTGACGAATGCCATGCTACCGATGCAACA 3966
QY 4155 CCGTGTGGGCAATTTGGAAAGGCTTAAACCGAAGCTCCATCCAAATAATGTTAGGCTTAGTGG 4214
Db 3967 CCGTGTGGGCAATTTGGAAAGGCTTAAACCGAAGCTCCATCCAAATAATGTTAGGCTTAGTGG 4026
QY 4215 TTCTTGCCACGGCTACCCCCCTGGAGTAAATCCCTACACCATGCCCCAACATAACTGAGA 4274
Db 4027 TTCTTGCCACGGCTACCCCCCTGGAGTAAATCCCTACACCATGCCCCAACATAACTGAGA 4086
QY 4275 TTCAATTAACCGATGAAGGCACTATCCCTTTTCAATGGAATAAGATTAAAGGGAATAATC 4334
Db 4087 TTCAATTAACCGATGAAGGCACTATCCCTTTTCAATGGAATAAGATTAAAGGGAATAATC 4146
QY 4335 TGAAGAAAGGAGACACCTTATCTTTAGGCTTACCAAAAAACACTGTGATGAGCTTGCTA 4394
Db 4147 TGAAGAAAGGAGACACCTTATCTTTAGGCTTACCAAAAAACACTGTGATGAGCTTGCTA 4206
QY 4395 ACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGGATGTGACATCTCAA 4454
Db 4207 ACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGGATGTGACATCTCAA 4266
QY 4455 AAATCCCTGAGGGGCACTGTGTAGTGTGCACTGATGCTCTTGTGTACAGGGTACACTG 4514
Db 4267 AAATCCCTGAGGGGCACTGTGTAGTGTGCACTGATGCTCTTGTGTACAGGGTACACTG 4326

Qy	4515	GTGACTTTGATTCGGTGATGACATGCGAGCCTCATGGTAGAAGGCACATGCCATGTTGACC	4574	
Db	4327	GTGACTTTGATTCGGTGATGACATGCGAGCCTCATGGTAGAAGGCACATGCCATGTTGACC	4386	
Qy	4575	TTGACCCCTACTTTTACCAATGGTGTTCGTGTGCGGGGTTTCAGCAATAGTTAAAGGCC	4634	
Db	4387	TTGACCCCTACTTTTACCAATGGTGTTCGTGTGCGGGGTTTCAGCAATAGTTAAAGGCC	4446	
Qy	4635	AGCGTAGGGGCGCACAGCCCGTGGGAGAGCTGGCATATATCTACTATGTAGACGGGAGTT	4694	
Db	4447	AGCGTAGGGGCGCACAGCCCGTGGGAGAGCTGGCATATATCTACTATGTAGACGGGAGTT	4506	
Qy	4695	GTACCCCTTCGGGTATGGTCTCTGAATGCAACATTTGTTGAAGCCTTGCAGCCGCAAGG	4754	
Db	4507	GTACCCCTTCGGGTATGGTCTCTGAATGCAACATTTGTTGAAGCCTTGCAGCCGCAAGG	4566	
Qy	4755	CATGATATGGTTTGTATCAACAGAGCTCAAACTATTCTGACACACTATCGCACCCCAAC	4814	
Db	4567	CATGATATGGTTTGTATCAACAGAGCTCAAACTATTCTGACACACTATCGCACCCCAAC	4626	
Qy	4815	CTGGGTTACCTCGCATAGGACAAATTTGGACGAGTGGGCTGATCTCTTTTCTATGGTCA	4874	
Db	4627	CTGGGTTACCTCGCATAGGACAAATTTGGACGAGTGGGCTGATCTCTTTTCTATGGTCA	4686	
Qy	4875	ACCCGAAACCTTCAATTTGTCAATATCTGCAAAAAGAACTGCTGCAAAATATGTTTGTGA	4934	
Db	4687	ACCCGAAACCTTCAATTTGTCAATATCTGCAAAAAGAACTGCTGCAAAATATGTTTGTGA	4746	
Qy	4935	CTGCAGCCCAACTACACTGCTGTCATCAGTATGCTATGCTGCTGCCCTTGACCGCGG	4994	
Db	4747	CTGCAGCCCAACTACACTGCTGTCATCAGTATGCTATGCTGCTGCCCTTGACCGCGG	4806	
Qy	4995	GGTGGCAGGAGCCCGGCTTGGGAAAAAACCTTGTGGGGTTCTGTGGCGCTTGACCGCGG	5054	
Db	4807	GGTGGCAGGAGCCCGGCTTGGGAAAAAACCTTGTGGGGTTCTGTGGCGCTTGACCGCGG	4866	
Qy	5055	CTGACGCTGTCTGTGGCCAGAGCCAGCGAGGTGACAGATACCAATATGCTTCACTG	5114	
Db	4867	CTGACGCTGTCTGTGGCCAGAGCCAGCGAGGTGACAGATACCAATATGCTTCACTG	4926	
Qy	5115	AAGTCAATACTTCTGGGACAGCCGACCTCGCTGTTGGGTTGGAGTGGCTATGCTTATC	5174	
Db	4927	AAGTCAATACTTCTGGGACAGCCGACCTCGCTGTTGGGTTGGAGTGGCTATGCTTATC	4986	
Qy	5175	TAGCCATTTGACACTTTTGGGCCCACTTGTGTGCGGCGTGTGCTGTCTATTATCAGTCC	5234	
Db	4987	TAGCCATTTGACACTTTTGGGCCCACTTGTGTGCGGCGTGTGCTGTCTATTATCAGTCC	5046	
Qy	5235	CTACCGGTGTCTGTGCGCCAGTGGTTGACGAAGAAGAAATCGTGGAGGAGTGTGCAT	5294	
Db	5047	CTACCGGTGTCTGTGCGCCAGTGGTTGACGAAGAAGAAATCGTGGAGGAGTGTGCAT	5106	
Qy	5295	CATTCAATCCCTTGGAGCCATGGTGTGCAATTTGACAGCTGAAGTACATCAACA	5354	
Db	5107	CATTCAATCCCTTGGAGCCATGGTGTGCAATTTGACAGCTGAAGTACATCAACA	5166	
Qy	5355	CAACTAGTCTCTTACACTTGGAAACCGCCCTTGAATAAACTTAAACCTTCTGGGCGCTC	5414	
Db	5167	CAACTAGTCTCTTACACTTGGAAACCGCCCTTGAATAAACTTAAACCTTCTGGGCGCTC	5226	
Qy	5415	ATCAGCTTACAAATCTTGTCTATCATAGAGTATGCTGTGGTTTATGCTCACTTTACCTGACA	5474	
Db	5227	ATCAGCTTACAAATCTTGTCTATCATAGAGTATGCTGTGGCTTATGCTCACTTTACCTGACA	5286	
Qy	5475	ATCCCTTTGCAATATGCGGTGTTTGTCTTCAATGGGGTATTTACTACCCCACTACTCACA	5534	
Db	5287	ATCCCTTTGCAATATGCGGTGTTTGTCTTCAATGGGGTATTTACTACCCCACTACTCACA	5346	
Qy	5535	AGATCAAAATGCTCTGTCTTATTTTGGAGGCGCAATTTGGCGTCCAAAGCTTACAGACGCTA	5594	
Db	5347	AGATCAAAATGCTCTGTCTTATTTTGGAGGCGCAATTTGGCGTCCAAAGCTTACAGACGCTA	5406	
Qy	5595	GAGCGCAGCTGGCGTTTCATGATGGCCGGGCTGCGGGAAACAGCTCTTTGGTACATGGACAT	5654	

Db	5407	GAGRCGCACTGGCGCTTCATGATGCGGGGCTGTGGGAAACAGCTCTTTGGTACATGGACAT	5466	
Qy	5655	CGGTGGGTTTTGTCTTTTGACATGCTAGGCGCTATGCTGCGGCTCATCCACTCTCTTGCT	5714	
Db	5467	CGGTGGGTTTTGTCTTTTGACATGCTAGGCGGCTATGCTGCGGCTCATCCACTCTTGCT	5526	
Qy	5715	TGACATTTAAATGCTTGATCGGTGAGTGGCCCACTATGGATCAGCTTGTGTTTGTAGTCT	5774	
Db	5527	TGACATTTAAATGCTTGATCGGTGAGTGGCCCACTATGGATCAGCTTGTGTTTGTAGTCT	5586	
Qy	5775	ACTCGCGTTTCAATCCGCGCGCAGGAGTCTGGGCGTCTTGTGAGCTTGTGCAATGTTTG	5834	
Db	5587	ACTCGCGTTTCAATCCGCGCGCAGGAGTCTGGGCGTCTTGTGAGCTTGTGCAATGTTTG	5646	
Qy	5835	CTTTTGACAAACAGAGGCGCAGATCAGCTGGGCCCAACAGACTTCTTATGCTTCTCTAGGA	5894	
Db	5647	CTTTTGACAAACAGAGGCGCAGATCAGCTGGGCCCAACAGACTTCTTATGCTTCTCTAGGA	5706	
Qy	5895	GCAACACTGATGTAATGAGTACTTTTATGGCACTCTGTGACATCCGAGGAAGATATCGG	5954	
Db	5707	GCAACACTGATGTAATGAGTACTTTTATGGCACTCTGTGACATCCGAGGAAGATATCGG	5766	
Qy	5955	GCATTCTGGAGGCACTTACCCCTGGAGTCTCATATCAGCTTGCATCCGTTGGCTCCACA	6014	
Db	5767	GCATTCTGGAGGCACTTACCCCTGGAGTCTCATATCAGCTTGCATCCGTTGGCTCCACA	5826	
Qy	6015	CCCCGAGGAGGATGATTGGCGGCTCATTTCTTGGGGTCTTAGATTTTGGCAGTATGTT	6074	
Db	5827	CCCCGAGGAGGATGATTGGCGGCTCATTTCTTGGGGTCTTAGATTTTGGCAGTATGTT	5886	
Qy	6075	GCAATTTCTTGTGATTTGCTTTTAAATGCTCTTAAAGCTGGAGTTTACAGCATGTTTAAACA	6134	
Db	5887	GCAATTTCTTGTGATTTGCTTTTAAATGCTCTTAAAGCTGGAGTTTACAGCATGTTTAAACA	5946	
Qy	6135	TTCTCTGTTGCTCTTCTACAGCTGCCAGAAAGGGGTACAAGGGCCCTTGGATTTGGATCAG	6194	
Db	5947	TTCTCTGTTGCTCTTCTACAGCTGCCAGAAAGGGGTACAAGGGCCCTTGGATTTGGATCAG	6006	
Qy	6195	GTATGCTCCAAGACACGCTGTCCATGCGGTGCTGAACCTCATCTTTCTTCTTGTAGAGAAATGGTT	6254	
Db	6007	GTATGCTCCAAGACACGCTGTCCATGCGGTGCTGAACCTCATCTTTCTTCTTGTAGAGAAATGGTT	6066	
Qy	6255	TTGCAAACTTTTACAAAGGACCCAGAACTTTGTTCAAATTAAGTGGAGGGGCTGTTCAG	6314	
Db	6067	TTGCAAACTTTTACAAAGGACCCAGAACTTTGTTCAAATTAAGTGGAGGGGCTGTTCAG	6126	
Qy	6315	TCAACGCTAGGCTGTGTGGGTGCGCTAGACCGGACCCCAACTGATTGGACTAGTCTTGTGCG	6374	
Db	6127	TCAACGCTAGGCTGTGTGGGTGCGCTAGACCGGACCCCAACTGATTGGACTAGTCTTGTGCG	6186	
Qy	6375	TCAATATGCGTTTGGGAGCTACTGTAAATATAGAGAAATTTGGAGATCACAATTTTGTGTA	6434	
Db	6187	TCAATATGCGTTTGGGAGCTACTGTAAATATAGAGAAATTTGGAGATCACAATTTTGTGTA	6246	
Qy	6435	CAGCAGTATCTCTCCTTCAAAATGCTGTTTCCACCCAGGTGCCCCCAACCTTGGAGAGCTGAG	6494	
Db	6247	CAGCAGTATCTCTCCTTCAAAATGCTGTTTCCACCCAGGTGCCCCCAACCTTGGAGAGCTGAG	6306	
Qy	6495	TGGCGGTGGAAGGGGTACAGGTTTCACTAGGTGAGCCCAAACTCTCCTTGGAGCA	6554	
Db	6307	TGGCGGTGGAAGGGGTACAGGTTTCACTAGGTGAGCCCAAACTCTCCTTGGAGCA	6366	
Qy	6555	CATCTGCTTCTGTTTACGGTCTTACGGTAAAGGTTAAATCTTTTAAAGCTTCCCTTCCGCG	6614	
Db	6367	CATCTGCTTCTGTTTACGGTCTTACGGTAAAGGTTAAATCTTTTAAAGCTTCCCTTCCGCG	6426	
Qy	6615	TTGACGCTTACACACCTTGTGTGCGCATGCAACTTAAATTTTGGGTGATGCACTTGGAGCAAA	6674	
Db	6427	TTGACGCTTACACACCTTGTGTGCGCATGCAACTTAAATTTTGGGTGATGCACTTGGAGCAAA	6486	
Qy	6675	ATGACTGTAAATTTCAAAACAACTCTCTTATGATGATGAAAGCGCGAGTGTCCGCTCTTGT	6734	

Db	4698	GAUGAUUGCGGCCUUAUUGUUGGGUUCUAGAGAUUUGGCAAGUUGGUGCAUUUUUUU	4757
Qy	6086	GTGATTGTCTTAATGTCTTAAAGCTGGAGTTTCAGAGCATGGTTAAACATTCTCGTGTGT	6145
Db	4758	GUGAUUGCUUAUUGUUCUUAAGCUGGAGUUCAGAGCAUGGUUACAUAUUCUGGUUGU	4817
Qy	6146	CTTTTCTACAGCTGCGAAGAGGGGTACAAGGGCCCTTGGATTGAGATCAGGTATGCTCAA	6205
Db	4818	CCUUCUACAGCUGCGAAGAGGGGUAACAAGGGCCCUUGGAUUGGAUCAGGUUAGUCCAA	4877
Qy	6206	GCAGCTGTCCATCGGGTCTGAACTCATCTTTTCTGTGTGAGATGTTTGTGAAAACCTT	6265
Db	4878	GCACGCUUGCAGUGGGUGGUAACUACUUCUUUUUGUUGGAGAUGGUUUGCAAAACUU	4937
Qy	6266	TACAAAGGACCCAGAACTTTGTTCAAAATTACTGTGAGAGGGGCTGTTCAGTCAACGCTAGG	6325
Db	4938	UACAAAGGACCCAGAACTTTGTTCAAAATTACTGTGAGAGGGGCTGTTCAGTCAACGCTAGG	4997
Qy	6326	CTGTGTGGGTGCGGTAGACCGGACCCAACTGATTGTGGACTAGTCTTGTGCTCAATTTATGGC	6385
Db	4998	CUGUGGGGUGCGGUCAGACCGGACCCAACTGATTGTGGACTAGTCTTGTGCTCAATTTATGGC	5057
Qy	6386	GTTAGGGACTACTGTAAATATGAGAAATGGGAGATCACATTTTGTGTACAGAGTATCC	6445
Db	5058	GUUAGGGACUACUGUAAAUAGAGAAAUUGGGAGAUCAUUCUUUUUACAGCAGUAUCC	5117
Qy	6446	TCTCAAATGTCTGTTTCAACCCAGGTGCCCCCAACTTTGAGAGCTGCAAGTGGCGTGGAC	6505
Db	5118	UCUCCAAUUGUCUUGUUCACCCAGGUGCCCCCACTTUGAGAGCUGCAGUGGGCCGUGGAC	5177
Qy	6506	GGCGTACAGGTTCAAGTTTACTAGGTGAGGCCCAAACTCTCTTGGACGACATCTGCTTGC	6565
Db	5178	GGCGTACAGGTTCAAGTTTACTAGGTGAGGCCCAAACTCTCTTGGACGACATCTGCTTGC	5237
Qy	6566	TGTTACGCTCTGACGGTAAAGGTAAAGCTGTTAAGCTTCCCTTCCGCTTGACGGTCCAC	6625
Db	5238	UGUUAACGUGUUCAGCGGUAAGGGUAAACUGUUUAAAGUUUCCUCCGCGUUGACGGUCCAC	5297
Qy	6626	ACACTGTGTGCGCATGCAACTTAAATTTGCGTGATGCATCTTGAGACAAATGACTGTAAT	6685
Db	5298	ACAACGUGUGCGCAUGCAUUAUUUUGGUGAUGCACAUGGAGACAAUAGAUGUAU	5357
Qy	6686	TCCACAAACAACTCTCTAGTGTGAAGCCGAGTGTCCGCTCTTGTGTTTCAAAACAGAG	6745
Db	5358	UCCACAAACAACTCTCTAGTGTGAAGCCGAGTGTCCGCTCTTGTGTTTCAAAACAGAG	5417
Qy	6746	TTGCGGCTTACAAACCAATCTGTGAGCAATTTTCAAGCTGCTGCTTCCCTTCCGCTTGACGGT	6805
Db	5418	UUGCGGCGUAACAAACCAUUGUUGAGGCAUUUUCAGCUGCGGUGUACACCAACCAACUG	5477
Qy	6806	CCAGCCCCCTCCATCGAAGAGGTAGTGTGAAGAAAGCGCCAGTTTCCGGGCAAGAACTGGT	6865
Db	5478	CCAGCCCCCTCCATCGAAGAGGTAGTGTGAAGAAAGCGCCAGTTTCCGGGCAAGAACTGGT	5537
Qy	6866	TCGCTTACCTTCCCTCCCGAGATCCGATCCGAGAGTGTCAATGTCTGTAAGAGCGTG	6925
Db	5538	UCGCUUACUUGCCGCCUCCGAGAUCCGUCGCCAGAGUGCAUGUCCUGGAAAGCCUG	5597
Qy	6926	CAAACGAGTACCCGTTAGAGGTCTTCAACCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT	6985
Db	5598	CAAACGAGTACCCGTTAGAGGTCTTCAACCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT	5657
Qy	6986	TTGGCCATCGCCGATGCCCTGTGGAGCGGGTGTGATTAACCTTTTCACTGCAATTTGA	7045
Db	5658	UUGGCCAUGCCGAGUCCUUGUUGGAGCGGGUAGUUAACCCUUUUCACUUGCAUUGGA	5717
Qy	7046	TGTGCAATGACCGAAGAGCGGCGCTGTGATTTTACCGATTTACCTTCCCTTCCCTTCCCT	7105
Db	5718	UUGGCAUUGACCGAAGAGCGGCGCTGTGATTTTACCGATTTACCTTCCCTTCCCTTCCCT	5777
Qy	7106	GAGGTCTCTGAATGGTACGAAAGTGGTTCGAGCGGCTACAAACCGCTTCCAGCTACGTT	7165
Db	5778	GAGGTCTCTGAATGGTACGAAAGTGGTTCGAGCGGCTACAAACCGCTTCCAGCTACGTT	5837
Qy	7166	ACTGGCCCCCGTACCCCTAAGATACGGGAAAGGATTTCCACTCAGTCAGCCCCCGCCAAA	7225
Db	5838	ACUGGCCCCCGUACCCCUAAGAUACGGGAAAGGAUUUCCACUCAGUCAGCCCCCGCCAAA	5897
Qy	7226	CGGCTACAAAAGAAAGTTGGGAAAGAGTGTGTTTCTGTCAGCATGAGCTACACCTGG	7285
Db	5898	CGGCUACAAAAGAAAGTTGGGAAAGAGTGTGTTTCTGTCAGCATGAGCTACACCTGG	5957
Qy	7286	ACGACGTGATTAGCTTTCAAAAACCTGCTTCTAAGTTTCTGTCGCAACTCTCGGCGCATCACT	7345
Db	5958	ACGACGTGATTAGCTTTCAAAAACCTGCTTCTAAGTTTCTGTCGCAACTCTCGGCGCATCACT	6017
Qy	7346	AGTGGTTTCTCAAAACAAAGATCAATCTGCTGTGTGATGAGCCGCGGATGCGGAGTGT	7405
Db	6018	AGUGUUUCCUACAAACAAAGAUCAUUGUGUAGUGAUCUGAGCCGCGGAGUCGAGCUU	6077
Qy	7406	AGAAAACAAAGTCACTATTATAGAACAACTCTGTTCCCGCCATCATACCAACACAA	7465
Db	6078	AGAAAACAAAGTCACTATTATAGAACAACTCTGTTCCCGCCATCATACCAACACAA	6137
Qy	7466	GTGAGATTGGCTAAGGAAAGCTTCAAAAAGTTGTTCGTTGTCTATGTGGGACTATGATGA	7525
Db	6138	GUGAGAUUGGCUAAGGAAAGCUUCAAAGUUGUGGUGUAGUGGAGGACUAGUAGAA	6197
Qy	7526	GTAGAGCTCACAGCGCCCTCTTAAGTCTGTAAGTCCCACTCACTGSCCTTTCGGGGCACT	7585
Db	6198	GUAGCAGUCACAGCGCCCTCTTAAGTCTGTAAGTCCCACTCACTGSCCTTTCGGGGCACT	6257
Qy	7586	GATGTTGTTCTGGAGCAGCCCGCAAGCTGTCTCGACTTTCGACATTCGACAGATGTGTCAGGCA	7645
Db	6258	GAUUGUUGUUGGAGCAGCCCGCAAGCTGTCTCGACTTTCGACATTCGACAGATGTGTCAGGCA	6317
Qy	7646	GGTGAGATACCGAGTCAATATCGGAAACTGTGTAGTTTCCAAAGGAGGAGTCTTCTCGT	7705
Db	6318	GGUAGAUACCGAGTCAATATCGGAAACTGTGTAGTTTCCAAAGGAGGAGTCTTCTCGT	6377
Qy	7706	AAGACCCCCCAGAAACCAACAAAGAAACCCCAAGGGTCTTCTCGTACCCCACTTGAA	7765
Db	6378	AAGACCCCCCAGAAACCAACAAAGAAACCCCAAGGGTCTTCTCGTACCCCACTTGAA	6437
Qy	7766	ATGAGATGTTTGAGAAAGTGTACTACGTTCAAGTGTCTCTGAGCTAGTTTAAAGCTGTC	7825
Db	6438	AUGAGAUUGUUGAAGAUAGUACUGGUGCAGGUGUCCUGUAGUUAUUAUUAUUAUUAUUA	6497
Qy	7826	ATGGGAGATGCTACGGGTTTGTAGATCCAGTACCGTGTCAAGCGTCTCTGTGTCGATG	7885
Db	6498	AUGGGAUGGCUACGGGUUUGUAGUACCGUACCGUACCGUACCGUACCGUACCGUACCGU	6557
Qy	7886	TGCTTACCCGATGCGATCGGAGCCACATGCGATACAGTGTGTTTGTGACGATCCATCA	7945
Db	6558	UGGUCACCCGAGUACGCGGAGCCACATGCGATACAGTGTGTTTGTGACGATCCATCA	6617
Qy	7946	CCGAGAGATATCATGTTGGAGAGACAGATCTACTCAGCAGTAACTCAGTGACCAACAC	8005
Db	6618	CCGAGAGATATCATGTTGGAGAGAGATCTACTCAGCAGTAACTCAGTGACCAACAC	6677
Qy	8006	CGAGCTGCAATTCACACATTTGCGAGGAGTTATACCTGCGAGGACCGATGATCGCTTAT	8065
Db	6678	CGAGCTGCAATTCACACATTTGCGAGGAGTTATACCTGCGAGGACCGATGATCGCTTAT	6737
Qy	8066	GATGGCCGAGAGATCGGATATCGTGTAGGTGTGTTTCCGCGCTTCTTACCTTCAAGT	8125
Db	6738	GAUGGCCGAGAGAUCCGUAUUGUAGUAGGUGUCCUGGCGUUAUUAUUAUUAUUAUUAUUA	6797
Qy	8126	TCCAAAGTTTGTACCTGCTGCTGAGGTAATGCTCTCAGCCGAAACAGGCTGGCATGAG	8185
Db	6798	UCCAAAGTTTGTACCTGCTGCTGAGGTAATGCTCTCAGCCGAAACAGGCTGGCATGAG	6857
Qy	8186	AACCTCTGCTTCTTATTTGCGGCGATGTTGACCGTAAATTTTGGAAAGAGCGCGGAGCA	8245
Db	6858	AACCTCTGCTTCTTATTTGCGGCGATGTTGACCGTAAATTTTGGAAAGAGCGCGGAGCA	6917

CC phage HGBV cDNA library. The cDNA clone AAT00052, which encodes the
CC proteins AAR2066-71 (the 6 possible reading frames), was rescued from
CC the lambda phage, searched against a sequence database and found to be an
CC unique HGBV sequence. Reagents which comprise the HGBV DNA, or its
CC protein prods. can be used for the diagnosis, therapy or in a vaccine to
CC prevent HGBV infection.. (Updated on 27-AUG-2003 to correct OS field.)
XX

SQ Sequence 4268 BP; 1036 A; 1063 C; 1063 G; 1086 T; 0 U; 20 Other;

Query Match 44.2%; Score 4159; DB 2; Length 4268;
Best Local Similarity 98.1%; Pred No. 0;
Matches 4215; Conservative 20; Mismatches 30; Indels 30; Gaps 2;
3456 TGGCTCATCCACAGGCTCTATACACCCCAATAACCGTTGACCGCGCTAATACACGAGCA 3515
Db 1 TGGCTCATCCACAGGCTCCATACACCCCAATAACCGTTGACCGCGCTAATACACGAGCA 60
3516 TCTATCAACCAACCATGTGGAGCTGGGTCCCTTACTCGGTCTCTTGGGGAGACCAAGG 3575
Db 61 TCTATCAACCAACCATGTGGAGCTGGGTCCCTTACTCGGTCTCTTGGGGAGACCAAGG 120
3576 GGTATCTGGTAACACGACTGGGTCATTGGTTGAGGTCAACAAATCCGATGACCCCTATT 3635
Db 121 GGTATCTGGTAACACGACTGGGTCATTGGTTGAGGTCAACAAATCCGATGACCCCTATT 180
3636 GGTGTGTGTGGGGCCCTTCCCATGGCTGTGTGCAAGGGTCTTTCAGGTGCCCGATTTC 3695
Db 181 GGTGTGTGTGGGGCCCTTCCCATGGCTGTGTGCAAGGGTCTTTCAGGTGCCCGATTTC 240
3696 TGTGTCCTCCGGGCATGTTATGGGATGTTTACCGCTGTCTAGAAATTCCTGGCGGTTCAG 3755
Db 241 TGTGTCCTCCGGGCATGTTATGGGATGTTTACCGCTGTCTAGAAATTCCTGGCGGTTCAG 300
3756 TCAGTCAGATTAGGTTAGGCGGTGGTGTGTCTGGATACCATCCCGAGTACACAGCAC 3815
Db 301 TCGGCCAGATTAGGTTAGGCGGTGGTGTGTCTGGATACCATCCCGAGTACACAGCAC 360
3816 ATGCCACTCTTGATACAAAACCTACTGTGCCTTAACGAGTATTCAGTGCAAATTTTAAATG 3875
Db 361 ATGCCACTCTTGATACAAAACCTACTGTGCCTTAACGAGTATTCAGTGCAAATTTTAAATG 420
3876 CCCCACCTGGCAGCGGCAAGTCAACCAATTAACGATTTCTTACGTGAGGAGAGTATG 3935
Db 421 CCCCACCTGGCAGCGGCAAGTCAACCAATTAACGATTTCTTACATGACGAGGAGTATG 480
3936 AGTCTTGGCTCTAAATCCAGTGGCTACAAAGCATCAATGCAAGTACATGACG 3995
Db 481 AGTCTTGGCTCTAAATCCAGTGGCTACAAAGCATCAATGCAAGTACATGACG 540
3996 CGAGTACGGGTGAATCCAAATTTGCTATTTTAAATGGCAATGTACCAACACAGGGGCTT 4055
Db 541 CGAGTACGGGTGAATCCAAATTTGCTATTTTAAATGGCAATGTACCAACACAGGGGCTT 600
4056 CACTTACGTACAGCAGCATATGGCATGTACCTGACCGGAGCATGTTCCCGAACTATGATG 4115
Db 601 CACTTACGTACAGCAGCATATGGCATGTACCTGACCGGAGCATGTTCCCGAACTATGATG 660
4116 TAATCATTTGTGAGCAATGCCATGTACCGATGCAACACCGTGTGGGCAATGGAAAGG 4175
Db 661 TAATCATTTGTGAGCAATGCCATGTACCGATGCAACACCGTGTGGGCAATGGAAAGG 720
4176 TCCTAACCGAAGCTCCATCCAAAATGTTAGGCTAGTGGTCTTGGCAACCGGTACCCCCC 4235
Db 721 TCCTAACCGAAGCTCCATCCAAAATGTTAGGCTAGTGGTCTTGGCAACCGGTACCCCCC 780
4236 CTGGAGTAATCCCTACACCAATGCGCAACATTAATCAATTAACCGATGAGGCA 4295
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4296 CTATCCCTCTTCATGGAAAAAGATTAAAGGAGGAAATCTGAAGAAAGGGAGACACCTTA 4355
Db 841 CTATCCCTCTTCATGGAAAAAGATTAAAGGAGGAAATCTGAAGAAAGGGAGACACCTTA 900

QY 4356 TCTTTGAGGCTACAAAAAAACACTGTGATGAGCTTGTCTAACGAGTGTAGCTCGAAGGGAA 4415
Db 901 TCTTTGAGGCTACCAAAAAACACTGTGATGAGCTTGTCTAACGAGTGTAGCTCGAAGGGAA 960
4416 TAACAGCTGTCTCTTACTATAGGGGATGTGACATCTCAAAATCCCTGAGGGCGACTGTG 4475
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Db 1861 TGGTTGCTGCAATTTGACAGCTGAAGTACAATCACCACAACTAGTCTTTTCAGATTGG 1920
5376 AAACCGCCCTTGAAAACTTAAACCTTTCTTGGGCTCTATGACAGTACAACTCTTGTCTA 5435
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5436 TCATAGAGTATGTGTGTTTGTAGTCACTTTTACCTGACAACTCCCTTTGTCATCATCGCTGT 5495

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Db	4174	TACCGAGTCATTATCGGCAAACTGTGTATAGTTCCAAAGGAGGAGGTCTTCTGTGAAGACCC	4233
QY	7713	CCCAGAAACCAACAAAGAGAAACCCCAAGGCTTATC	7747
Db	4234	CCCAGAAACCAACAAAGAGAAACCCCAAGGCTTATC	4268
RESULT 14			
AAA55298			
ID	AAA55298 standard; DNA; 4268 BP.		
XX	AC	AAA55298;	
XX	AC		
DT	06-AUG-2003	(revised)	
DT	30-AUG-2000	(first entry)	
XX	Hepatitis GB virus nucleotide sequence SEQ ID NO:80.		
XX			
KW	Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;		
KW	detection; characterisation; hepatitis; ss.		
XX			
OS	Hepatitis GB virus.		
XX			
PN	US6051374-A.		
PD	18-APR-2000.		
XX			
PF	07-JUN-1995;	95US-00488445.	
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PR	13-MAY-1994;	94US-00242654.	
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PR	23-NOV-1994;	94US-00344185.	
PR	23-NOV-1994;	94US-00344190.	
PR	30-JAN-1995;	95US-00377557.	
XX			
PA	(ABBO) ABBOTT LAB.		
XX			
PI	Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;		
PI	Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;		
XX			
DR	WPI; 2000-338307/29.		
PT	Detecting target hepatitis GB virus nucleic acid in a test sample		
PT	suspected of containing HGBV comprises reacting the test sample the HGBV		
PT	polynucleotide probe and detecting the complex that contains target HGBV.		
XX			
PS	Example 5; Col 205-210; 369pp; English.		
XX			
CC	The present invention describe a method for detecting target hepatitis GB		
CC	virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of		
CC	containing HGBV. The method involves reacting (T) with a HGBV		
CC	polynucleotide probe (I) containing 15 contiguous nucleotides, and which		
CC	selectively hybridises to the HGBV genome or its full complement, and		
CC	detecting the complex that contains THN, indicating the presence of		
CC	target HGBV. The method is used for detecting target HGBV nucleic acid in		
CC	the test sample suspected of containing HGBV and for characterisation of		
CC	newly ascertained etiological agent of non-A, non-B, non-C, non-D and non		
CC	-E hepatitis causing agents collectively termed as hepatitis GB virus.		
CC	AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and		
CC	protein sequences used in the exemplification of the present invention.		
CC	(Updated on 06-AUG-2003 to correct OS field.)		
XX			
SQ	Sequence 4268 BP; 1036 A; 1063 C; 1063 G; 1086 T; 0 U; 20 Other;		
Query Match 44.2%; Score 4159; DB 3; Length 4268;			
Best Local Similarity 98.1%; Pred.No. 0;			
Matches 4215; Conservative 20; Mismatches 30; Indels 30; Gaps 2;			
QY	3456	TGGCTCATCCACAGGCTCTATACACCAATAACCGTTGACGGGCTTAATGACCAGACA	3515

Db 1081 ACTGACGCTCATGTAGAGGCACATGCCATGTGTGACCTTGACCTTACCCTACTTTCCACATGG 1140
Qy 4596 GTGTTCTGTGTGCGGGTTTTCAGCAATAGTTTAAAGGCCAGGTAGGGGCCGACAGGCC 4655
Db 1141 GTGTTCTGTGTGCGGGTTTTCAGCAATAGTTTAAAGGCCAGGTAGGGGCCGACAGGCC 1200
Qy 4656 GTGGAGAGCTGGGCATATACTACTATGTAGACGGGAGTTGTACCCCTTTCGGGTATGGTTC 4715
Db 1201 GTGGAGAGCTGGGCATATACTACTATGTAGACGGGAGTTGTACCCCTTTCGGGTATGGTTC 1260
Qy 4716 CTGAATGCAACATTTGTTGAAGCTTCGACGCGAGCCAAAGGCATGGTATGGTGTGTCATCAA 4775
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Qy 5436 TCATAGATATGCTGTGGTTTAGTCACTTTACCTGCAAAATCCCTTTGATCATGCGGTGT 5495
Db 1981 TCATAGATATGCTGTGGTTTAGTCACTTTACCTGCAAAATCCCTTTGATCATGCGGTGT 2040
Qy 5496 TTGCTTTTCAATTCGGGTATTTACTACCCACTACCTCACAAATGTTTCTGTCAT 5555
Db 2041 TTGCTTTTCAATTCGGGTATTTACTACCCACTACCTCACAAATGTTTCTGTCAT 2100
Qy 5556 TATTTGGAGGCGCAATTTGCGTCAAGCTTTACAGCGCTAGAGCGCAGCTGGCGTTTCATGA 5615
Db 2101 TATTTGGAGGCGCAATTTGCGTCAAGCTTTACAGCGCTAGAGCGCAGCTGGCGTTTCATGA 2160
Qy 5616 TGGCCGGGCTGCGGGAACAGCTCTTTGTGTATGTGACATCGGTGGGTTTGTCTTTGACA 5675
Db 2161 TGGCCGGGCTGCGGGAACAGCTCTTTGTGTATGTGACATCGGTGGGTTTGTCTTTGACA 2220

Qy 5676 TGCTAGGCGCTATGCTGCGCCTCATCCACTGCTTGTCTTGACATTTAAATGCTTGATGG 5735
Db 2221 TGCTAGGCGCTATGCTGCGCCTCATCCACTGCTTGTCTTGACATTTAAATGCTTGATGG 2280
Qy 5736 GTGAGTGGCCCACTATGATCAGCTTGTGTGTGTAGTCTACTCCGCGTTCAATCCGGCGG 5795
Db 2281 GTGAGTGGCYCACTATGATCAGCTTGTGTGTGTAGTCTACTCCGCGTTCAATCCGGCGG 2340
Qy 5796 CAGGAGTTGTGGGGCTTGTGTGAGTGTGCAATGTTTGTGACACACAGAGGCCAG 5855
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Qy	6836	AGAAAGCGCCAGTTCCGGGCAAGAACTGGTTGCTTACCTTGCCCTCCGCCCTCCGAGATC	6894
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Search completed: October 30, 2005, 11:07:26
Job time : 2963 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 08:56:10 ; Search time 25672 Seconds
(without alignments)
17740.362 Million cell updates/sec

Title: US-10-009-002-1

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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3	9376.6	99.8	9399	12	AY243572 Synthetic
4	9338.6	99.4	9397	6	AX805212 Sequence
5	9338.6	99.4	9397	14	HGB277947
6	9133	97.2	9139	6	AX057394
7	9059.8	96.4	9143	6	AX075140
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12	9059.8	96.4	9143	6	AR350538
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14	9059.8	96.4	9143	6	AR494272
15	9059.8	96.4	9143	6	AR494275
16	9059.8	96.4	9143	14	HGU22304
17	8692.6	92.5	8912	6	AR230335
18	8692.6	92.5	8912	6	AR310030
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22	6088	64.8	8069	6	AX805211	AX805211 Sequence
23	4159	44.2	4268	6	AR230353	AR230353 Sequence
24	4159	44.2	4268	6	AR310048	AR310048 Sequence
25	4159	44.2	4268	6	AR350460	AR350460 Sequence
26	4159	44.2	4268	6	AR494194	AR494194 Sequence
27	1223.4	13.0	1233	14	AY534875	AY534875 Hepatitis
28	1223.4	13.0	1233	14	AY534877	AY534877 Hepatitis
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31	1215.4	12.9	1233	14	AY534874	AY534874 Hepatitis
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34	449.8	4.8	479	6	AR230433	AR230433 Sequence
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36	449.8	4.8	479	6	AR310128	AR310128 Sequence
37	449.8	4.8	479	6	AR350453	AR350453 Sequence
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43	319.6	3.4	337	6	AR230426	AR230426 Sequence
44	319.6	3.4	337	6	AR310045	AR310045 Sequence
45	319.6	3.4	337	6	AR310121	AR310121 Sequence

ALIGNMENTS

RESULT 1
AX057392
LOCUS AX057392 9399 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 1 from Patent WO0075337.
ACCESSION AX057392
VERSION AX057392.1 GI:12310132
KEYWORDS
SOURCE
ORGANISM Hepatitis GB virus B
Hepatitis GB virus B
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
REFERENCE 1
AUTHORS Bukh.J., Yanagi.M., Emerson.S.U. and Purcell,R.H.
TITLE Infectious cdna clone of gb virus b and uses thereof
JOURNAL Patent: WO 0075337-A 1 14-DEC-2000;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:39113"

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	Matches 9399;	Conservative	0;	Mismatches	0;	Indels
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Db	1	ACCACAAACTCCAGTTTGTACACTCCGCTAGGAATGCTCTGGAGCACC	CCCCCTAG	60		
Qy	61	CAGGGCTGGGGATTTCCCTGCTGCGAGAGGGTGGAGCCAACTTAGTAT	120			
Db	61	CAGGGCTGGGGATTTCCCTGCTGCGAGAGGGTGGAGCCAACTTAGTAT	120			
Qy	121	GTAGGCGCGGGACTCATGCGCTCGGCTGATGACAGCGCCAGCTTGCTGGATGGC	180			
Db	121	GTAGGCGCGGGACTCATGCGCTCGGCTGATGACAGCGCCAGCTTGCTGGATGGC	180			
Qy	181	CCTGATGGGCTTCATGGTTCGGTGTGGCGCTTTAGGCAGCTTCCACGCCACCA	240			
Db	181	CCTGATGGGCTTCATGGTTCGGTGTGGCGCTTTAGGCAGCTTCCACGCCACCA	240			

QY 241 CCTCCAGATAGAGCGGCGGCACTGTAGGGAAGACC GGGGACCGGTCACTACCAAGGACG 300
DB |||||
241 CCTCCAGATAGAGCGGCGGCACTGTAGGGAAGACC GGGGACCGGTCACTACCAAGGACG 300
QY 301 CAGACCTCTTTTGTAGTATCAGCCCTCGGGAAGTAGTTGGGGAAGCCCACTTATATGTGT 360
DB |||||
301 CAGACCTCTTTTGTAGTATCAGCCCTCGGGAAGTAGTTGGGGAAGCCCACTTATATGTGT 360
QY 361 TGGGATGTTGGGTTAGCCATCCATACCGTACTGCCCTGATAGGGTCTCTTGGAGGGGAT 420
DB |||||
361 TGGGATGTTGGGTTAGCCATCCATACCGTACTGCCCTGATAGGGTCTCTTGGAGGGGAT 420
QY 421 CTGGGAGTCTCGTAGACGTTAGCACATGCTGTATTTCTACTCAAAACAAGTCTCTGTACC 480
DB |||||
421 CTGGGAGTCTCGTAGACGTTAGCACATGCTGTATTTCTACTCAAAACAAGTCTCTGTACC 480
QY 481 TGGCCCAAGACCGGCAAGAACCAAGCAGACGCGAGGCTTCATATCTGTGTCCATTTAAAC 540
DB |||||
481 TGGCCCAAGACCGGCAAGAACCAAGCAGACGCGAGGCTTCATATCTGTGTCCATTTAAAC 540
QY 541 ATCTGTTGAAAGGGGACAACGAGCAAGCGCAAGGTCCAGCGCGATGCTCGGCCCTCGTAA 600
DB |||||
541 ATCTGTTGAAAGGGGACAACGAGCAAGCGCAAGGTCCAGCGCGATGCTCGGCCCTCGTAA 600
QY 601 TTACAAAATTGCTGTATCCATGATGGCTTGCGAGACATTTGGCTCAGGCTGCTTTGCCACG 660
DB |||||
601 TTACAAAATTGCTGTATCCATGATGGCTTGCGAGACATTTGGCTCAGGCTGCTTTGCCACG 660
QY 661 TCATGGTTGGGACCGCCAGACCTCGGCCATAAGTCTCGCAATCTTGGAACTCTTCTCGGA 720
DB |||||
661 TCATGGTTGGGACCGCCAGACCTCGGCCATAAGTCTCGCAATCTTGGAACTCTTCTCGGA 720
QY 721 TTACCCCTTTGGGGTGGATTGGTGAAGTTACAACTCACACACCTCTAGTAGGCCCGCTGCT 780
DB |||||
721 TTACCCCTTTGGGGTGGATTGGTGAAGTTACAACTCACACACCTCTAGTAGGCCCGCTGCT 780
QY 781 GGCAGAGCGGTCTGTCAGACAGTCTGCCAGATAGTACGCTTTGCTGGAGGATGGAGTCAA 840
DB |||||
781 GGCAGAGCGGTCTGTCAGACAGTCTGCCAGATAGTACGCTTTGCTGGAGGATGGAGTCAA 840
QY 841 CTGGGCTACTGGTTGGTTGGTGTCCACCTTTTGTGGTATGTCTGTCTATCTTTGGCCCTG 900
DB |||||
841 CTGGGCTACTGGTTGGTTGGTGTCCACCTTTTGTGGTATGTCTGTCTATCTTTGGCCCTG 900
QY 901 TCCCTGTAGTGGGCGCGGTCACCTGACCCAGACACAATACCAATCCTGACCAATTG 960
DB |||||
901 TCCCTGTAGTGGGCGCGGTCACCTGACCCAGACACAATACCAATCCTGACCAATTG 960
QY 961 CTGCCAGCGTAATCAGGTTATCTATTGTTCTCCTTCCACTTGGCTTACAGGCTGGTTG 1020
DB |||||
961 CTGCCAGCGTAATCAGGTTATCTATTGTTCTCCTTCCACTTGGCTTACAGGCTGGTTG 1020
QY 1021 TGTGATCTGTGGGACGAGTGTGGGTTCCGCCAATCGGTACATCTCACACCTTCCAA 1080
DB |||||
1021 TGTGATCTGTGGGACGAGTGTGGGTTCCGCCAATCGGTACATCTCACACCTTCCAA 1080
QY 1081 TTGGAGTGGCAGGACTCTCTTCTGCTGACCAATTTGATTTGTTATGGGCGCTCTTGT 1140
DB |||||
1081 TTGGAGTGGCAGGACTCTCTTCTGCTGACCAATTTGATTTGTTATGGGCGCTCTTGT 1140
QY 1141 GACCTGTGACGCCCTTGACATTTGGTGAAGTGTGTGGTGGTGTATTTAGTCTGGTGAAGT 1200
DB |||||
1141 GACCTGTGACGCCCTTGACATTTGGTGAAGTGTGTGGTGGTGTATTTAGTCTGGTGAAGT 1200
QY 1201 GCTTGTCAAGGCACTGGCTTTATTCATAGACCTCAATGAATCTGTACTTGTACTCTGGA 1260
DB |||||
1201 GCTTGTCAAGGCACTGGCTTTATTCATAGACCTCAATGAATCTGTACTTGTACTCTGGA 1260
QY 1261 AGTGCCCACTGGAATAGATCTCTGGGTTCTAGGGTTTATCGGTTGGATGGCGGCAAGGT 1320
DB |||||
1261 AGTGCCCACTGGAATAGATCTCTGGGTTCTAGGGTTTATCGGTTGGATGGCGGCAAGGT 1320
QY 1321 CGAGGCTGTCTATCTCTTTGACCAAACTGGCTTTCACAAAGTACCATACGCTATTTCGCACTAT 1380

DB |||||
1321 CGAGGCTGTCTATCTCTTTGACCAAACTGGCTTTCACAAAGTACCATACGCTATTTCGCACTAT 1380
QY 1381 GTTTAGCAGTGTACTACTACCTGGCGGTTGGCGCTCTGATCTACTATGCTCTCTCGGGGCAA 1440
DB |||||
1381 GTTTAGCAGTGTACTACTACCTGGCGGTTGGCGCTCTGATCTACTATGCTCTCTCGGGGCAA 1440
QY 1441 GTGGTATCAGTTGCTCTTAGCGCTTATGCTTTTACATAGAAGGACCTCTCGAAACCCCAT 1500
DB |||||
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QY 1501 CAGGGTGCCCACTGGATGCTCAATAGCTGAGTGTTCGCTTTGATGATACCATGTC 1560
DB |||||
1501 CAGGGTGCCCACTGGATGCTCAATAGCTGAGTGTTCGCTTTGATGATACCATGTC 1560
QY 1561 TTGCCACTCTTTTGTAGTGAAGTGTGTCAGAAGTCAATTTGTACAGTCCAAAGTGGAC 1620
DB |||||
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DB |||||
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DB |||||
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DB |||||
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QY 1801 CGAAGCATCGGCTGTAAACCATGCTTAAACAAACCGCATGGCACAAACGCTCAGCCCTGAA 1860
DB |||||
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QY 1861 ATTGGCTATATTACAATACCTCGGCTCTAAAGAAATGTTTAAACCTCATAAATTGGATGTC 1920
DB |||||
1861 ATTGGCTATATTACAATACCTCGGCTCTAAAGAAATGTTTAAACCTCATAAATTGGATGTC 1920
QY 1921 AGGCCATTTGTTTGTAGGGATCAGATACCCCTATAGTTTACTTTTATGACCTGTGCAA 1980
DB |||||
1921 AGGCCATTTGTTTGTAGGGATCAGATACCCCTATAGTTTACTTTTATGACCTGTGCAA 1980
QY 1981 TTCACCTCTCTACACCGAGAGTGGGCTAGGTTGCCCGGTACCCACCTGTGGTACG 2040
DB |||||
1981 TTCACCTCTCTACACCGAGAGTGGGCTAGGTTGCCCGGTACCCACCTGTGGTACG 2040
QY 2041 TGGTCTTGGTTACAGGTTCCGCAAGGGTTTTACAGTGTGTGAAAGACCTAGGCCACAGG 2100
DB |||||
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QY 2101 ATTGATCACCACCAAGACCAAGCTCGGAAATTTATCAGGCTTATATTCGGCCACGGGTGC 2160
DB |||||
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DB |||||
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QY 2221 CAGCAAGTATCTTATTTTAGCCTACCTCTGTACTTGTTCCTTTTGTGGCGCGCTTC 2280
DB |||||
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QY 2281 TGGTTACCCCTTGGCTCTGTCTCCATCCAGTCTGTATCTCCAAAGTGGCTGGGATGT 2340
DB |||||
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QY 2341 TTTGTCTAAAGCTCAAGTAGTCTCTTTTGTCTTCAATTTCTCATCTGTGTCTACTCCG 2400
DB |||||
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DB |||||

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Db 2821 TGTGCTGGTTGTTTCCCGGTGCGACATATGACGCGCTGGTACTTCTGTGTGTCA 2880
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ORIGIN

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VERSION AY243572.1 GI:33090377
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ORGANISM
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1 (bases 1 to 9399)
Martin, A., Bodola, F., Sangar, D. V., Goettge, K., Popov, V.,
Rijnbrand, R., Lanford, R. E. and Lemon, S. M.
Chronic hepatitis associated with GB virus B persistence in a
tamarin after intrahepatic inoculation of synthetic viral RNA
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9962-9967 (2003)
12907703
AUTHORS
JOURNAL
PUBMED
2 (bases 1 to 9399)
Martin, A., Bodola, F., Sangar, D. V., Goettge, K., Popov, V.,
Rijnbrand, R., Lanford, R. E. and Lemon, S. M.
Direct Submission
Submitted (25-FEB-2003) Virology and Immunology, University of
Texas Medical Branch, 301 University Boulevard, Galveston, TX
77555, USA
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QY ||||| 5581 GCTTACAGACGCTAGAGCGCACTGGCGTTTCATGATGCCCGGGCTGCGGGAACAGCTCT 5640
Db ||||| 5581 GCTTACAGACGCTAGAGCGCACTGGCGTTTCATGATGCCCGGGCTGCGGGAACAGCTCT 5640
QY ||||| 5641 TGGTACATGAGCATCGGTGGGTTTGTCTTTTGACATGCTAGCGGCTATGCTGCGGCTC 5700
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Db	6061	TTGGCAGTAT	GTGTGCAAT	TCTTTGTG	ATTTGCTT	TAAATG	CTTAAAG	CTGAGTTC	A	6120
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Db	6121	GAGCATGGT	TAAATTC	TCTGGTGT	CTCTTTCT	ACAGCT	GGCAG	AGGGGTCA	AAAGGCC	6180
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Db	6181	CTGGAATGG	ATCAGTAT	GTCTCC	AAAGCAC	GTGTCC	ATGCGG	TGCTG	AACTCATCT	6240
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Db	7081	TTTATACC	CAGTTAC	CCCTCC	CAAAA	AGGAGT	CTCT	GAAAT	TGTC	CAGAC	GAAGTT	TGGT	7140
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VERSION AJ277947.1 GI:13162187
KEYWORDS ORF1; polyprotein.
SOURCE Hepatitis GB virus B
ORGANISM Hepatitis GB virus B
REFERENCE 1
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
AUTHORS Sbardellati,A., Scarselli,B., Verschoor,E., De Tomassi,A.,
Lazaro,D. and Traboni,C.
TITLE Generation of infectious and transmissible virions from a GB virus
B full-length consensus clone in tamarins
J. Gen. Virol. 82 (Pt 10), 2437-2448 (2001)
JOURNAL 21446677
MEDLINE 11562537
PUBMED 2 (bases 1 to 9397)
AUTHORS Traboni,C.
DIRECT Submision
TITLE Submitted (15-MAY-2000) Traboni C., Biochemistry, IRBM P.
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Qy	241	CCTCCAGATAGAGCGGGGACCTGTAGGGAAGA.CCGGGAGCCGGTCACTACAGGAGC	300						
Db	241	CCTCCAGATAGAGCGGGGACCTGTAGGGAAGA.CCGGGAGCCGGTCACTACAGGAGC	300						
Qy	301	CAGACCTCTTTTTCAGTATCAGCGCTCCGGAAGTAGTTGGGCAAGCCCACTATATGT	360						
Db	301	CAGACCTCTTTTTCAGTATCAGCGCTCCGGAAGTAGTTGGGCAAGCCCACTATATGT	360						
Qy	361	TGGGATGGTTGGGGTTAGCCATCCATACCGTACTCGCTGTAGGGTCCCTTCGAGGGGAT	420						
Db	361	TGGGATGGTTGGGGTTAGCCATCCATACCGTACTCGCTGTAGGGTCCCTTCGAGGGGAT	420						
Qy	421	CTGGAGTCTCGTAGACCGTAGACATGCTGTTATTTCTACTCAAAAGTCTGTACC	480						
Db	421	CTGGAGTCTCGTAGACCGTAGACATGCTGTTATTTCTACTCAAAAGTCTGTACC	480						
Qy	481	TGCCCCAGACGCGCAGACAGACGACGCGCTTCATATCCTGTGTCATTAATAAC	540						
Db	481	TGCCCCAGACGCGCAGACAGACGACGCGCTTCATATCCTGTGTCATTAATAAC	540						

Qy	541	ATCTGTTGAAAGGGGAACAACGAGCAAAAGCCGCAAAAGTCACGCGCATGCTCGGCCCTGTA	600
Db	541	ATCTGTTGAAAGGGGAACAACGAGCAAAAGCCGCAAAAGTCACGCGCATGCTCGGCCCTGTA	600
Qy	601	TTACAAATTTGCTGGTATCATATGATGCTTGCAGACATTTGGCTCAGGCTGCTTTGCCAGC	660
Db	601	TTACAAATTTGCTGGTATCATATGATGCTTGCAGACATTTGGCTCAGGCTGCTTTGCCAGC	660
Qy	661	TCATGTTGGGGACGCCAAGACCCCTCGCCATTAAGTCTCGCAATCTTGGAAATCTCTCTGGA	720
Db	661	TCATGTTGGGGACGCCAAGACCCCTCGCCATTAAGTCTCGCAATCTTGGAAATCTCTCTGGA	720
Qy	721	TTACCTTTTGGGGTGGATTTGGTATGTTTCAACTCACACACCTCTAGTAGCCCGCTGGT	780
Db	721	TTACCTTTTGGGGTGGATTTGGTATGTTTCAACTCACACACCTCTAGTAGCCCGCTGGT	780
Qy	781	GGCAGGAGCGGTCTGTCGACAGTCTGCCAGATAGTACGCTTGTCTGAGAGTGGAGTCAA	840
Db	781	GGCAGGAGCGGTCTGTCGACAGTCTGCCAGATAGTACGCTTGTCTGAGAGTGGAGTCAA	840
Qy	841	CTGGGCTACTGGTTGGTTCCACCTTTTGTGGTATGTCTGCTATCTTTTGGGCTG	900
Db	841	CTGGGCTACTGGTTGGTTCCACCTTTTGTGGTATGTCTGCTATCTTTTGGGCTG	900
Qy	901	TCCCTGTAGTGGGGCGGGTCACTGACCCAGACACAAATACCAATCTCTGACCAATTG	960
Db	901	TCCCTGTAGTGGGGCGGGTCACTGACCCAGACACAAATACCAATCTCTGACCAATTG	960
Qy	961	CTGCCAGCTAATCAGGTATCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1020
Db	961	CTGCCAGCTAATCAGGTATCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1020
Qy	1021	TGTGATCTGTGCGGACGAGTCTGGGTTCCGCCAATCCGTACATCTCACACCTTCCAA	1080
Db	1021	TGTGATCTGTGCGGACGAGTCTGGGTTCCGCCAATCCGTACATCTCACACCTTCCAA	1080
Qy	1081	TTGGAATGGGACGAGTCTCTTCTTGGCTGACCAATTGATTTTGTATGGGCTCTTGT	1140
Db	1081	TTGGAATGGGACGAGTCTCTTCTTGGCTGACCAATTGATTTTGTATGGGCTCTTGT	1140
Qy	1141	GACCTGTGACGCGCTTACATTTGATGTTGTGGTGGTGTGTTAGTCTGGTACTG	1200
Db	1141	GACCTGTGACGCGCTTACATTTGATGTTGTGGTGGTGTGTTAGTCTGGTACTG	1200
Qy	1201	GCTTGTGAGGCACTGGCTTATTCATAGACCTCAATGAAATCTGGTACTTGTACTTGA	1260
Db	1201	GCTTGTGAGGCACTGGCTTATTCATAGACCTCAATGAAATCTGGTACTTGTACTTGA	1260
Qy	1261	AGTGCCCACTGGGAATAGATCTGGGTTCTTAGGTTTATCGGGTGGATGGCCGGCAAGT	1320
Db	1261	AGTGCCCACTGGGAATAGATCTGGGTTCTTAGGTTTATCGGGTGGATGGCCGGCAAGT	1320
Qy	1321	CGAGGCTGTCATCTTTGACCAAACTGGCTTCAAAAGTACCATACGCTATTGGGACTAT	1380
Db	1321	CGAGGCTGTCATCTTTGACCAAACTGGCTTCAAAAGTACCATACGCTATTGGGACTAT	1380
Qy	1381	GTTTGTAGCAGTGTACATACCTTGGCGGTGGCGCTCTGATCTACTATGCTCTCGGGGCA	1440
Db	1381	GTTTGTAGCAGTGTACATACCTTGGCGGTGGCGCTCTGATCTACTATGCTCTCGGGGCA	1440
Qy	1441	GTGGTATCAGTTGCTCTAGGCTTATGCTTTTACATAGACGACCTCTGGAACCCCAT	1500
Db	1441	GTGGTATCAGTTGCTCTAGGCTTATGCTTTTACATAGACGACCTCTGGAACCCCAT	1500
Qy	1501	CAGGGTCCCACTGGATGCTCAATAGCTGAGTTTGTCTCGCTTTGTATGATACCATGTC	1560
Db	1501	CAGGGTCCCACTGGATGCTCAATAGCTGAGTTTGTCTCGCTTTGTATGATACCATGTC	1560
Qy	1561	TTGCCACTCTTATTTGAGTGAGATGTGTGAGAGTCAATTTGTTACAGTCCAAAGTGAC	1620
Db	1561	TTGCCACTCTTATTTGAGTGAGATGTGTGAGAGTCAATTTGTTACAGTCCAAAGTGAC	1620
Qy	1621	CAGGCTATCACTCTAGAGTATAAACAATCCATATCTTGGTACCCCTATACAAATCCCTGG	1680

Db 1621 ||||| CAGGCTCTCACTAGAGTATAACAACCTCCATATCTTGGTACCCCTATACAAATCCCTGG 1680
QY 1681 TGCAGGGGATGTATGGTTAAATTCABAAATACACATGGGGTCTCCGCTATTCGCA 1740
Db 1681 TGCAGGGGATGTATGGTTAAATTCABAAATACACATGGGGTCTCCGCTATTCGCA 1740
QY 1741 TGTGCATCTGACTACACTATGGGCACTGATGAGTGTGGAAACGACACTCGCAACACTTA 1800
Db 1741 TGTGCCATCGTACTGCACTATGGGCACCTGATGCACTGTGGAACGACACTCGCAACACTTA 1800
QY 1801 CGAAGCATCGGTGTAAACACATATGGCTTAACACCGCATGGGCAACACGGCTAGCCCTGAA 1860
Db 1801 CGAAGCATCGGTGTAAACACATATGGCTTAACACCGCATGGGCAACACGGCTAGCCCTGAA 1860
QY 1861 ATTGGCTATATTACAAATACCCCTGGCTTAAGAAATGTTTAAACCTCATATTTGATGTC 1920
Db 1861 ATTGGCTATATTACAAATACCCCTGGCTTAAGAAATGTTTAAACCTCATATTTGATGTC 1920
QY 1921 AGGCCATTTGATTTAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGAA 1980
Db 1921 AGGCCATTTGATTTAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGAA 1980
QY 1981 TTCCACTCTCTACACCGGAGAGTGGGCTAGGTTGCCCGGTACCCACCTGTGGTAGG 2040
Db 1981 TTCCACTCTCTACACCGGAGAGTGGGCTAGGTTGCCCGGTACCCACCTGTGGTAGG 2040
QY 2041 TGGTTCTTGGTTACAGGTTCCGCAAGGGTTTACAGTGTATGTAAGAGACCTTAGCCACAGG 2100
Db 2041 TGGTTCTTGGTTACAGGTTCCGCAAGGGTTTACAGTGTATGTAAGAGACCTTAGCCACAGG 2100
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Db 2101 ATTGATCACCAAGACCAAGCCTGGAATAATATCAGGTCCTTATATTCGCGCACGGGTGC 2160
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Db 2161 TTGTCTCTTACGGAGTTACCAAGCGCGTGTGCTAATCTCTGTGGGTTGTGG 2220
QY 2221 CAGCAAGTATCTTATTTAGCCTACTCTGTACTTGTCCCTTCTTTTGGCGCGCTTC 2280
Db 2221 CAGCAAGTATCTTATTTAGCCTACTCTGTACTTGTCCCTTCTTTTGGCGCGCTTC 2280
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Db 2281 TGGTTACCCCTTTGCGTCTGCTCCCAATCCAGTCTGATCTCCAGTCTGGCTGGAGTGT 2340
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Db 2341 TTGTCTAAAGCTCAAGTAGCTCTTTTGTCTTTGATTTTCTTCACTGTGTCTATCTCGG 2400
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Db 2401 CTGCAGGCTACGTTATGCTGCCCTTTAGGGTTTGTGCCATGGCTGGGGCTGCCCT 2460
QY 2461 AACTTTCTTTTGTGACGAGCTGCTGCCCAACAGATATGACTGGTGGGTCGACTGCT 2520
Db 2461 AACTTTCTTTTGTGACGAGCTGCTGCCCAACAGATATGACTGGTGGGTCGACTGCT 2520
QY 2521 AGTGCAGGGTTAGTTTGTGGGCGCGCGTAACCGTGGTCAACCGATAGCTCTGCTGT 2580
Db 2521 AGTGCAGGGTTAGTTTGTGGGCGCGCGTGACCGTGGTCAACCGATAGCTCTGCTGT 2580
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Db 2581 AGGCTCTTGGCTCTGTTAGCGCTTTTAAACCTCTTGCATTTGGTTAGCCCTGCTCAGC 2640
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Db 2641 TTTTGACACCGAGATAATTGGAGGGCTGACAAATACCACTGTAGTAGCAATTAGTTGTAT 2700
QY 2701 GTCTGTTTGGCTCTTGTCTCACTTGTATACCTCGCTGTGCTTTAGTTAACTCCTATCT 2760
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Db 2701 GTCTGTTTGGCTCTTGTCTCACTTGTATACCTCGCTGTGCTTTAGTTAACTCCTATCT 2760
QY 2761 TTGGCAACGTTGGGAGAAATGGTTTTGGAAAGTTTACACTAAGACCGGAGAGGTTTTCTCT 2820
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Db 2821 TGTGCTGTTTGTTCCTCCCGTGCACATATGACGCGCTGGTGACTTTCTGTGTGTGCA 2880
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Db 2881 CGTAGCTCTCTATATGTTTAAACATCCAGTGCAGCATCGTTCTTTGGGACGACTCTAGGGT 2940
QY 2941 TAGGGCCCATAGAAATGTTGGTGGCTCGGAAAGTGTCACTGCTGGTATTTCTCATATATGT 3000
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Db 3781 GGTGTGTCTGGATACCATCCCGAGTACACAGCATGCCACTCTTGATACAAACCTTAC 3840
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|||||

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Qy 7261 TTGCTGAGCATGAGCTACACTGAGCCGAGCTGATTAAGCTTCAAACTGCTTCTAAAGT 7320
Db 7261 TTGCTGAGCATGAGCTACACTGAGCCGAGCTGATTAAGCTTCAAACTGCTTCTAAAGT 7320
Qy 7321 TCTGTCTGCAACTCGGGCCATCAGTGTGGTTTCTCTCAAAAGAGATCATTTGGTGTATGT 7380
Db 7321 TCTGTCTGCAACTCGGGCCATCAGTGTGGTTTCTCTCAAAAGAGATCATTTGGTGTATGT 7380
Qy 7381 GACTGAGCCGCGGATCGGAGCTTTAGAAAAAAGTCTACTTAAATAGACAACTCT 7440
Db 7381 GACTGAGCCGCGGATCGGAGCTTTAGAAAAAAGTCTACTTAAATAGACAACTCT 7440
Qy 7441 GTTCCCCCATCATACCAAGCAAGTGAGATTGGCTTAAGAAAAAGCTTCAAAAGTTGT 7500
Db 7441 GTTCCCCCATCATACCAAGCAAGTGAGATTGGCTTAAGAAAAAGCTTCAAAAGTTGT 7500
Qy 7501 CGGTGTCTGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTAAGTCTGCTAAAGTC 7560
Db 7501 CGGTGTCTGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTAAGTCTGCTAAAGTC 7560
Qy 7561 CCACATCACTGCGCTTCCGGGCACTGATGTTGTTCTGGAGCAGCCCGCAAGGCTGTTCT 7620
Db 7561 CCACATCACTGCGCTTCCGGGCACTGATGTTGTTCTGGAGCAGCCCGCAAGGCTGTTCT 7620
Qy 7621 GGACTTGAGAAAGTGTGTGAGGAGAGGTGAGATACCGAGTCATTTATCGGCAAACTGTGAT 7680
Db 7621 GGACTTGAGAAAGTGTGTGAGGAGAGGTGAGATACCGAGTCATTTATCGGCAAACTGTGAT 7680
Qy 7681 AGTTCCAAAGAGAGGTCCTTCTGTAAGACCCCGCAGAAACCAACAAAGAAACCCCAAG 7740
Db 7681 AGTTCCAAAGAGAGGTCCTTCTGTAAGACCCCGCAGAAACCAACAAAGAAACCCCAAG 7740
Qy 7741 GCTTATCTCTGATCCGCCCACTTGAATGAGATGTGTTGAGAAAGATGTACTACGTCAGT 7800
Db 7741 GCTCATCTCTGATCCGCCCACTTGAATGAGATGTGTTGAGAAAGATGTACTACGTCAGT 7800
Qy 7801 TGCTCTGACGTAGTTAAAGCTGTCTGAGGAGATGCGTACCGGTTTGTAGATCCACGTCAC 7860
Db 7801 TGCTCTGACGTAGTTAAAGCTGTCTGAGGAGATGCGTACCGGTTTGTAGATCCACGTCAC 7860
Qy 7861 CCGTGTCAAGCTGTGTTGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 7920
Db 7861 CCGTGTCAAGCTGTGTTGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 7920
Qy 7921 AGTGTGTTTTGACAGTACCATCACACCGAGGATATCATGTTGGAGACAGACATCTACTCTC 7980
Db 7921 AGTGTGTTTTGACAGTACCATCACACCGAGGATATCATGTTGGAGACAGACATCTACTCTC 7980
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Db 7981 AGCAGCTAAACTCAGTACCAACACCGAGCTGGCAATTCACACCATTTGGGAGCAGTTATA 8040
Qy 8041 CGCTGGAGACCGATGATCGCTTATGATGGCGGAGAGATCGATATCGTAGGTGTAGGTC 8100
Db 8041 CGCTGGAGACCGATGATCGCTTATGATGGCGGAGAGATCGATATCGTAGGTGTAGGTC 8100
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Db 8101 TTCCGCGCTCTATCTACTACTCAAGTTCCAAAGTTTGAACCTGCTGGCTGAAGGTAAATGC 8160
Qy 8161 TGCAGCCGAAACAGGCTGGCATGAAGAACCTTCTTCTTATTTGCGGCGATGATGTCAC 8220
Db 8161 TGCAGCCGAAACAGGCTGGCATGAAGAACCTTCTTCTTATTTGCGGCGATGATGTCAC 8220

Qy	8221	CGTAATTTGAAAGCCCGAGCAGATGCAGACAAACAAAGCAATGCGTGTCTTTGCTAG	8280
Db	8221	CGTAATTTGGAAGCCCGAGCAGATGCAGACAAACAAAGCAATGCGTGTCTTTGCTAG	8280
Qy	8281	CTGGATGAAGGTGATGGTGCACACAAAGATGTGTGCCTCAACCCAAATACAGTTTGG	8340
Db	8281	CTGGATGAAGGTGATGGTGCACACAAAGATGTGTGCCTCAACCCAAATACAGTTTGG	8340
Qy	8341	AGAATTAACATCATCAATGTTACCTCTGGAAATACCAAAAGTGCAGCCCTTA	8400
Db	8341	AGAATTAACATCATCAATGTTACCTCTGGAAATACCAAAAGTGCAGCCCTTA	8400
Qy	8401	CTACTTTCTTACAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
Db	8401	CTACTTTCTTACAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
Qy	8461	ATACAACCCAGTGTCTCGTGGATTGGGTATCTAATACATCACTACCCATGTGTTGTGGT	8520
Db	8461	ATACAACCCAGTGTCTCGTGGATTGGGTATCTAATACATCACTACCCATGTGTTGTGGT	8520
Qy	8521	TAGCCGTGTGTGGCTGTCCATTTTCATGAGCAGATGCTCTTTGAGGACAAACTTCCCGA	8580
Db	8521	TAGCCGTGTGTGGCTGTCCATTTTCATGAGCAGATGCTCTTTGAGGACAAACTTCCCGA	8580
Qy	8581	GACTGTGACCTTTGACTGGTATGGGAAAAATTTATACGGTGTCTGTAGAAGATCTGCCAG	8640
Db	8581	GACTGTGACCTTTGACTGGTATGGGAAAAATTTATACGGTGTCTGTAGAAGATCTGCCAG	8640
Qy	8641	CATCATTTGCTGTGTGACCGTATTGAGGCTTTCTCGTGTGTGGCTGTACCAACGCTGA	8700
Db	8641	CATCATTTGCTGTGTGACCGTATTGAGGCTTTCTCGTGTGTGGCTGTACCAACGCTGA	8700
Qy	8701	GATCCTCAGAGTTTCCAACTCACTAACAGACATGACCATGCCCTCTGCGAGCTCGCG	8760
Db	8701	GATCCTCAGAGTTTCCAACTCACTAACAGACATGACCATGCCCTCTGCGAGCTCGCG	8760
Qy	8761	AAAGAAAGCAGGGCGGTCTCGCCAGGCCAAGAGGCGTGGCGAGACACACGAAATT	8820
Db	8761	AAAGAAAGCAGGGCGGTCTCGCCAGGCCAAGAGGCGTGGCGAGACACACGAAATT	8820
Qy	8821	GGCTCGCTTCTCTCTGGCATGTACATCTAGACCTCTACCAATTTGGATTAAGACGAG	8880
Db	8821	GGCTCGCTTCTCTCTGGCATGTACATCTAGACCTCTACCAATTTGGATTAAGACGAG	8880
Qy	8881	CGTGGCTCGGTACACCATTTTCAATTAATGTGATGTTTACTCCCGGAGGGGATGTGT	8940
Db	8881	CGTGGCTCGGTACACCATTTTCAATTAATGTGATGTTTACTCCCGGAGGGGATGTGT	8940
Qy	8941	TATTACACCAAGAGATTTGCAGAGTTCTTGTGAAGTATTTGCTGTCAATTTGTTTT	9000
Db	8941	TATTACACCAAGAGATTTGCAGAGTTCCTTGTGAAGTATTTGCTGTCAATTTGTTTT	9000
Qy	9001	TGCCCTAGGGCTCAATGCTGTGGATTAGCCATCAGCTGAACCCCAAAATTCAAAATTA	9060
Db	9001	TGCCCTAGGGCTCAATGCTGTGGATTAGCCATCAGCTGAACCCCAAAATTCAAAATTA	9060
Qy	9061	CTAACAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	9120
Db	9061	CTAACAG - TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	9118
Qy	9121	TTAACGACCCCGCGATGTGATTTGGCGACCATGTGTGATCAAAACCTTTTCGGGTGAA	9180
Db	9119	TTAACGACCCCGCGATGTGATTTGGGACCATGTGTGATCAAAACCTTTTCGGGTGAA	9178
Qy	9181	GCCATGCTCTGAAGGGATGACGTCCCTTCTGGCTCATCCAACAAAAACCGTCTCGGTGG	9240
Db	9179	GCCATGCTCTGAAGGGATGACGTCCCTTCTGGCTCATCCAACAAAAACCGTCTCGGTGG	9238
Qy	9241	GTGAGGAGTCTTGCTGTGTGGGAAGCAGTCAAGTATTAATTTCCCGTGTGTGTGTGACGC	9300
Db	9239	GTGAGGAGTCTTGCTGTGTGGGAAGCAGTCAAGTATTAATTTCCCGTGTGTGTGTGACGC	9298

Qy	9301	CTCAGCAGCTATTATTGTCGCTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTG	9306
Db	9299	CTCAGCAGCTATTATTGTCGCTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTG	9358
Qy	9361	TTCCAAGCGGAGGCGCAACCCCGCTTGGAAATTAATAACT	9399
Db	9359	TTCCAAGCGGAGGCGCAACCCCGCTTGGAAATTAATAACT	9397
RESULT 6			
AX057394		9139 bp	DNA
LOCUS	AX057394	Sequence 3 from Patent WO0075337.	linear PAT 17-JAN-2001
DEFINITION	AX057394		
ACCESSION	AX057394.1	GI:12310133	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
ORIGIN			
Query Match		97.2%; Score 9133; DB 6; Length 9139;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 9133; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ACCAACAACACTCCAGTTTGTACATCCCGTAGGAATGCTCTGGAGCACCCCCCTAG	60
Db	1	ACCACAACAACACTCCAGTTTGTACATCCCGTAGGAATGCTCTGGAGCACCCCCCTAG	60
Qy	61	CAGGGCTGTGGGGATTTCCCTCGCCGCTGCGAGAGGGTGGAGCCAAACACCTTAGTAT	120
Db	61	CAGGGCTGTGGGGATTTCCCTCGCCGCTGCGAGAGGGTGGAGCCAAACACCTTAGTAT	120
Qy	121	GTAGGCGCGGGACTCATAGCGCTCGCGTGATGACAAGCGCCAAAGCTTGATGGATGGC	180
Db	121	GTAGGCGCGGGACTCATAGCGCTCGCGTGATGACAAGCGCCAAAGCTTGATGGATGGC	180
Qy	181	CTGTATGGGCGTTTCATGGGTTGGGTGTGGTGGCGCTTTAGGCGAGCTCCACGCCACCA	240
Db	181	CCTGATGGGCGTTTCATGGGTTGGGTGTGGTGGCGCTTTAGGCGAGCTCCACGCCACCA	240
Qy	241	CCTCCAGATAGACGGCGGCACGTGTAGGAAGACCGGGACCGGTCACTACCAAGGACG	300
Db	241	CCTCCAGATAGACGGCGGCACGTGTAGGAAGACCGGGACCGGTCACTACCAAGGACG	300
Qy	301	CAGACCTCTTTTGTAGTATCACGCTCCGAAAGTAGTTGGGCAAGCCACCTATATGTGT	360
Db	301	CAGACCTCTTTTGTAGTATCACGCTCCGAAAGTAGTTGGGCAAGCCACCTATATGTGT	360
Qy	361	TGGGATGGTTGGGTTAGCCATCATACCGTACTGCTGTATAGGGTCTTTCGCGAGGGAT	420
Db	361	TGGGATGGTTGGGTTAGCCATCATACCGTACTGCTGTATAGGGTCTTTCGCGAGGGAT	420
Qy	421	CTGGGAGTCTGTAGACCGTAGCACATGCTGTATTCTTCTACTCAACAAAGTCTCTGACC	480
Db	421	CTGGGAGTCTGTAGACCGTAGCACATGCTGTATTCTTCTACTCAACAAAGTCTCTGACC	480
Qy	481	TGGCCCCAGAACCGCGAAGAACCAAGCAGACGCGAGCTTCATATCCTGTGTCATTAAAC	540
Db	481	TGGCCCCAGAACCGCGAAGAACCAAGCAGACGCGAGCTTCATATCCTGTGTCATTAAAC	540
Qy	541	ATCTGTTGAAAGGGGACAACAGCGCAAGCGCAAGTCCAGCGGATGCTCGGCTCTGTAA	600

Db 541 ATCTGTTGAAAGGACAAACGAGCAAAAGCGCAAAGTCCAGCGCGATGCTCGCGCTCGTAA 600
QY 601 TTACAAAATGCTGTATCTCATGATGGCTTGAGACATTTGGCTCAGGCTGCTTTGCCAGC 660
Db 601 TTACAAAATGCTGTATCTCATGATGGCTTGAGACATTTGGCTCAGGCTGCTTTGCCAGC 660
QY 661 TCATGTTGGGAGCCCAAGACCTTCGCGCATAGTCTCGCAATCTTTGGAATCTTTCTGGA 720
Db 661 TCATGTTGGGAGCCCAAGACCTTCGCGCATAGTCTCGCAATCTTTGGAATCTTTCTGGA 720
QY 721 TTACCTTTGGGTTGGATTTGGTATGTTTAACTACACACCTCTAGTAGGCGCGCTGGT 780
Db 721 TTACCTTTGGGTTGGATTTGGTATGTTTAACTACACACCTCTAGTAGGCGCGCTGGT 780
QY 781 GCGAGGCGGTCTGTTCCAGACAGTCTGCAGATAGTACGCTTGCCTGGAGGATGAGTCAA 840
Db 781 GCGAGGCGGTCTGTTCCAGACAGTCTGCAGATAGTACGCTTGCCTGGAGGATGAGTCAA 840
QY 841 CTGGGCTACTGTTGGTTGGTGTCCACCTTTTGTGTATGTTCTGCTATCTTTGGCGCTG 900
Db 841 CTGGGCTACTGTTGGTTGGTGTCCACCTTTTGTGTATGTTCTGCTATCTTTGGCGCTG 900
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Db 901 TCCCTGTAGTGGGCGCGGCTCACTGA CCGAGACA CAAATACCA CAATCCTGACCAATTG 960
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Db 1081 TTGGACTGCGACGACTCTCTTCTGGCTGACCAATTTGATTTGTTATGGGCGCTCTTGT 1140
QY 1141 GACCTGTACGCGCTTGACATTTGGTGTGAGTGTGCTGCTGCTGATTTAGTTCGGTGACTG 1200
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Db 1201 GCTTGTACGGCACTGGCTTTATTCATAGACCTCAATGAAACTGGTACTTTGTACTCTGGA 1260
QY 1261 AGTGCCCACTGGAATAGATCTCTGGGTTCTAGGGTTTATCGGGTGGATGGCCGGCAAGT 1320
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Db 1321 CGAGGCTGTCTCTTTGACCAAACTGGCTTTCACAGTACCATACGCTATTTCGCACTAT 1380
QY 1381 GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCTCTCGGGGCA 1440
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QY 1801 CGAAGCATCCGGTGTAAACACCATGGCTAAACCGCATGGCAGACAGGCTCAGCCCTGAA 1860
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QY 1861 ATTGGCTATATTAACAATACCTCGGTCTTAAAGAAATGTTTAAACCTCAATAATTGGATGTC 1920
Db 1861 ATTGGCTATATTAACAATACCTCGGTCTTAAAGAAATGTTTAAACCTCAATAATTGGATGTC 1920
QY 1921 AGGCCATTTGTTTGAAGGATCAGATA CCCCCTATAGTTTACTTTTATAGACCTCTGTGAA 1980
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QY 1981 TTCCACTCTCTTACCA CCGGAGAGTGGGCTAGGTTGCCCGGTACCCCACTGTGGTAGC 2040
Db 1981 TTCCACTCTCTTACCA CCGGAGAGTGGGCTAGGTTGCCCGGTACCCCACTGTGGTAGC 2040
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RESULT 7
AR075140
LOCUS
DEFINITION Sequence 32 from patent US 5955318.
ACCESSION AR075140
VERSION AR075140.1 GI:10001892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

AR075140 9143 bp DNA linear PAT 28-AUG-2000

Unclassified.
1 (bases 1 to 9143)
Simons, J.N., Desai, S. M. and Mushahwar, I. K.
Reagents and methods useful for controlling the translation of
hepatitis GBV proteins
Patent: US 5953118-A 32 21-SEP-1999;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 96.4%; Score 9059.8; DB 6; Length 9143;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 9096; Conservative 0; Mismatches 37; Indels 4; Gaps 1;

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DB 61 CAGGCGTGGGGATTTCCTCCCTGCCCTCTGCAGAAAGGTGGAGCCAAACCCTTAGTAT 120

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DB 121 GTAGCGCGGGACTCATGACGCTCGCGTGTGACAAAGCGCAAGCTTGACTTGGATGGC 180

QY 181 CTTGATGGGCGTTCAATGGGTTCCGTTGGTGGTGGCGCTTTAGGACGCTCCAGCCCAACA 240
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DB 241 CTTCCAGATAGAGCGGGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGAGC 300

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VERSION AR230431.1 GI:27270570
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UnClassified.
REFERENCE 1 (bases 1 to 9143)
AUTHORS Simons,J.N., Pilot-Matias,T.J., Dawson,G.J., Schlauder,G.G.,
Deesi,S.M., Leary,T.P., Muerhoff,A.S., Erker,J.C., Buijk,S.L. and
Mushahwar,i.K.
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Qy 2101 ATTGATCACCAAGACAAAGCCTTGAAAAATTTATCAGGTCCTTATTTCCGCCACGGGTGC 2160
Db 2101 ATTGATCACCAAGACAAAGCCTTGAAAAATTTATCAGGTCCTTATTTCCGCCACGGGTGC 2160
Qy 2161 TTTGTCTCTACGGGAGTTACCAACAGGCCGCTGGTCTAAATCTTGTGGGTTGTGTGG 2220
Db 2161 TTTGTCTCTTACGGGAGTTACCAACAGGCCGCTGGTCTAAATCTTGTGGGTTGTGTGG 2220

Qy 2221 CAGCAAGTATCTTATTTTAGCCTACCTCTGTACTTGTCCCTTTGTTTGGCGCGGCTTC 2280
Db 2221 CAGCAAGTATCTTATTTTAGCCTACCTCTGTACTTGTCCCTTTGTTTGGCGCGGCTTC 2280
Qy 2281 TGGTTACCCTTTGGGTCCTGTCTCCCATCCAGTCGTATCTCCAAGCTGGCTGGGATGT 2340
Db 2281 TGGTTACCCTTTGGGTCCTGTCTCCCATCCAGTCGTATCTCCAAGCTGGCTGGGATGT 2340
Qy 2341 TTTGTCTAAAGCTCAAGTAGCTCTCTTTTGTCTTTGATTTTCTCATCTCTGTTGCTATCTCCG 2400
Db 2341 TTTGTCTAAAGCTCAAGTAGCTCTCTTTTGTCTTTGATTTTCTCATCTCTGTTGCTATCTCCG 2400
Qy 2401 CTGAGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCATAGGCTCGGGCTTGCCTCT 2460
Db 2401 CTGAGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCATAGGCTCGGGCTTGCCTCT 2460
Qy 2461 AACTTTCTTTTGTGACGACGCTGCTGCCAAACAGATTATGACTGGTGGGTGCCACTGTCT 2520
Db 2461 AACTTTCTTTTGTGACGACGCTGCTGCCAAACAGATTATGACTGGTGGGTGCCACTGTCT 2520
Qy 2521 AGTGGCAGGGTTAGTTTGTGGGCGGCGCTAACCGTGGTCAACGCTAGCTCTGCTGTGT 2580
Db 2521 AGTGGCAGGGTTAGTTTGTGGGCGGCGCTGACCGTGGTCCAGTATAGCTCTGCTGTGT 2580
Qy 2581 AGTCTCTTGGCTCTGCTAGCGCTTTTAAACCTCTTGCATTTGGTTACGCTCTGCTCAGC 2640
Db 2581 AGTCTCTTGGCTCTGCTAGCGCTTTTAAACCTCTTGCATTTGGCTACGCTCTGCTCAGC 2640
Qy 2641 TTTTGTATACCGAGATAATTCGAGGGCTGACATAACACCTGTAGTAGCATTAGTTGTCTAT 2700
Db 2641 TTTTGTATACCGAGATAATTCGAGGGCTGACATAACACCTGTAGTAGCATTAGTTGTCTAT 2700
Qy 2701 GTCTCGTTTGGCTTCTTGTCTCACTTGTGTACCTCGCTGCTGTAGTTAGTTAACTCTCATCT 2760
Db 2701 GTCTCGTTTGGCTTCTTGTCTCACTTGTGTACCTCGCTGCTGTAGTTAGTTAACTCTCATCT 2760
Qy 2761 TTGGCAAGCTTGGGAGAAATTTGGTTTGGAACTGTACATAAGACCCGAGAGGTTTTCCT 2820
Db 2761 TTGGCAAGCTTGGGAGAAATTTGGTTTGGAACTGTACATAAGACCCGAGAGGTTTTCCT 2820
Qy 2821 TGTGCTGGTTTGTTCCTCCCGTGGGACATATAGCGGCTGGTGAATTTCTGTGTGTGTCA 2880
Db 2821 TGTGCTGGTTTGTTCCTCCCGTGGGACATATAGCGGCTGGTGAATTTCTGTGTGTGTCA 2880
Qy 2881 CGTAGCTCTTCTATGTTTAACTCCAGTCAGCATCGTCTTTGGGACTGACTCTAGGGT 2940
Db 2881 CGTAGCTCTTCTATGTTTAACTCCAGTCAGCATCGTCTTTGGGACTGACTCTAGGGT 2940
Qy 2941 TAGGGCCCATAGAAATGTTGGTGGCTCTCGGAAAGTGTCTATGCTTGGTATTTCTCATTTATGT 3000
Db 2941 TAGGGCCCATAGAAATGTTGGTGGCTCTCGGAAAGTGTCTATGCTTGGTATTTCTCATTTATGT 3000
Qy 3001 TCTTAAAGTTTCTCTTCTTAGTGTGGTGAAGTGGTGTGTCTTCTATAGACACTTGTCA 3060
Db 3001 TCTTAAAGTTTCTCTTCTTAGTGTGGTGAAGTGGTGTGTCTTCTATAGACACTTGTCA 3060
Qy 3061 TGGTGATGTCTTGCTAAATGATTTTGGCTCGAACTACCATTTGCCATTTGCCATTTTTCCT 3120
Db 3061 TGGTGATGTCTTGCTAAATGATTTTGGCTCGAACTACCATTTGCCATTTTTCCT 3120
Qy 3121 TTTTGAAGGCAAGGAGGCTTATAGGAATGAAGGAAGAGCGTTGGCTGTGGGGACAC 3180
Db 3121 TTTTGAAGGCAAGGAGGCTTATAGGAATGAAGGAAGAGCGTTGGCTGTGGGGACAC 3180
Qy 3181 GGTGTATGGTTTGGCGGCTCTCGGGACCTTGTGTTCAGGAGGTTGGCTAT 3240
Db 3181 GGTGTATGGTTTGGCGGCTCTCGGGACCTTGTGTTCAGGAGGTTGGCTAT 3240
Qy 3241 GCGGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTCAGTGTCTCTCTGAACGTGG 3300
Db 3241 GCGGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTCAGTGTCTCTCTGAACGTGG 3300

QY 3301 CACGCTGTGAGCGATGGCAGTGGTCAATGACTGGTATAGACCCCGAACTTGGACTGGAAAC 3360
DB 3301 CACGCTGTGAGCGATGGCAGTGGTCAATGACTGGTATAGACCCCGAACTTGGACTGGAAAC 3360
QY 3361 TATCTTCAGATTAGGATCTCTGGCCACATGACTAGCTACATGGGATTTGTTGTGACAAACGTGTT 3420
DB 3361 TATCTTCAGATTAGGATCTCTGGCCACATGACTAGCTACATGGGATTTGTTGTGACAAACGTGTT 3420
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DB 3421 GTATAGTCTCAACCATGGCAGCAAGGGCGCGGTGGTGGTCAATCCACAGGCTCTATACA 3480
QY 3481 CCCAATAACCGTTGACGGCGCTTAATGACACAGAGACATCTATCAACCAACCATGATGGAGCTGG 3540
DB 3481 CCCAATAACCGTTGACGGCGCTTAATGACACAGAGACATCTATCAACCAACCATGATGGAGCTGG 3540
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DB 3541 GTCCCTTACTCGGTGCTCTTGGCGGGAGACCAAGGGGTATCTGGTAAACAGACTGGGGTC 3600
QY 3601 ATTGGTTGAGGTCAACAATAACGATCGATGACCCCTTATTTGGTGTGTGCGGGGCCCTTCCCAT 3660
DB 3601 ATTGGTTGAGGTCAACAATAACGATGACCCCTTATTTGGTGTGTGCGGGGCCCTTCCCAT 3660
QY 3661 GCGTGTTCGCAAGGGTCTTTCAGAGTGCCCGGATTTCTGTGCTCCTCGGGGCATGTTATTGG 3720
DB 3661 GCGTGTTCGCAAGGGTCTTTCAGAGTGCCCGGATTTCTGTGCTCCTCGGGGCATGTTATTGG 3720
QY 3721 GATGTTACCGCTGTCTAGAAATCTTGGCGGTTTCAGTCACTAGATAGGTTAGGCGCGTT 3780
DB 3721 GATGTTACCGCTGTCTAGAAATCTTGGCGGTTTCAGTCACTAGATAGGTTAGGCGCGTT 3780
QY 3781 GGTGTGTGCTGATACCATCCCGAGTACACAGACATGCGACTCTTGTATACAAAACCTTAC 3840
DB 3781 GGTGTGTGCTGATACCATCCCGAGTACACAGACATGCGACTCTTGTATACAAAACCTTAC 3840
QY 3841 TGTGCTTAAACGAGTATTCAGTCAAAATTTTAAATGCCCCCACTGGCAGCGGCAAGTCAAC 3900
DB 3841 TGTGCTTAAACGAGTATTCAGTCAAAATTTTAAATGCCCCCACTGGCAGCGGCAAGTCAAC 3900
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DB 3901 CAAATTACCACTTTCTTACATGACGAGAGATGATGAGTCTTGGTCTTAAATCCAGTGT 3960
QY 3961 GGCTACACAGCATCAATGSCAAAGTACATGACGCGAGTACGGGTGAATCCAAATTG 4020
DB 3961 GGCTACACAGCATCAATGSCAAAGTACATGACGCGAGTACGGGTGAATCCAAATTG 4020
QY 4021 CTATTTTAAATGGCAATGTACCAACACAGGGGCTTCACTTTAGGTACAGCACATATGGCAT 4080
DB 4021 CTATTTTAAATGGCAATGTACCAACACAGGGGCTTCACTTTAGGTACAGCACATATGGCAT 4080
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DB 4081 GTACCTGACCGGAGCATGTTCCGGAACTATGACGTCACTATTGTGACGAATGCCATGC 4140
QY 4141 TACCGATGCAACCAACCGTGTGGGCAATGGAAAGGTTCTAACCGAAGCTTCCATCCAAAAA 4200
DB 4141 TACCGATGCAACCAACCGTGTGGGCAATGGAAAGGTTCTAACCGAAGCTTCCATCCAAAAA 4200
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DB 4201 TGTTAGGCTAGTGGTCTTGGCACCGGCTACCCCGCTGGAGTAATCCCTTACACCATGC 4260
QY 4261 CAACTAATCTAGATTCAATTAAACCGATGAAGGCACTATCCCTTTCATGGAAAAAAGAT 4320
DB 4261 CAACTAATCTAGATTCAATTAAACCGATGAAGGCACTATCCCTTTCATGGAAAAAAGAT 4320
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DB 4321 TAAAGAGGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACCTG 4380
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DB 4381 TGATGAGCTTGCTAAACAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGG 4440
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DB 4441 ATGTGACATCTCAAAAATCCCTGAGGGGCACTGTGTAGTAGTGTGCCACTGATGCCTTGTG 4500
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DB 4561 ATGCCATGTTGACCTTGACCCCTAATTTCACCATGGGTTCGTGTGCGGGGTTTCAGC 4620
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DB 4621 AATAGTTAAAGCCAGCGTAGGGCCCGCACAGGCGCTGGGAGAGCTGGCATATACTACTA 4680
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DB 4681 TGTAGACGGGAGTTGTATCCCTTCGGGTATCGTTTCTGGAATGCAACATTTGTGAAAGCCTT 4740
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DB 4801 CTATGCGACCCCAACCTGGGTTACTCGATAGGAGCAAAATTTGGACGAGTGGGCTGATCT 4860
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DB 4921 TTAATGTTTGTGTGACTGACGCCCAACTACAACTGTGTCACTAGTATGCTATGCTGCTCC 4980
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Qy 5521 CCCACTACCTCAAGATCAAAATGTTCTGTGTCAATTATTTGGAGCGCAATTTGGTCCAA 5580
Db 5521 CCCACTACCTCAAGATCAAAATGTTCTGTGTCAATTATTTGGAGCGCAATTTGGTCCAA 5580
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Db 5701 ATCCACTGCTTGTGTCATTTAAATGCTTGATGGGTGAGTGGCCCACTATGATCAGCT 5760
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Db 6061 TTGGCAGTATGTGCAATTTCTTTTGTGATTTGTCTTTAAATGCTTAAAGCTGGAGTTCA 6120
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Db 6121 GAGCATGGTTAAACATTCCTGTTGTCTTTCTTACAGCTGCCAGAGGGGTTCAAGGGGCC 6180
Qy 6181 CTGGATTTGGATCAGGTATGCTCCAAAGCAACGCTGTCCATGCGGTGCTGAACATCTTTTC 6240
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Db 6301 AGGGGCTGTTCCAGTCAACGTAAGCTGTGTGGGTGCGCTAGACCGGACCCCAACTGATTG 6360
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Db 6361 GACTAGTCTGTGCTCAATTAATGGCTTAGGGACTACTGTAATAATGAGAAATGGGNGA 6420
Qy 6421 TCACATTTTGTGACAGCAGTATCTCTCCAAATGCTGTGTTTACCCAGGTCGCCCCCAAC 6480
Db 6421 TCACATTTTGTGACAGCAGTATCTCTCCAAATGCTGTGTTTACCCAGGTCGCCCCCAAC 6480
Qy 6481 CTTGAGAGCTCAGTGGCCGTGGAACGCGTACAGGTTCAAGTGTATCTAGGTAGGCCCAA 6540
Db 6481 CTTGAGAGCTCAGTGGCCGTGGAACGCGTACAGGTTCAAGTGTATCTAGGTAGGCCCAA 6540
Qy 6541 AACTCCTTGGACGACATCTGCTGTGTAGCGTTCCTGACCGGTAAAGGTAAACCTGTAA 6600
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Qy 6601 GCTTCCCTTCCGGTTGACCGGTACACACACTGTGFTGCGGATGCAACTTAATTTGCGTGA 6660
Db 6601 GCTTCCCTTCCGGTTGACCGGTACACACACTGTGFTGCGGATGCAACTTAATTTGCGTGA 6660
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Db 6661 TGCACATTGACACAAATGACCTGTAATTTCCATAAACACACACTCTAGTATGAAGCGCGAGT 6720
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Db 6721 GTCCGCTCTTTGTTTCAAACACAGGAGTTGCGGCGTACAAACCAATTTGCTTGAAGCAATTC 6780
Qy 6781 AGCTGGGTTGACACACCAAACTGCCAGCCCTCCATCGAAGAGTAGTGTGAAGAA 6840
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Qy 7201 TTCCACTCAGTCAGCCCCCGCCAAACGGCTTACAAAAGAGTTGGGAAGAGTGAAGT 7260
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Db 7501 CGGTGTCTATGTTGGGACATGATGAAGTAGCAGCTCACACGCCCTTCTAAGTCTGTAAAGTC 7560
Qy 7561 CCACATCACTGGCCCTCGGGGCACTGATGTTCTGTTCTGAGAGCAGCCGCAAGGCTGTCT 7620
Db 7561 CCACATCACTGGCCCTCGGGGCACTGATGTTCTGTTCTGAGAGCAGCCGCAAGGCTGTCT 7620
Qy 7621 GGACTTCCAGAGTGTCTCGAGGCGAGTGAATACCGAGTCAATTTATCGGCAAACTGTGAT 7680
Db 7621 GGACTTCCAGAGTGTCTCGAGGCGAGTGAATACCGAGTCAATTTATCGGCAAACTGTGAT 7680

Qy	7681	AGTTCCAAAGAGGAGGAGTCTTTGTTGAAGACCCCCCCAGAAACCAACAAAGAAAACCCCAAG	7740
Db	7681	AGTTCCAAAGAGGAGGAGTCTTCGTGAAGACCCCCCCAGAAACCAACAAAGAAAACCCCAAG	7740
Qy	7741	GCTTATCTCGTACCCCAACCTTGAATAGAGATGTGTTGAGAAAGTGTACTACCGTCAGGT	7800
Db	7741	GCTTATCTCGTACCCCAACCTTGAATAGAGATGTGTTGAGAAAGTGTACTACCGTCAGGT	7800
Qy	7801	TGCTCCTGACGTAGTTAAAGCTGTCAATGGAGATGCGTACGGGTTTGTAGATCCACGTAC	7860
Db	7801	TGCTCCTGACGTAGTTAAAGCTGTCAATGGAGATGCGTACGGGTTTGTAGATCCACGTAC	7860
Qy	7861	CCGTGTCAAGCGTCTGTGTGTCGATCAACCCGAGGATATCATCGTGGAGACACATGCGATAC	7920
Db	7861	CCGTGTCAAGCGTCTGTGTGTCGATCAACCCGAGGATATCATCGTGGAGACACATGCGATAC	7920
Qy	7921	AGTGTGTTTTTGACAGTACCATCAACCCGAGGATATCATCGTGGAGACACATCTACTTC	7980
Db	7921	AGTGTGTTTTTGACAGTACCATCAACCCGAGGATATCATCGTGGAGACACATCTACTTC	7980
Qy	7981	AGCAGCTAAACTCAGTGCACCAACACCGAGCTGGCATTACACCAATTCGGAGGCAGTTATA	8040
Db	7981	AGCAGCTAAACTCAGTGCACCAACACCGAGCTGGCATTACACCAATTCGGAGGCAGTTATA	8040
Qy	8041	CGTGGAGGACCGATGATCGCTTATGATGCGCGAGAGATCGGATATCGTAGGTGTAGTTC	8100
Db	8041	CGCTGGAGGACCGATGATCGCTTATGATGCGCGAGAGATCGGATATCGTAGGTGTAGTTC	8100
Qy	8101	TTCCGGCGTCTATACTACTCTCAAGTTTCCACACAGTTTGACCTGTGGCTGAAGTAAATGC	8160
Db	8101	TTCCGGCGTCTATACTACTCTCAAGTTTCCACACAGTTTGACCTGTGGCTGAAGTAAATGC	8160
Qy	8161	TGCAGCCGAAACAGGCTGCGCATGAAGAACCTTCGCTCTTATTTTGGCGCGATGATGTCAC	8220
Db	8161	TGCAGCCGAAACAGGCTGCGCATGAAGAACCTTCGCTCTTATTTTGGCGCGATGATGTCAC	8220
Qy	8221	CGTAAATTTGGAAGACGCCGAGCAGATGCAGACAAACAAAGCAATGCGTCTTTGCTAG	8280
Db	8221	CGTAAATTTGGAAGACGCCGAGCAGATGCAGACAAACAAAGCAATGCGTCTTTGCTAG	8280
Qy	8281	CTGAGTAAGGTGATGGGTGCACCAAGAGTTGTGTGCTCAACCCCAAAATACAGTTTGGTA	8340
Db	8281	CTGAGTAAGGTGATGGGTGCACCAAGAGTTGTGTGCTCAACCCCAAAATACAGTTTGGTA	8340
Qy	8341	AGAAATTAACATCATGCTCATCAAAATGTTTACCTCTGGAAATTACCAAAAGTGGCAAGCCTTA	8400
Db	8341	AGAAATTAACATCATGCTCATCAAAATGTTTACCTCTGGAAATTACCAAAAGTGGCAAGCCTTA	8400
Qy	8401	CTACTTTTCTTACAAGAGATCCTCGTATCCCTTTGGCAGGTGCTCTGCCGAGGTCCTGGG	8460
Db	8401	CTACTTTTCTTACAAGAGATCCTCGTATCCCTTTGGCAGGTGCTCTGCCGAGGTCCTGGG	8460
Qy	8461	ATACAAACCCAGTCTCGTGGATTTGGGTATCTAAATACATCACTACCCATGTTTGTGGGT	8520
Db	8461	ATACAAACCCAGTCTCGTGGATTTGGGTATCTAAATACATCACTACCCATGTTTGTGGGT	8520
Qy	8521	TAGCCGTGTGTGGCTGTGCATTTTCATGAGACAGATGCTCTTTTGAGACACAACTTCCCGA	8580
Db	8521	TAGCCGTGTGTGGCTGTGCATTTTCATGAGACAGATGCTCTTTTGAGACACAACTTCCCGA	8580
Qy	8581	GACTGTGACCTTTGACTGGTATGGGAAAAATTTATACGGTGCCTGTAGAAGATCTGCCACG	8640
Db	8581	GACTGTGACCTTTGACTGGTATGGGAAAAATTTATACGGTGCCTGTAGAAGATCTGCCACG	8640
Qy	8641	CATCAATTGCTGGTGTGACCGGTATTGAGGCTTTCTCGGTGGTGGCTTACACCAACGCTGA	8700
Db	8641	CATCAATTGCTGGTGTGACCGGTATTGAGGCTTTCTCGGTGGTGGCTTACACCAACGCTGA	8700
Qy	8701	GATCCTCAGAGTGTTCCTAACTACCTAAACAGATCATGACATGCCCCCTCGGAGCTGGCG	8760
Db	8701	GATCCTCAGAGTGTTCCTAACTACCTAAACAGATCATGACATGCCCCCTCGGAGCTGGCG	8760
Qy	8761	AAAGAAAACCCAGGGCGGTCTCTGCCAGCGCCAGAGGCGTGGCGGAGACACACGAAAATT	8820

[illegible]

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Qy 301 CAGACCTCTTTTGGAGTATCAGCGCTCCGGAAGTAGTTGGGCAAGCCCACTATATGT 360
Db 301 CAGACCTCTTTTGGAGTATCAGCGCTCCGGAAGTAGTTGGGCAAGCCCACTATATGT 360
Qy 361 TGGGATGGTTGGGTTAGCCATCATACCGTACTGCGCTGTAGGGTCTTGGCAGGGGAT 420
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Qy 421 CTGGGAGTCTCGTAGCGTAGCATGCGCTGTATTTCTACTCAAAACAAGTCTGTACC 480
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RESULT 10

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LOCUS AR310126 9143 bp DNA linear PAR 12-JUN-2003

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ACCESSION AR310126

VERSION AR310126.1 GI:31702404

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1. (bases 1 to 9143)

AUTHORS Simons J.N., Pilot-Matias T.J., Dawson G.J., Schlauder G.G., Desai S.M., Leary T.P., Muerhoff A.S., Erker J.C., Buijck S.I. and Mushahwar I.K.

TITLE Non-A, non-B, non-C, non-D, non-E hepatitis reagents and methods for their use

JOURNAL Patent: US 655898-A 390 06-MAY-2003;

FEATURES

source Location/Qualifiers

1..9143

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/mol_type="genomic DNA"

ORIGIN

Query Match 96.4%; Score 9059.8; DB 6; Length 9143;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 9096; Conservative 0; Mismatches 37; Indels 4; Gaps 1;

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ACCESSION AR310129
VERSION AR310129.1 GI:31702407

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 9143)
AUTHORS Simons J.N., Pilot-Matias T.J., Daweon, G.J., Schlauder G.G.,
Desai, S.M., Leary, T.P., Muerhoff, A.S., Erker, J.C., Buijk, S.I., and
Mushahwar, I.K.
TITLE Non-A, non-B, non-C, non-D, non-E hepatitis reagents and methods
for their use
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Query Match 96.4%; Score 9059.8; DB 6; Length 9143;
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ACCESSION AR350538
VERSION AR350538.1 GI:33751681
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9143)
AUTHORS Simons,J.N., Pilot-Matias,T.J., Dawson,G.J., Schlauder,G.G.,
Desai,S.M., Leary,T.P., Muerhoff,A.S., Erker,J.C., Buifk,S.L. and
Muehahwar,I.K.
TITLE Non-A, non-B, non-C, non-D, non-E hepatitis reagents and methods
for their use
JOURNAL Patent: US 6586568-A 390 01-JUL-2003;
FEATURES Location/Qualifiers
source 1. 9143
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SOURCE	Unknown.		
ORGANISM	Unclassified.		
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AUTHORS	Simons,J.N., Pilot-Matias,T.J., Dawson,G.J., Schlauder,G.G., Desai,S.M., Leary,T.P., Muerhoff,A.S., Erker,J.C., Buijk,S.L. and Mushahwar,I.K.		
TITLE	Non-A, non-B, non-C, non-D, non-E hepatitis reagents and methods for their use		
JOURNAL	Patent: US 6586568-A 393 01-JUL-2003;		
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Best Local Similarity	99.6%;	Pred. No. 0;	
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QY	3661	GGCTGTGCCAAGGGTCTTCAAGGTGCCCCGATCTGTGCTCCTCGGGCATGTTATTGG	3720		Db	4741	CGACGACGCAAGGCATGGTATGGTTGTCTCATCAACAGAGCTCAAACTTCTTGACAC	4800	
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QY	3721	GATGTTACCGCTGTAGAAATTTCTGGCGGTTTCACTGAGCCAGATTTAGGGTTAGGCCGTT	3780		Db	4801	CTATCGCACCCAACTGGGTACCTGCGATAGGAGCAAAATTTGGACGAGTGGGCTGATCT	4860	
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VERSION AR494272.1 GI:47267258
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9143)
AUTHORS Simons,J.N., Pilot-Matias,T.J., Dawson,G.J., Schlauder,G.G.,
Desai,S.M., Leary,T.P., Muerhoff,A.S., Erker,J.C., Buijck,S.B. and
Mushahwar,I.K.
TITLE Non-a, non-b, non-c, non-d, non-e hepatitis reagents and
methods for their use
JOURNAL Patent: US 6720166-A 390 13-APR-2004;
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ORIGIN
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DB |||||
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Db	901	TCCCTGTAGTGGGCGGGGTCATGACCCAGACACAAATACCAATCTGTACCAATATG	960
Qy	961	CTGCCAGGTAATCAGGTATCTATTGTTCTCTCCACTGCTTGCCTACAGAGCTGGTTG	1020
Db	961	CTGCCAGGTAATCAGGTATCTATTGTTCTCTCCACTGCTTGCCTACAGAGCTGGTTG	1020
Qy	1021	TGTGATCTGTGCGGACGAGTGTCTGGGTTCCGCCAAATCCGTACATCTCACACCTTCCAA	1080
Db	1021	TGTGATCTGTGCGGACGAGTGTCTGGGTTCCGCCAAATCCGTACATCTCACACCTTCCAA	1080
Qy	1081	TTGGAATGGCAACGACTCCTTCTTTGGGTGACCAATGATTTGTATGGGCGCTCTTGT	1140
Db	1081	TTGGAATGGCAACGACTCCTTCTTTGGGTGACCAATGATTTGTATGGGCGCTCTTGT	1140
Qy	1141	GACCTGTGACGCCCTTGACATTTGATGTTGTGTGTGTGTGTATTTAGTCGTGACTG	1200
Db	1141	GACCTGTGACGCCCTTGACATTTGATGTTGTGTGTGTGTATTTAGTCGTGACTG	1200
Qy	1201	GCTTGTGAGGCACTGGCTTATTACATAGACCTCAATGAAACTGGTACTTGTACCTGGGA	1260
Db	1201	GCTTGTGAGGCACTGGCTTATTACATAGACCTCAATGAAACTGGTACTTGTACCTGGGA	1260
Qy	1261	AGTGCCCACTGGAAATAGATCCTGGGTTCTTAGGGTTTATCGGGTGGATGCGCGCAAGGT	1320
Db	1261	AGTGCCCACTGGAAATAGATCCTGGGTTCTTAGGGTTTATCGGGTGGATGCGCGCAAGGT	1320
Qy	1321	CGAGGCTGTATCTTTGTGACCAAACTGGCTTACAAAGTACCATACGCTATTGGGACTAT	1380
Db	1321	CGAGGCTGTATCTTTGTGACCAAACTGGCTTACAAAGTACCATACGCTATTGGGACTAT	1380
Qy	1381	GTTTATGAGAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCCCTCTCGGGGCAA	1440
Db	1381	GTTTATGAGAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCCCTCTCGGGGCAA	1440
Qy	1441	GTGGTATCAGTTGCTCCTAGGCTTATGCTTTTACATAGAAAGCACTCTCGAAACCCCAT	1500
Db	1441	GTGGTATCAGTTGCTCCTAGGCTTATGCTTTTACATAGAAAGCACTCTCGAAACCCCAT	1500
Qy	1501	CAGGGTGCACCTGGATGCTCAATAGCTGAGTTTGTCTCGGCTTTGATGATACCATGTCC	1560
Db	1501	CAGGGTGCACCTGGATGCTCAATAGCTGAGTTTGTCTCGGCTTTGATGATACCATGTCC	1560

Qy	1561	TTGCCACTCTTATTTTGAGTGAGAAATGTCAGAAAGTCATTTGTTACAGTCCAAAGTGGAC	1620
Db	1561	TTGCCACTCTTATTTTGAGTGAGAAATGTCAGAAAGTCATTTGTTACAGTCCAAAGTGGAC	1620
Qy	1621	CAGGCCTATCACTCTAGAGTATAACAACCTCCATATCTTGTTACCCCTATACAAATCCCTGG	1680
Db	1621	CAGGCCTGTCACTCTAGAGTATAACAACCTCCATATCTTGTTACCCCTATACAAATCCCTGG	1680
Qy	1681	TGCGAGGGGATGTATGTTAAATTCAAAATTAACATAGGGTGTGCTGCCTATTTCGCAA	1740
Db	1681	TGCGAGGGGATGTATGTTAAATTCAAAATTAACATAGGGTGTGCTGCCTATTTCGCAA	1740
Qy	1741	TGTGCCATCGTACTGCATATGCGCATGATGCGATGTGGAACGACATCTGCGAAACTTAA	1800
Db	1741	TGTGCCATCGTACTGCATATGCGCATGATGCGATGTGGAACGACATCTGCGAAACTTAA	1800
Qy	1801	CGAAGCATGCGGTGTAACACCATGGCTAACNACCGCATGGCACNAGGCTCAGCCCTGAA	1860
Db	1801	CGAAGCATGCGGTGTAACACCATGGCTAACNACCGCATGGCACNAGGCTCAGCCCTGAA	1860
Qy	1861	ATTGGCTATATTACAATACCCCTGGGTCTAAAGAAATGTTTAAACCTCATAAATGGATGTC	1920
Db	1861	ATTGGCTATATTACAATACCCCTGGGTCTAAAGAAATGTTTAAACCTCATAAATGGATGTC	1920
Qy	1921	AGGCCATTTGTATTTTGGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAA	1980
Db	1921	AGGCCATTTGTATTTTGGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAA	1980
Qy	1981	TTGCATCTCCTACACACCGAGAGTGGGTAGTTGCCCGGTACCCACACTGTGTGATCG	2040
Db	1981	TTCCACTCTCCTACACACCGAGAGTGGGTAGTTGCCCGGTACCCACACTGTGTGATCG	2040
Qy	2041	TGTTCTCTGGTTACAGTTCCGCAAGGTTTTACAGTGATGTGAAGACCTAGCCACAGG	2100
Db	2041	TGTTCTCTGGTTACAGTTCCGCAAGGTTTTACAGTGATGTGAAGACCTAGCCACAGG	2100
Qy	2101	ATTGATCACCAAGACAAAGCCTGGAAAAATTATCAGGTCTTATATTCGCCACACGGGTGC	2160
Db	2101	ATTGATCACCAAGACAAAGCCTGGAAAAATTATCAGGTCTTATATTCGCCACACGGGTGC	2160
Qy	2161	TTTGTCTCTTACGGGAGTTACGACCAAGGCGGTGGTCTAAATCTGTGGGGTGTGTGG	2220
Db	2161	TTTGTCTCTTACGGGAGTTACGACCAAGGCGGTGGTCTAAATCTGTGGGGTGTGTGG	2220
Qy	2221	CAGCAGATCTTATTTTAGCCTACCTCTGTACTTTGTCCCTTTGTTTGGCGCGCTTC	2280
Db	2221	CAGCAGATCTTATTTTAGCCTACCTCTGTACTTTGTCCCTTTGTTTGGCGCGCTTC	2280
Qy	2281	TGGTTACCCCTTTCGCTCCTGTGCTCCCATCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340
Db	2281	TGGTTACCCCTTTCGCTCCTGTGCTCCCATCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340
Qy	2341	TTTGTCTTAAAGCTCAAGTAGCTCCTTTTGTCTTGAATTTCTTCATCTGTGTCTATCTCG	2400
Db	2341	TTTGTCTTAAAGCTCAAGTAGCTCCTTTTGTCTTGAATTTCTTCATCTGTGTCTATCTCG	2400
Qy	2401	CTGAGGCTACGTTATGCTGCCCTTTTAGGGTTTGCCCATGGCTCGCGGCTTGCCTCT	2460
Db	2401	CTGAGGCTACGTTATGCTGCCCTTTTAGGGTTTGCCCATGGCTCGCGGCTTGCCTCT	2460
Qy	2461	AACCTTTCTTTGTTGCAGCAGCTGCTGCCAACACAGATATGACTGTGTGGTGGGACTGTCT	2520
Db	2461	AACCTTTCTTTGTTGCAGCAGCTGCTGCCAACACAGATATGACTGTGTGGTGGGACTGTCT	2520
Qy	2521	AGTGGCAGGGTATGTTTGTGGGCGGCGCGTAACCGTGTGTCAACCGATAGCTCTGTCTGT	2580
Db	2521	AGTGGCAGGGTATGTTTGTGGGCGGCGCGTAACCGTGTGTCAACCGATAGCTCTGTCTGT	2580
Qy	2581	AGTCTCTTGCCCTCTGGTAGCGCTTTTAAACCTCTTTGCAATTTGGTTACGCCCTGCTTCAGC	2640
Db	2581	AGTCTCTTGCCCTCTGGTAGCGCTTTTAAACCTCTTTGCAATTTGGTTACGCCCTGCTTCAGC	2640

QY	2641	TTTTGATACGAGATAATTGGAGGCTGACAAATACCACCTGTAGTAGCATTTGTGTAT	2700
Db	2641	TTTTTGACACCGAGATAATTGGAGGCTGACAAATACCACCTGTAGTAGCATTTGTGTAT	2700
QY	2701	GTCTCGTTTGGCTTCTTTGCTCACTGTGTACTGTGTACTCGTGTGCTTTAGTTAACTCCTATCT	2760
Db	2701	GTCTCGTTTGGCTTCTTTGCTCACTGTGTACTGTGTACTCGTGTGCTTTAGTTAACTCCTATCT	2760
QY	2761	TTGGCAACGTTGGAGAAATGGTTTGGAAAGTATACACTAAGACCGAGAGGTTTTCCT	2820
Db	2761	TTGGCAACGTTGGAGAAATGGTTTGGAAAGTATACACTAAGACCGAGAGGTTTTCCT	2820
QY	2821	TGTGCTGGTTTGTTCCTCCCGTGCACATATAGCGCTGTGTACTTTCTGTGTGTGCA	2880
Db	2821	TGTGCTGGTTTGTTCCTCCCGTGCACATATAGCACGCTGTGTACTTTCTGTGTGTGCA	2880
QY	2881	CGTAGCTCTTATGTTTAAATCCAGTGCAGATCGTTCTTTTGGGACTGACTCTAGGGT	2940
Db	2881	CGTAGCTCTTATGTTTAAATCCAGTGCAGATCGTTCTTTTGGGACTGACTCTAGGGT	2940
QY	2941	TAGGGCCCATAGAAATGGTGGCTCTCGGAAGTGCATGCTTGTATTTCTCATATGT	3000
Db	2941	TAGGGCCCATAGAAATGGTGGCTCTCGGAAGTGCATGCTTGTATTTCTCATATGT	3000
QY	3001	TCTTAAGTTTTCCTTTAGTGTGGTGAGAAATGGTGTGTTTCTATAAGCACTTGCA	3060
Db	3001	TCTTAAGTTTTCCTTTAGTGTGGTGAGAAATGGTGTGTTTCTATAAGCACTTGCA	3060
QY	3061	TGGTAGTGTCTTGCCTAATGATTTTGCCTCGAAACTACCATTTGCAAGGCCAATTTTCCC	3120
Db	3061	TGGTAGTGTCTTGCCTAATGATTTTGCCTCGAAACTACCATTTGCAAGGCCAATTTTCCC	3120
QY	3121	TTTTGAAGCAAGGCAAGGCTCTATAGGAATCAAGGAAGACGCTTGGCGTGTGGGGACAC	3180
Db	3121	TTTTGAAGCAAGGCAAGGCTCTATAGGAATCAAGGAAGACGCTTGGCGTGTGGGGACAC	3180
QY	3181	GGTTGATGTTTGGCCGTTTGGTGGCTCTCGGCGACCTTGTTTTCGACAGGCTTGGCTAT	3240
Db	3181	GGTTGATGTTTGGCCGTTTGGTGGCTCTCGGCGACCTTGTTTTCGACAGGCTTGGCTAT	3240
QY	3241	GCCGCCAGATGGGTGGGCCATTTACGCGACCTTTTACGTCGAGTGTCTCTGAAAGCTGG	3300
Db	3241	GCCGCCAGATGGGTGGGCCATTTACGCGACCTTTTACGTCGAGTGTCTCTGAAAGCTGG	3300
QY	3301	CACGCTGTACAGATGGGCACTGCTCATGCTGATAGACCCCGAACTTGGACCTGGAAAC	3360
Db	3301	CACGCTGTACAGATGGGCACTGCTCATGCTGATAGACCCCGAACTTGGACCTGGAAAC	3360
QY	3361	TATCTTTCAGATTAGGATCTCTGGCCACTAGCTACATGGGATTTGTTTGTGACAAAGTGT	3420
Db	3361	TATCTTTCAGATTAGGATCTCTGGCCACTAGCTACATGGGATTTGTTTGTGACAAAGTGT	3420
QY	3421	GTATATCTGCTACATGGCAGCAAGGGCGCGGTGGCTGTATCCCAAGGCTCTATACA	3480
Db	3421	GTATATCTGCTACATGGCAGCAAGGGCGCGGTGGCTGTATCCCAAGGCTCTATACA	3480
QY	3481	CCCAATAACCGTTGACGCGGCTTAAAGCAGGACATCTATCAACCAACCATGTTGGAGCTGG	3540
Db	3481	CCCAATAACCGTTGACGCGGCTTAAAGCAGGACATCTATCAACCAACCATGTTGGAGCTGG	3540
QY	3541	GTCCCTTACTCGGTGTCTTTGGGGGAGACCAAGGGGTATCTGGTAAACGACTGGGGTC	3600
Db	3541	GTCCCTTACTCGGTGTCTTTGGGGGAGACCAAGGGGTATCTGGTAAACGACTGGGGTC	3600
QY	3601	ATTGGTTGAGGTCAACAAATCCGATGAAACCTTATTTGGTGTGTGTGGGGGCCCTTCCCAT	3660
Db	3601	ATTGGTTGAGGTCAACAAATCCGATGAAACCTTATTTGGTGTGTGTGGGGGCCCTTCCCAT	3660
QY	3661	GGCTGTGCAAGGGTCTTTCAGGTTGCCCGGATCTGTGCTCCTCGGGCATGTTATTGG	3720
Db	3661	GGCTGTGCAAGGGTCTTTCAGGTTGCCCGGATCTGTGCTCCTCGGGCATGTTATTGG	3720
QY	3721	GATGTTTACCGCTGTAGAAAATTTCTGGCGGTTTCAGTCACTCAGATTAGGCTTAGGCCGTT	3780

Db	3721	GATGTTTACCGCTGTAGAAAATTTCTGGCGGTTTCAGTACGCCAGATTAGGGTTAGGCCGTT	3780
QY	3781	GGTGTGTCTGGATACCATCCCGAGTACACAGCACATGCCACTCTTGATACAAAACCTTAC	3840
Db	3781	GGTGTGTCTGGATACCATCCCGAGTACACAGCACATGCCACTCTTGATACAAAACCTTAC	3840
QY	3841	TGTGCTTAAACGAGTATTCAAGTGCAAAATTTTAAATTTGCCCCCACTGGCAGCGCAAGTCAAC	3900
Db	3841	TGTGCTTAAACGAGTATTCAAGTGCAAAATTTTAAATTTGCCCCCACTGGCAGCGCAAGTCAAC	3900
QY	3901	CAAAATTTACCATTTCTTACATGACAGGAGAGTATGAGTCTTGGTCTTAAATTTCCAGTGT	3960
Db	3901	CAAAATTTACCATTTCTTACATGACAGGAGAGTATGAGTCTTGGTCTTAAATTTCCAGTGT	3960
QY	3961	GGCTAACACACATCAATGCCCANAATGATACATGACGCGAGCTACGCGGCTGAATCCAAATG	4020
Db	3961	GGCTAACACACATCAATGCCCANAATGATACATGACGCGAGCTACGCGGCTGAATCCAAATG	4020
QY	4021	CTATTTTAAATGGCAAAATGTACAAACACAGGGGCTTCACTTACGTACACACATATGGCAT	4080
Db	4021	CTATTTTAAATGGCAAAATGTACAAACACAGGGGCTTCACTTACGTACACACATATGGCAT	4080
QY	4081	GTACTGTACCGGAGCATGTTCCCGAACTATGATGTATATCAATTTTGTGACGAATGCCATGC	4140
Db	4081	GTACTGTACCGGAGCATGTTCCCGAACTATGATGTATATCAATTTTGTGACGAATGCCATGC	4140
QY	4141	TACCGATCAACACCAACCGGTTTGGGCAATTTGGAAGGCTCTTACCGAGCTCCATCCANAAA	4200
Db	4141	TACCGATCAACACCAACCGGTTTGGGCAATTTGGAAGGCTCTTACCGAGCTCCATCCANAAA	4200
QY	4201	TGTTAGGCTAGTGGTCTTTCGACGGCTACCCCGCTGGAGTAACTCCCTACACACATGC	4260
Db	4201	TGTTAGGCTAGTGGTCTTTCGACGGCTACCCCGCTGGAGTAACTCCCTACACACATGC	4260
QY	4261	CAACATAA CTGAGATTCAATTAACCGATGAAGGCACTATCCCTTTTCATGGAAGAAAGAT	4320
Db	4261	CAACATAA CTGAGATTCAATTAACCGATGAAGGCACTATCCCTTTTCATGGAAGAAAGAT	4320
QY	4321	TAGGAGGAAAATCTGAAGAAAGGAGACACTTATCTTTCGAGGCTACCAAAAACACTG	4380
Db	4321	TAGGAGGAAAATCTGAAGAAAGGAGACACTTATCTTTCGAGGCTACCAAAAACACTG	4380
QY	4381	TGATGAGCTGTCTAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGG	4440
Db	4381	TGATGAGCTGTCTAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGG	4440
QY	4441	ATGTGACATCTCAAAAATCCCTGAGGGCGACTGTGTAGTGTGCTGCACTGTATGCTTGTG	4500
Db	4441	ATGTGACATCTCAAAAATCCCTGAGGGCGACTGTGTAGTGTGCTGCACTGTATGCTTGTG	4500
QY	4501	TACAGGGTACACTGTGTGACTTTGATTCCTGTATGACTGCAGCCTCATGGTAGAAGGCAC	4560
Db	4501	TACAGGGTACACTGTGTGACTTTGATTCCTGTATGACTGCAGCCTCATGGTAGAAGGCAC	4560
QY	4561	ATGCCATGTGACCTTGACCTTCACTTCCACCATGGGTGTTTGTGTGTGCGGGTTTCAGC	4620
Db	4561	ATGCCATGTGACCTTGACCTTCACTTCCACCATGGGTGTTTGTGTGTGCGGGTTTCAGC	4620
QY	4621	AATAGTTTAAAGGCCACGCTAGGGGCCGCAAGGGCGTGGGAGAGCTGGCATATCTACTA	4680
Db	4621	AATAGTTTAAAGGCCACGCTAGGGGCCGCAAGGGCGTGGGAGAGCTGGCATATCTACTA	4680
QY	4681	TGTAGACGGGAGTTGTACCCCTTGGGTATGGTTCCTGAATGCACATTTTGAAGCCTT	4740
Db	4681	TGTAGACGGGAGTTGTACCCCTTGGGTATGGTTCCTGAATGCACATTTTGAAGCCTT	4740
QY	4741	CGACGACGCAAGGCTATGTTTGTCTCATCAACAGAGCTCAAACTATTCTCGACAC	4800
Db	4741	CGACGACGCAAGGCTATGTTTGTCTCATCAACAGAGCTCAAACTATTCTCGACAC	4800
QY	4801	CTATCCGACCCCAACCTGGGTTTACCTGCAATAGGAGCAAAATTTGGACGAGTGGGCTGATCT	4860

Db 4801 CTATCGCACCCAACTGGGTACTCTGGATAGGAGCAAAATTTGACGAGTGGGTGATCT 4860
Qy 4861 CTTTTCATGTCAACCCGAACTCTCATTTGTCAATACTACTGCAAAAAGAACTGCTGACAA 4920
Db 4861 CTTTTCATGTCAACCCGAACTCTCATTTGTCAATACTACTGCAAAAAGAACTGCTGACAA 4920
Qy 4921 TTATGTTTTGTGATCTGAGGCCAACTTACAATCTGTGTCAATCAGTATGGCTATGCTGCTCC 4980
Db 4921 TTATGTTTTGTGATCTGAGGCCAACTTACAATCTGTGTCAATCAGTATGGCTATGCTGCTCC 4980
Qy 4981 CAATGACGACACCGGTGGAGGAGCCGGCTTTGGGAAAAAACTTTGTGGGGTTCTGTG 5040
Db 4981 CAATGACGACACCGGTGGAGGAGCCGGCTTTGGGAAAAAACTTTGTGGGGTTCTGTG 5040
Qy 5041 GCGCTTGGACGGCGCTGACGCGCTGTCTGGCCAGAGCCACGAGGTGACAGATACCA 5100
Db 5041 GCGCTTGGACGGCGCTGACGCGCTGTCTGGCCAGAGCCACGAGGTGACAGATACCA 5100
Qy 5101 AATGTGCTTCACTGAATCAATCTTCTGGGACAGCGCACTCGCTGTGGCGTTGGAGT 5160
Db 5101 AATGTGCTTCACTGAATCAATCTTCTGGGACAGCGCACTCGCTGTGGCGTTGGAGT 5160
Qy 5161 GGCTATGCTTATCTAGCCATTGACACTTTTGGCGCCACTTTGTGGCGGCTTGTCTGCTC 5220
Db 5161 GGCTATGCTTATCTAGCCATTGACACTTTTGGCGCCACTTTGTGGCGGCTTGTCTGCTC 5220
Qy 5221 TATTACATCACTCCCTACCGGTGCTACTGTGCGCCAGTGTGACGAAAGAAATCGT 5280
Db 5221 TATTACATCACTCCCTACCGGTGCTACTGTGCGCCAGTGTGACGAAAGAAATCGT 5280
Qy 5281 GGAGAGTGTGCATCAATTCCTTGGAGGCCAATGTTGCTGCAATTTGAAGCTGAA 5340
Db 5281 GGAGAGTGTGCATCAATTCCTTGGAGGCCAATGTTGCTGCAATTTGAAGCTGAA 5340
Qy 5341 GAGTACATCACCACTAGCTCTTTCACATTTGGAAACCGCCCTGAAAACTTAAAC 5400
Db 5341 GAGTACATCACCACTAGCTCTTTCACATTTGGAAACCGCCCTGAAAACTTAAAC 5400
Qy 5401 CTTTCTTGGGCTCATGAGCTACAATCTTGTCTATCATAGATATTGCTGTGTTAGT 5460
Db 5401 CTTTCTTGGGCTCATGAGCTACAATCTTGTCTATCATAGATATTGCTGTGCTTAGT 5460
Qy 5461 CACTTTACCTGAAATCTTGTGATCATGCGTGTGCTTTTCAATTTGGAGGCGCAATTTGCGTCCA 5520
Db 5461 CACTTTACCTGAAATCTTGTGATCATGCGTGTGCTTTTCAATTTGGAGGCGCAATTTGCGTCCA 5520
Qy 5521 CCCACTACCTCAGAGTCAAAATGTTCTCTGATTTTGGAGGCGCAATTTGCGTCCA 5580
Db 5521 CCCACTACCTCAGAGTCAAAATGTTCTCTGATTTTGGAGGCGCAATTTGCGTCCA 5580
Qy 5581 GCTTACAGACGCTAGAGCGCACTGGCGTTTCATGATGGCGGGCTGCGGAAACAGCTCT 5640
Db 5581 GCTTACAGACGCTAGAGCGCACTGGCGTTTCATGATGGCGGGCTGCGGAAACAGCTCT 5640
Qy 5641 TGGTACATGGACATCGGTGGGTTTGTCTTTGACATGCTAGCGGCTATGCTGCGGCTC 5700
Db 5641 TGGTACATGGACATCGGTGGGTTTGTCTTTGACATGCTAGCGGCTATGCTGCGGCTC 5700
Qy 5701 ATCCACTGCTTGTGACATTTAAATGCTTGAATGGGTGAGTGGCCCACTATGGATCAGCT 5760
Db 5701 ATCCACTGCTTGTGACATTTAAATGCTTGAATGGGTGAGTGGCCCACTATGGATCAGCT 5760
Qy 5761 TGCTGGTTTACTCTACTCCGGTTCAATCCGGCGCAGGAGTGTGGCGCTTTGTGACG 5820
Db 5761 TGCTGGTTTACTCTACTCCGGTTCAATCCGGCGCAGGAGTGTGGCGCTTTGTGACG 5820
Qy 5821 TTGTGCAATGTTGCTTTGACACAGCAGGCGCAAGTCACTTGGCCCAACAGACTTCTTAC 5880
Db 5821 TTGTGCAATGTTGCTTTGACACAGCAGGCGCAAGTCACTTGGCCCAACAGACTTCTTAC 5880
Qy 5881 TATGCTTGTAGGACCAACACTGTATGTAATGAGTACTTTTATTTGCCACTCGTGACATCCG 5940
Db 5881 TATGCTTGTAGGACCAACACTGTATGTAATGAGTACTTTTATTTGCCACTCGTGACATCCG 5940

Qy 5941 CAGGAAAGATCTGGGCAATCTGAGGCAATCTACCCCTGGAGTGTCAATACAGCTTGCAAT 6000
Db 5941 CAGGAAAGATCTGGGCAATCTGAGGCAATCTACCCCTGGAGTGTCAATACAGCTTGCAAT 6000
Qy 6001 CCGTTGCTCCACACCCCGAGCGAGGATGATGGGCTCATTTGCTTTGGGCTTAGAGAT 6060
Db 6001 CCGTTGCTCCACACCCCGAGCGAGGATGATGGGCTCATTTGCTTTGGGCTTAGAGAT 6060
Qy 6061 TTGGCAGTATGTGTGCAATTTCTTTGTGATTTGCTTTAAATGTCTTAAAGCTGGAGTTCA 6120
Db 6061 TTGGCAGTATGTGTGCAATTTCTTTGTGATTTGCTTTAAATGTCTTAAAGCTGGAGTTCA 6120
Qy 6121 GAGCATGTTAAATCTCCTGTTGCTCTTCTACAGCTGCCAGAAAGGGGTTCAAGGGGCC 6180
Db 6121 GAGCATGTTAAATCTCCTGTTGCTCTTCTACAGCTGCCAGAAAGGGGTTCAAGGGGCC 6180
Qy 6181 CTGGATTTGATCAGGTATGCTTCAAGCACGCTGTCCATGCGGTCTGAACTCATCTTTTC 6240
Db 6181 CTGGATTTGATCAGGTATGCTTCAAGCACGCTGTCCATGCGGTCTGAACTCATCTTTTC 6240
Qy 6241 TGTGAGAAATGGTTTTGCAAAAATTTTAAAGAGCCAGAACTTTGTTCAAATTAAGTGGAG 6300
Db 6241 TGTGAGAAATGGTTTTGCAAAAATTTTAAAGAGCCAGAACTTTGTTCAAATTAAGTGGAG 6300
Qy 6301 AGGGCTGTTTCCAGTCAACGCTAGGCTGTGTGGGTGCGGTAGACCGGACCCAACTGATTG 6360
Db 6301 AGGGCTGTTTCCAGTCAACGCTAGGCTGTGTGGGTGCGGTAGACCGGACCCAACTGATTG 6360
Qy 6361 GACTAGTCTTGTGCTCAATTTATGCGTATGCGTTAGGGACTACTGTAAATATAGAAATTTGGGAGA 6420
Db 6361 GACTAGTCTTGTGCTCAATTTATGCGTATGCGTTAGGGACTACTGTAAATATAGAAATTTGGGAGA 6420
Qy 6421 TCACATTTTGTGTACAGCAGTATCTCTCCAAATGTCTGTTTACCCAGGTGCCCCAAC 6480
Db 6421 TCACATTTTGTGTACAGCAGTATCTCTCCAAATGTCTGTTTACCCAGGTGCCCCAAC 6480
Qy 6481 CTTGAGAGCTGCAATGCGCTGGAACGCTGACAGTTTCAAGTTTCAAGTTTATCTAGGTGAGCCCAA 6540
Db 6481 CTTGAGAGCTGCAATGCGCTGGAACGCTGACAGTTTCAAGTTTCAAGTTTATCTAGGTGAGCCCAA 6540
Qy 6541 AACTCTTGGACGACATCTGCTGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTAC 6600
Db 6541 AACTCTTGGACGACATCTGCTGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTAC 6600
Qy 6601 GCTTCCCTTCCGCTTGCAGCTCACACCTGCTGCTGCGATGCAACTTAAATTTTGGCTGA 6660
Db 6601 GCTTCCCTTCCGCTTGCAGCTCACACCTGCTGCTGCGATGCAACTTAAATTTTGGCTGA 6660
Qy 6661 TGCACTTTGAGACAAATGACTGTAAATTTCCAAACCAACACTCTTAGTGTAGTGAAGCCGCACT 6720
Db 6661 TGCACTTTGAGACAAATGACTGTAAATTTCCAAACCAACACTCTTAGTGTAGTGAAGCCGCACT 6720
Qy 6721 GTCGCTCTTGTTTTCAAACAGGAGTTGCGGCTGACAAACCAATTTGCTTGAAGCAATTTTC 6780
Db 6721 GTCGCTCTTGTTTTCAAACAGGAGTTGCGGCTGACAAACCAATTTGCTTGAAGCAATTTTC 6780
Qy 6781 AGCTGGGTTGACACACCAAACTGCGAGCCCTCCATCGAAGAGGTAGTGTGAAGAAA 6840
Db 6781 AGCTGGGTTGACACACCAAACTGCGAGCCCTCCATCGAAGAGGTAGTGTGAAGAAA 6840
Qy 6841 GCGCAGTTCCGGGCAAGAACTGGTTCGCTTACCTTCCCTCCCTCCGAGATCCGTCCTC 6900
Db 6841 GCGCAGTTCCGGGCAAGAACTGGTTCGCTTACCTTCCCTCCCTCCGAGATCCGTCCTC 6900
Qy 6901 AGGAGTGTCTATGCTGCTGAAAGCTGCAACGAAAGTGAACCGTTAGAGGTTCTTCAAACCT 6960
Db 6901 AGGAGTGTCTATGCTGCTGAAAGCTGCAACGAAAGTGAACCGTTAGAGGTTCTTCAAACCT 6960
Qy 6961 CCCTCTTCAACCACTGCTTCTACAGTTGGCAGTCCCGATGCCCTGTTGGAGCGGGTGA 7020
Db 6961 CCCTCTTCAACCACTGCTTCTACAGTTGGCAGTCCCGATGCCCTGTTGGAGCGGGTGA 7020

Qy	7021	GTGTAAACCC	TTTCACTGCAAT	TTGGATGTGCAAT	TGACCGA	AAACAGGCGAGG	CCCTCAT	G	7080			
Db	7021	GTGTAAACCC	TTTCACTGCAAT	TTGGATGTGCAAT	TGACCGA	AAACAGGCGAGG	CCCTCAT	G	7080			
Qy	7081	TTTACCAG	TTACCCCTCC	CAAAAGGAGG	GTCTCTGA	ATGTCAGACGA	AGATTTGG	TCGAC	7140			
Db	7081	TTTACCAG	TTACCCCTCC	CAAAAGGAGG	GTCTCTGA	ATGTCAGACGA	AGATTTGG	TCGAC	7140			
Qy	7141	GGCTACAA	CCGCTTCC	CAGCTAC	GTACTTGG	CCCCCCCC	TACCTTAA	GATACGGGAAAGGA	7200			
Db	7141	GACTACAA	CCGCTTCC	CAGCTAC	GTACTTGG	CCCCCCCC	TACCTTAA	GATACGGGAAAGGA	7200			
Qy	7201	TTCCACT	CAGTCAG	CCCCCCCC	CAAAAGG	CGCTTACAA	AAAAAGAA	GTGGGAAAGAGTCGAT	7260			
Db	7201	TTCCACT	CAGTCAG	CCCCCCCC	CAAAAGG	CGCTTACAA	AAAAAGAA	GTGGGAAAGAGTCGAT	7260			
Qy	7261	TTGGTGCAG	CATGAGCT	TACACCTT	GGACCGAG	CTGATTAG	CTTCAAA	ACTGCTTCTTAAAGT	7320			
Db	7261	TTGGTGCAG	CATGAGCT	TACACCTT	GGACCGAG	CTGATTAG	CTTCAAA	ACTGCTTCTTAAAGT	7320			
Qy	7321	TCTGTCTG	CAACTCG	GGGCCAT	CAC	TAGTGGT	TTCCCTCA	AAAGATCATTTGGTGAT	7380			
Db	7321	TCTGTCTG	CAACTCG	GGGCCAT	CAC	TAGTGGT	TTCCCTCA	AAAGATCATTTGGTGAT	7380			
Qy	7381	GACTGAG	CCCGGGAT	CGGAGCT	TTAGAA	CAAAAGT	CAC	TATTAA	TAGACAACTCT	7440		
Db	7381	GACTGAG	CCCGGGAT	CGGAGCT	TTAGAA	CAAAAGT	CAC	TATTAA	TAGACAACTCT	7440		
Qy	7441	GTTTCCCC	CCCATCAT	CACAA	AGCAGT	GAGATTGG	CTTACG	GA	AAAGCTTCA	AAAGTTGT	7500	
Db	7441	GTTTCCCC	CCCATCAT	CACAA	AGCAGT	GAGATTGG	CTTACG	GA	AAAGCTTCA	AAAGTTGT	7500	
Qy	7501	CGGTGTC	ATGTTGG	GA	CTATGAT	GAAGTAG	CAGCTCAC	AGCCCTCT	TAAGTCT	CTAAGTC	7560	
Db	7501	CGGTGTC	ATGTTGG	GA	CTATGAT	GAAGTAG	CAGCTCAC	AGCCCTCT	TAAGTCT	CTAAGTC	7560	
Qy	7561	CCACAT	CAC	TGGCCT	TCGGGG	CACTGAT	TTGGT	TTCTG	GAGACCG	CGCAAGGCT	7620	
Db	7561	CCACAT	CAC	TGGCCT	TCGGGG	CACTGAT	TTGGT	TTCTG	GAGACCG	CGCAAGGCT	7620	
Qy	7621	GGACTT	GCAGAG	TTGTG	CGAGG	CAGTGAG	ATACCG	AGT	CATTTAT	CGGCAAACTGT	7680	
Db	7621	GGACTT	GCAGAG	TTGTG	CGAGG	CAGTGAG	ATACCG	AGT	CATTTAT	CGGCAAACTGT	7680	
Qy	7681	AGTTTCAA	AGGAGAG	GTCTT	CGTAG	AGACCC	CCCGAG	AAACCA	AAAGAA	CCCCCAAG	7740	
Db	7681	AGTTTCAA	AGGAGAG	GTCTT	CGTAG	AGACCC	CCCGAG	AAACCA	AAAGAA	CCCCCAAG	7740	
Qy	7741	GCTTAT	CTCGTAC	CCCCC	ACCTTGA	ATGATG	TTGTTG	GAGA	AGATGT	ACTACGGT	7800	
Db	7741	GCTTAT	CTCGTAC	CCCCC	ACCTTGA	ATGATG	TTGTTG	GAGA	AGATGT	ACTACGGT	7800	
Qy	7801	TGCTCT	CGACGTAG	TTAAAG	CTGT	CATG	GGAGAT	TCG	GTACGG	GTGTTGTAG	7860	
Db	7801	TGCTCT	CGACGTAG	TTAAAG	CTGT	CATG	GGAGAT	TCG	GTACGG	GTGTTGTAG	7860	
Qy	7861	CCGTGTC	AAAGCG	CTGTG	TCGAT	GTGTC	ACCG	ATGTCAG	TGCG	AGCCACAT	7920	
Db	7861	CCGTGTC	AAAGCG	CTGTG	TCGAT	GTGTC	ACCG	ATGTCAG	TGCG	AGCCACAT	7920	
Qy	7921	AGTGTG	TTTGGAC	AGTACC	ATCA	CA	CCGAGG	ATATCAT	GGTGG	AGACACAT	7980	
Db	7921	AGTGTG	TTTGGAC	AGTACC	ATCA	CA	CCGAGG	ATATCAT	GGTGG	AGACACAT	7980	
Qy	7981	AGCAGCT	TA	AACTCAG	TAC	CA	CGAG	CTGG	CA	TTCAC	CCATTCG	8040
Db	7981	AGCAGCT	TA	AACTCAG	TAC	CA	CGAG	CTGG	CA	TTCAC	CCATTCG	8040
Qy	8041	CGCTG	GAGG	ACCG	ATGATCG	CTTAT	GATG	CCCG	AGAG	TCGGA	TATCGT	8100
Db	8041	CGCTG	GAGG	ACCG	ATGATCG	CTTAT	GATG	CCCG	AGAG	TCGGA	TATCGT	8100
Qy	8101	TTCCGG	CGCT	CTAT	ACTAC	CTTCA	ACAG	TTTG	ACCT	CTG	GGCTGA	8160

Db	8101	 TTCCGGCGTCTATACCTCAAGTTCCACAGTTTGACCTGCTGGCTGAAGTAATGC	8160
Qy	8161	TGCAGCGCAACGGCTGGCATGAAGAACCCCTCCGCTCTCTTATTTGGCGCGATGATTCGAC	8220
Db	8161	TGCAGCGCAACGGCTGGCATGAAGAACCCCTCCGCTCTCTTATTTGGCGCGATGATTCGAC	8220
Qy	8221	CGTAATTTGGAAGAGCGCGGAGCAGATGCAGACAAACGAAGCAATCGTGCTCTTTGCTAG	8280
Db	8221	CGTAATTTGGAAGAGCGCGGAGCAGATGCAGACAAACGAAGCAATCGTGCTCTTTGCTAG	8280
Qy	8281	CTGGATGAAGGTGATGGGTGCACCAACAGATTTGTGTGCCTCAACCCAAATACACAGTTTGG	8340
Db	8281	CTGGATGAAGGTGATGGGTGCACCAACAGATTTGTGTGCCTCAACCCAAATACACAGTTTGG	8340
Qy	8341	AGAATTAAACATCATGCTCATCAAAATGTTACTCTGGAATTACCAAAAGTGGCAAGCCCTTA	8400
Db	8341	AGAATTAAACATCATGCTCATCAAAATGTTACTCTGGAATTACCAAAAGTGGCAAGCCCTTA	8400
Qy	8401	CTACTTTCTTCAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
Db	8401	CTACTTTCTTCAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
Qy	8461	ATACNACCCAGTCTGCGTGGATTCGGGTATCTAATACATCACTACCCATGTTTGTGGGT	8520
Db	8461	ATACNACCCAGTCTGCGTGGATTCGGGTATCTAATACATCACTACCCATGTTTGTGGGT	8520
Qy	8521	TAGCCGTGTCTGGCTGTCCATTTTCATGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA	8580
Db	8521	TAGCCGTGTCTGGCTGTCCATTTTCATGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA	8580
Qy	8581	GACTGTGACCTTTGACTGTATGGGAAAAATATACGGTGCCTGTAGAGATCTGCCCGAG	8640
Db	8581	GACTGTGACCTTTGACTGTATGGGAAAAATATACGGTGCCTGTAGAGATCTGCCCGAG	8640
Qy	8641	CATCATTTGCTGGTGTGCACGGTATTGAGGCTTTTCTCGGTGGTGGCTACACCAACGCTGA	8700
Db	8641	CATCATTTGCTGGTGTGCACGGTATTGAGGCTTTTCTCGGTGGTGGCTACACCAACGCTGA	8700
Qy	8701	GATCCTCAGAGTTTCCCAATCACTAACACAGACATGACCATGCCCCCTCGCGAGCCTGGCG	8760
Db	8701	GATCCTCAGAGTTTCCCAATCACTAACACAGACATGACCATGCCCCCTCGCGAGCCTGGCG	8760
Qy	8761	AAAGAAAGCAGGGCGGTCTCGCCAGCGCCAGAGGCGTGGCGGAGCAGACACGCAAAATT	8820
Db	8761	AAAGAAAGCAGGGCGGTCTCGCCAGCGCCAGAGGCGTGGCGGAGCAGACACGCAAAATT	8820
Qy	8821	GGCTCGCTTCTCTGGCATGCTACATCTAGACCTTACACAGATTGAGATAGACGAG	8880
Db	8821	GGCTCGCTTCTCTGGCATGCTACATCTAGACCTTACACAGATTGAGATAGACGAG	8880
Qy	8881	CGTGGCTCGGTACACCACTTTCAATTATTTGTGATGTTTACTCCCGGAGGGGATGTGTT	8940
Db	8881	CGTGGCTCGGTACACCACTTTCAATTATTTGTGATGTTTACTCCCGGAGGGGATGTGTT	8940
Qy	8941	TATTACACACAGAGAATTCAGAAAGTTCCTTGTGAAGTATTTGGCTGTCTATGTTTT	9000
Db	8941	TATTACACACAGAGAATTCAGAAAGTTCCTTGTGAAGTATTTGGCTGTCTATGTTTT	9000
Qy	9001	TGCCCTAGGGCTCATTTGCTGTGGATTAGCCATCAGCTGAACCCCAAAATTCAAAATTA	9060
Db	9001	TGCCCTAGGGCTCATTTGCTGTGGATTAGCCATCAGCTGAACCCCAAAATTCAAAATTA	9060
Qy	9061	CTAACAG-----TTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGGGCAGCGCAACAGGGGAGACCCC	9116
Db	9061	TTAACAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGGGCAGCGCAACAGGGGAGACCCC	9120
Qy	9117	GGGCTTAACAGCCCCCG 9133	
Db	9121	GGGCTTAACAGCCCCCG 9137	

AR494275	AR494275	Sequence 393 from patent US 6720166.	9143 bp	DNA	linear	PAT 15-MAY-2004
LOCUS	DEFINITION	Accession				
ACCESSION	VERSION	AR494275.1	GI:47267264			
KEYWORDS	SOURCE	Unknown.				
ORGANISM	REFERENCE	Authors				
		Simons, J.N., Pilot-Matias, T.J., Dawson, G.J., Schlauder, G.G.,				
		Desai, S.M., Leary, T.P., Muerhoff, A.S., Erker, J.C., Buijk, S.L. and				
		Mushaiwar, I.K.				
	TITLE	Non-a, non-b, non-c, non-d, non-e hepatitis reagents and				
	JOURNAL	methods for their use				
	FEATURES	Patent: US 6720166-A 393 13-APR-2004;				
	source	Location/Qualifiers				
		1..9143				
	ORIGIN	/organism="unknown"				
		/mol_type="genomic DNA"				
		Query Match	95.4%;	Score 9059.8;	DB 6;	Length 9143;
		Best Local Similarity	99.6%;	Pred. No. 0;		
		Matches 9096;	Conservative 0;	Mismatches 37;	Indels 4;	Gaps 1;
Qy	1	ACCACAACTCCAGTTTGTACACTCCGCTAGGAATGCTCTCGAGACACCCCCCTAG	60			
Db	1	ACCACAACTCCAGTTTGTACACTCCGCTAGGAATGCTCTCGAGACACCCCCCTAG	60			
Qy	61	CAGGGCGTGGGGATTTCCCTGCGCTGTGCAGAGGGTGGAGCCAAACCACTTAGTAT	120			
Db	61	CAGGGCGTGGGGATTTCCCTGCGCTGTGCAGAGGGTGGAGCCAAACCACTTAGTAT	120			
Qy	121	GTAGCGCGGGACTCATGACGCTCGGTGTGTGACAGCGCCACAGCTTGACTGGATGCC	180			
Db	121	GTAGCGCGGGACTCATGACGCTCGGTGTGTGACAGCGCCACAGCTTGACTGGATGCC	180			
Qy	181	CCTGATGGCGCTTCATGGGTTTCGGTGTGTGGCGCTTTTAGCGAGCCTCCACGCCACCA	240			
Db	181	CCTGATGGCGCTTCATGGGTTTCGGTGTGTGGCGCTTTTAGCGAGCCTCCACGCCACCA	240			
Qy	241	CCTCCAGATAGACGGCGGCACCTGTAGGGAAGACCGGGACCGGTCACTACCAAGGACG	300			
Db	241	CCTCCAGATAGACGGCGGCACCTGTAGGGAAGACCGGGACCGGTCACTACCAAGGACG	300			
Qy	301	CAGACCTCTTTTTCAGTATCAGCCTCCGGAGTAGTGTGGCAGACCCCACTATATGCT	360			
Db	301	CAGACCTCTTTTTCAGTATCAGCCTCCGGAGTAGTGTGGCAGACCCCACTATATGCT	360			
Qy	361	TGGATGTTGGGTTAGCCATCATACCGTACTGCTGTAGGGTCTCTGCGAGGGAT	420			
Db	361	TGGATGTTGGGTTAGCCATCATACCGTACTGCTGTAGGGTCTCTGCGAGGGAT	420			
Qy	421	CTGGAGTCTCGTAGACCGTAGACATGCCTGTTATTTCTACTCAAAACAAGTCTGTACC	480			
Db	421	CTGGAGTCTCGTAGACCGTAGACATGCCTGTTATTTCTACTCAAAACAAGTCTGTACC	480			
Qy	481	TGCGCCAGAACGGCGAAGAACAGACAGACCGAGGCTTCATATCTGTGTCCATTAAC	540			
Db	481	TGCGCCAGAACGGCGAAGAACAGACAGACCGAGGCTTCATATCTGTGTCCATTAAC	540			
Qy	541	ATCTGTTGAAAGGGACAAACAGACAAAGCGAAAGTCCAGCGCATGCTCGGCTCGTAA	600			
Db	541	ATCTGTTGAAAGGGACAAACAGACAAAGCGAAAGTCCAGCGCATGCTCGGCTCGTAA	600			
Qy	601	TTACAAATTCCTGATTCATATGATGGCTTGACACATTTGGCTCAGGCTGCTTTGCCAGC	660			
Db	601	TTACAAATTCCTGATTCATATGATGGCTTGACACATTTGGCTCAGGCTGCTTTGCCAGC	660			
Qy	661	TCATGTTGGGAGCGCCAAACCTCGCCATAAGTCTCGCAATCTTGGAAATCTCTTGGGA	720			
Db	661	TCATGTTGGGAGCGCCAAACCTCGCCATAAGTCTCGCAATCTTGGAAATCTCTTGGGA	720			

Qy	721	TTACCC	TTTTGGGG	TGGATG	TTGTAACA	CTCA	CACACCT	CTAGT	AGGCCCG	CGCTGGT	780
Db	721	TTACCC	TTTTGGGG	TGGATT	GTGTAACA	CTCA	CACACCT	CTAGT	AGGCCCG	CGCTGGT	780
Qy	781	GGCAGG	ACGGT	CGTTCCG	ACAGT	CTCC	CAGATAGT	ACGCTT	GCTG	GAGGATGGAGTCAA	840
Db	781	GGCAGG	ACGGT	CGTTCCG	ACAGT	CTCC	CAGATAGT	ACGCTT	GCTG	GAGGATGGAGTCAA	840
Qy	841	CTGGG	CTACT	TGGTTCGG	TGTCAC	CTTT	TTTGTGGT	ATGCTG	TATCT	TTTGGGCGTG	900
Db	841	CTGGG	CTACT	TGGTTCGG	TGTCAC	CTTT	TTTGTGGT	ATGCTG	TATCT	TTTGGGCGTG	900
Qy	901	TCCCT	GATAGT	GGGGCGGG	CTCACT	GAC	CACAAAT	TACCACA	ATCT	CCTGACCAATG	960
Db	901	TCCCT	GATAGT	GGGGCGGG	CTCACT	GAC	CACAAAT	TACCACA	ATCT	CCTGACCAATG	960
Qy	961	CTGCC	ACGCT	TAATCAGG	TATCTATT	TGTTCT	CCCTTCC	ACTTGC	CTAC	CAGAGCTG	1020
Db	961	CTGCC	ACGCT	TAATCAGG	TATCTATT	TGTTCT	CCCTTCC	ACTTGC	CTAC	CAGAGCTG	1020
Qy	1021	TGTG	ATCTGT	GGGACG	AGTCTGG	TTCCG	CCCAAT	CCGTAC	ATCTCA	CACACCTTCAA	1080
Db	1021	TGTG	ATCTGT	GGGACG	AGTCTGG	TTCCG	CCCAAT	CCGTAC	ATCTCA	CACACCTTCAA	1080
Qy	1081	TTGG	ACTGG	GCACGG	ACTCTTT	TGGCTG	ACCA	CATTGTT	TGTTAT	GGCGCTCTTGT	1140
Db	1081	TTGG	ACTGG	GCACGG	ACTCTTT	TGGCTG	ACCA	CATTGTT	TGTTAT	GGCGCTCTTGT	1140
Qy	1141	GAC	CTGTGA	CGCCCT	TCACAT	TGGT	GATG	TGTGTGG	TGTGTAT	TAGTCG	1200
Db	1141	GAC	CTGTGA	CGCCCT	TCACAT	TGGT	GATG	TGTGTGG	TGTGTAT	TAGTCG	1200
Qy	1201	GCT	TGTCAG	GCACCT	GGCTTAT	TCAT	CATAG	ACCTCA	ATGAA	CTGGTACT	1260
Db	1201	GCT	TGTCAG	GCACCT	GGCTTAT	TCAT	CATAG	ACCTCA	ATGAA	CTGGTACT	1260
Qy	1261	AGT	GCCCACT	TGGA	TAGAT	CCTCGG	TTTCT	TAGG	TTTTAT	CGGTCG	1320
Db	1261	AGT	GCCCACT	TGGA	TAGAT	CCTCGG	TTTCT	TAGG	TTTTAT	CGGTCG	1320
Qy	1321	CG	AGGCTGT	CATCTTT	TGACCA	AACTGG	CTTAC	AGTACCA	TACCG	TATGCG	1380
Db	1321	CG	AGGCTGT	CATCTTT	TGACCA	AACTGG	CTTAC	AGTACCA	TACCG	TATGCG	1380
Qy	1381	GTT	TAGCAG	GTAC	ATCA	CTAC	CTGG	CGGTGCG	CTCGAT	CTACTATG	1440
Db	1381	GTT	TAGCAG	GTAC	ATCA	CTAC	CTGG	CGGTGCG	CTCGAT	CTACTATG	1440
Qy	1441	GT	G	TATCAG	TGCTCT	AGCG	TTATG	CTTTTAC	ATAGAA	CGGACCT	1500
Db	1441	GT	G	TATCAG	TGCTCT	AGCG	TTATG	CTTTTAC	ATAGAA	CGGACCT	1500
Qy	1501	C	AGG	TGCCCACT	GGATGT	CTCA	TAGCTG	AGT	TTTTGCT	CGCTTTGAT	1560
Db	1501	C	AGG	TGCCCACT	GGATGT	CTCA	TAGCTG	AGT	TTTTGCT	CGCTTTGAT	1560
Qy	1561	TTG	CACTCT	TTAT	TGAGT	GAGA	TG	TG	TG	TG	1620
Db	1561	TTG	CACTCT	TTAT	TGAGT	GAGA	TG	TG	TG	TG	1620
Qy	1621	C	AGG	CTTAT	CACT	AGT	TAA	CAACT	CTG	ATATCT	1680
Db	1621	C	AGG	CTTAT	CACT	AGT	TAA	CAACT	CTG	ATATCT	1680
Qy	1681	TG	C	AGG	GGG	AT	GTAT	TG	GT	TAAAT	1740
Db	1681	TG	C	AGG	GGG	AT	GTAT	TG	GT	TAAAT	1740
Qy	1741	TG	T	GCC	AT	CTG	CACT	ATG	G	CACT	1800
Db	1741	TG	T	GCC	AT	CTG	CACT	ATG	G	CACT	1800

QY	1801	CGAAGCATGCGGTGTAACAACCATATGGCTAAACAACCGCATGGCAACAACGGCTCAGCCCTGAA	1860	Db	2881	CGTAGCTCTCTATGTTTAAACATCCAGTGCAGCATCGTCTTTGGGACTGACTCTAGGGT	2940
Db	1801	CGAAGCATGCGGTGTAACAACCATATGGCTAAACAACCGCATGGCAACAACGGCTCAGCCCTGAA	1860	QY	2941	TAGGGCCCATAGAAATGTTGGTGGCTCTCGGAAGTGTCAATCTTGGTATCTCTATTATGT	3000
QY	1861	ATTGGCTATATTACAAATACCCCTGGGTCTAAAGAAATGTTTAAACCTCATAAATTGATGTC	1920	Db	2941	TAGGGCCCATAGAAATGTTGGTGGCTCTCGGAAGTGTCAATCTTGGTATCTCTATTATGT	3000
Db	1861	ATTGGCTATATTACAAATACCCCTGGGTCTAAAGAAATGTTTAAACCTCATAAATTGATGTC	1920	QY	3001	TCTTAAAGTTTTTCCCTCTTAGTGTGTTGGTGAATGTTGTTGTTTCTATAAGCACTTGCA	3060
QY	1921	AGGCCATTTGTATTGTTAGGGATCAGATACCCCTATAGTTTACTTTATGACCCCTGTGAA	1980	Db	3001	TCTTAAAGTTTTTCCCTCTTAGTGTGTTGGTGAATGTTGTTTCTATAAGCACTTGCA	3060
Db	1921	AGGCCATTTGTATTGTTAGGGATCAGATACCCCTATAGTTTACTTTATGACCCCTGTGAA	1980	QY	3061	TGGTGATGTCCTTGCCCTAATGATTTTGGCTCGAAACTACCATTTGCAAGAGCCATTTTCCG	3120
QY	1981	TTCCACTCTCTTAACAACCGGAGAGTGGGCTAGGTTGCCCGTAACCCACCTGTGGTAGG	2040	Db	3061	TGGTGATGTCCTTGCCCTAATGATTTTGGCTCGAAACTACCATTTGCAAGAGCCATTTTCCG	3120
Db	1981	TTCCACTCTCTTAACAACCGGAGAGTGGGCTAGGTTGCCCGTAACCCACCTGTGGTAGG	2040	QY	3121	TTTTGAAGGCAAGGCAAGGGCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGGACAC	3180
QY	2041	TGGTTCTTGGTTACAGGTTCCGCAAGGTTTTTACAGTGATGTGAAGACCTTAGCCACAGG	2100	Db	3121	TTTTGAAGGCAAGGCAAGGGCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGGACAC	3180
Db	2041	TGGTTCTTGGTTACAGGTTCCGCAAGGTTTTTACAGTGATGTGAAGACCTTAGCCACAGG	2100	QY	3181	GTTTGATGTTTGGCCGTTGTTGGCGGACCTTGTGTTTTCGCAGGGTTGGCTAT	3240
QY	2101	ATTGATCACCAAGACAAAGCCCTGGAAAAATTTATCAGGTCCTTATATTCGCGCCACCGGTGC	2160	Db	3181	GTTTGATGTTTGGCCGTTGTTGGCGGCTCTCGGCGACCTTGTGTTTCGCAGGGTTAGCTAT	3240
Db	2101	ATTGATCACCAAGACAAAGCCCTGGAAAAATTTATCAGGTCCTTATATTCGCGCCACCGGTGC	2160	QY	3241	GCCGCGAGATGGGTGGGCCATTACCGCACCTTTTACGCTGCAGTGTCTCTCTGAACGTGG	3300
QY	2161	TTTGTCTCTTACGGGAGTTACCAACGAGGCTGGTGTGTAATCTCTGTTGGGGTTGTGTGG	2220	Db	3241	GCCGCGAGATGGGTGGGCCATTACCGCACCTTTTACGCTGCAGTGTCTCTCTGAACGTGG	3300
Db	2161	TTTGTCTCTTACGGGAGTTACCAACGAGGCTGGTGTGTAATCTCTGTTGGGGTTGTGTGG	2220	QY	3301	CACGCTGTCAGCGATGGCAGTGGTATGACCTGATAGACCTTGGTATAGACCCCGCACTTGGAC	3360
QY	2221	CAGCAAGTATCTTATTTTAGCCCTACCTCTGTTTACTTGTGTCCTTTGTTTGGGCGGCTTC	2280	Db	3301	CACGCTGTCAGCGATGGCAGTGGTATGACCTGATAGACCTTGGTATAGACCCCGCACTTGGAC	3360
Db	2221	CAGCAAGTATCTTATTTTAGCCCTACCTCTGTTTACTTGTGTCCTTTGTTTGGGCGGCTTC	2280	QY	3361	TATCTTCAGATTAGGATCTCTGGGCCACTAGCTACATGATGGGATTTGTTTGTGACAACTGTT	3420
QY	2281	TGGTTACCCCTTGGCTGCTGCCATCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340	Db	3361	TATCTTCAGATTAGGATCTCTGGGCCACTAGCTACATGATGGGATTTGTTTGTGACAACTGTT	3420
Db	2281	TGGTTACCCCTTGGCTGCTGCCATCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340	QY	3421	GTATCTGCTCACCATGGCAGAAAGGGCGCGGTGGCTCATGCCACAGGCTCTATACA	3480
QY	2341	TTTGTCTAAAGCTCAAGTAGCTCTTTTGTGCTTGAATTTCTTCTCATCTGTGTATCTCCG	2400	Db	3421	GTATCTGCTCACCATGGCAGAAAGGGCGCGGTGGCTCATGCCACAGGCTCTATACA	3480
Db	2341	TTTGTCTAAAGCTCAAGTAGCTCTTTTGTGCTTGAATTTCTTCTCATCTGTGTATCTCCG	2400	QY	3481	CCCAATAACCCCTGACCGGGCTTAATGACAGGACATCTATCAACCCATGTTGGAGCTGG	3540
QY	2401	CTGCAGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCCATGGCTGGGGCTTGCCCT	2460	Db	3481	CCCAATAACCCCTGACCGGGCTTAATGACAGGACATCTATCAACCCATGTTGGAGCTGG	3540
Db	2401	CTGCAGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCCATGGCTGGGGCTTGCCCT	2460	QY	3541	GTCCCTTACTCGGTGCTCTTGGGGGAGACCAAGGGGTATCTGGTAAACAGCACTGGGTC	3600
QY	2461	AACTTTCTTTGTTGAGCAGCTGCTGCCCAACAGATTATGACTGGTGGTGGCACTGCT	2520	Db	3541	GTCCCTTACTCGGTGCTCTTGGGGGAGACCAAGGGGTATCTGGTAAACAGCACTGGGTC	3600
Db	2461	AACTTTCTTTGTTGAGCAGCTGCTGCCCAACAGATTATGACTGGTGGTGGCACTGCT	2520	QY	3601	ATTGGTTGAGTCAACAAATCCGATGACCTTATTGGTGTGTGTGGGGGCCCTTCCCAT	3660
QY	2521	AGTGCAGGGTTAGTTTGTGGGCGGCGGTAAACCGTGGTCAACGATAGCTCTGCTTGT	2580	Db	3601	ATTGGTTGAGTCAACAAATCCGATGACCTTATTGGTGTGTGTGGGGGCCCTTCCCAT	3660
Db	2521	AGTGCAGGGTTAGTTTGTGGGCGGCGGTAAACCGTGGTCAACGATAGCTCTGCTTGT	2580	QY	3661	GGCTGTTGCCAAGGGTTCTTCAGGTGCCCGATCTGCTGCTCCCGGCGCATGTTATTGG	3720
QY	2581	AGGTCCCTTGGCTCTGTTAGCGCTTTTAAACCTCTTGCAATTTGGTTAGCCCTGCTCAGC	2640	Db	3661	GGCTGTTGCCAAGGGTTCTTCAGGTGCCCGATCTGCTGCTCCCGGCGCATGTTATTGG	3720
Db	2581	AGGTCCCTTGGCTCTGTTAGCGCTTTTAAACCTCTTGCAATTTGGTTAGCCCTGCTCAGC	2640	QY	3721	GATGTTCAACCCCTGCTAGAAAATTTCTGGCGGTTTCAGTCAAGTATGAGTTAGGCTTAGG	3780
QY	2641	TTTTGATACCGGAGATAATTGGAGGGCTGACAATACCACTGTAGTAGCAATTAGTTGTAT	2700	Db	3721	GATGTTCAACCCCTGCTAGAAAATTTCTGGCGGTTTCAGTCAAGCAGATTTAGGCTTAGG	3780
Db	2641	TTTTGATACCGGAGATAATTGGAGGGCTGACAATACCACTGTAGTAGCAATTAGTTGTAT	2700	QY	3781	GGTGTGCTGGATACCAATCCCGAGTACACAGCATGCCACTCTTTGATACAAAACCTTAC	3840
QY	2701	GTCTCGTTTGGCTTTCTTTGCTCACTTTGCTTACCTCGCTGTGCTTTAGTTAACTCCTATCT	2760	Db	3781	GGTGTGCTGGATACCAATCCCGAGTACACAGCATGCCACTCTTTGATACAAAACCTTAC	3840
Db	2701	GTCTCGTTTGGCTTTCTTTGCTCACTTTGCTTACCTCGCTGTGCTTTAGTTAACTCCTATCT	2760	QY	3841	TGTGCTTAAACAGATTTCAGTGCAAAATTTTAAATTTGCCCGCTGCGGCGCAAGTCAAC	3900
QY	2761	TTGGCAACGTTGGGAGAAATGTTTTTGGAAAGTTTGGAAAGTTTGGAAAGTTTGGAAAGTTTGG	2820	Db	3841	TGTGCTTAAACAGATTTCAGTGCAAAATTTTAAATTTGCCCGCTGCGGCGCAAGTCAAC	3900
Db	2761	TTGGCAACGTTGGGAGAAATGTTTTTGGAAAGTTTGGAAAGTTTGGAAAGTTTGGAAAGTTTGG	2820	QY	3901	CAAAATTAACCTTTCTTACATGCGAGGAGATGATGAGGTCTTTGGTCTTAAATCCAGTGT	3960
QY	2821	TGTGCTGTTGTTTCTTCCCGGTGGACATATGACCGGCTGGTGAATTTCTGTGTGTGTCA	2880	Db	3901	CAAAATTAACCTTTCTTACATGCGAGGAGATGATGAGGTCTTTGGTCTTAAATCCAGTGT	3960
Db	2821	TGTGCTGTTGTTTCTTCCCGGTGGACATATGACCGGCTGGTGAATTTCTGTGTGTGTCA	2880	QY	3961	GGCTTAAACAGCATCAATGGCCAAAGTATACATGCGAGGAGTACGGCGTGAATTCGAAATG	4020
QY	2881	CGTAGCTCTTCTATGTTTAAATCCAGTGCAGCATCGTCTTTTGGGACTGACTCTAGGGT	2940				

Db 3961 GGCTACAAACGATCAATGCGCAAGTACATGCACCGCAGCTACCGCGTGAATCCAAATTG 4020
Qy 4021 CTAATTTAAATGGCAAAATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT 4080
Db 4021 CTAATTTAAATGGCAAAATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT 4080
Qy 4081 GTACTGACCGGAGCATGTTCCCGGAACATATGATGTAAATCAATTTGTGACGAATGCCATGC 4140
Db 4081 GTACTGACCGGAGCATGTTCCCGGAACATATGACGTCATCATTTGTGACGAATGCCATGC 4140
Qy 4141 TACCGATCAACACCGGTGTTGGCAATTTGGAAGGCTCTAACCCGAAGCTCCATCCAAAA 4200
Db 4141 TACCGATCAACACCGGTGTTGGCAATTTGGAAGGCTCTAACCCGAAGCTCCATCCAAAA 4200
Qy 4201 TGTAGGCTAGTGGTTCCTTGCCACGGCTACACCCCGCTGGAGTAATCCCTACACACATGC 4260
Db 4201 TGTAGGCTAGTGGTTCCTTGCCACGGCTACACCCCGCTGGAGTAATCCCTACACACATGC 4260
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 09:45:50 ; Search time 17780 Seconds
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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_est2.*

3: gb_btc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gsl1.*

9: gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1	CNS016HG	1101 bp	DNA	linear	GSS 26-JUL-1999
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DEFINITION	BACN16J15 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL106750				
VERSION	AL106750.1	GI:5623622			
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				
REFERENCE	1 (bases 1 to 1101)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.				
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ORIGIN					
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Db	686	KITYITBFCYKIGTCTSYVVCCTCVKTYCTYCTTCTCTCSGSGSGBGGTCCCGG	745		

[illegible]

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QY 2659 TGGAGGGCTGCAATACCACTGTAGTAGCATTAGTGTGATGCTCGTTTGGCTTCTT 2718
Db 884 YTYHYTYTYTYTYCYCYCCCTSYCYCTYTYTYTYTYTYTYTYTYTYTYTYTYTY 943
QY 2719 TGCTCACTGTGTACCTGCTGTGCTTTAGTTAGTTAACTTCCTATCTTT 2762
Db 944 TTTTCTCTCTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTY 987

RESULT 6
CNS0073W 922 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BAC14D09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL066784
VERSION AL066784.1 GI:4945247
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 922)
AUTHORS Direct Submission
TITLE Drosophila melanogaster (fruit fly)
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoss in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source
1..922
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BAC14D09"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN
Query Match 0.5%; Score 48; DB 9; Length 922;
Best Local Similarity 21.4%; Pred. No. 0.1;
Matches 79; Conservative 120; Mismatches 171; Indels 0; Gaps 0;

QY 2678 CCTGTAGTAGCATTAGTTGTCATGTCGTTTGGCTTCTTTGCTCACTTGTACCTCGC 2737
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Db 471 CCYCTTGCTGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 530
QY 2738 TGTGCTTTAGTTAACTCTCTAATCTTTGGCAAGTTTGGGAGAATTGGTTTGGAACTTACA 2797
Db 531 KTGGGTKGKGTCTTTTSTGTGKTGTGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 590
QY 2798 CTAAGACCGGAGAGAGTTTTCCTTTGTGCTGCTTTTCCCGGTTGCGACATATGACCG 2857
Db 591 GTSTGKGGKGGTGTCTTTGCTGCTTTGCTGCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 650
QY 2858 CTGTGACTTCTGTGTGTGTCAGTAGCTCTCTATGTTTAAACATCCAGTGCAGCATCG 2917
Db 651 KTGTGTGGGKKTCTTTTCTTTGCTGCTTTGCTGCTTTTCTTTTCTTTTCTTTTCTTTT 710
QY 2918 TTCCTTTGGGACTGACTCTAGGGTTAGGCCCATAGAGTTTGGTGCCTCTCGAAAGTGT 2977
Db 711 KKTTKTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 770
QY 2978 CATGCTTGGTATTCATTATGTTCTTTAAAGTTTTCCTCTTCTTTGTTGGTGAAGTGT 3037
Db 771 TGGGKGGKGGKGGKGGKGGKGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830
QY 3038 GTGTTTCTTCT 3047
Db 831 KKGKTKKGT 840

RESULT 7
CNS006ST/c 937 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BAC14F16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL065880
VERSION AL065880.1 GI:4944848
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 937)
AUTHORS Direct Submission
TITLE Drosophila melanogaster (fruit fly)
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoss in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source
1..937
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BAC14F16"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN
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[illegible]

ORIGIN

Query Match	0.5%	Score 46;	DB 9;	Length 895;	
Best Local Similarity	21.5%;	Pred. No. 0.4;			
Matches	81;	Conservative 128;	Mismatches 163;	Indels 4;	Gaps 1;
Qy	2711	GGCTCTCTTGCTCACCTTGGTTAACTCGCTGCTGCTTTAGTTAACTCCTATCTTTGGCAACGT	2770		
Db	481	KGKGKTKTTTKTGGTKTKKKKKKGGGGGKGKGKGGKGGKTKKKKTKTGTGKKG	540		
Qy	2771	TGGAGAAATTTGGTTTTTGGAAACGTTTACACTAAGACCGAGAGGTTTTCTTGTGCTGGTT	2830		
Db	541	TGKGTKKKKKGKTKTGKGGKKGGTGTTKTKKTKTGKTKKTKGKTKGGTKGKGGTKGKKG	600		
Qy	2831	TGTTTCCCGGTGGACATATGACGCGCTGGTGACATTCTGTGTGTGTGCTACAGTAGCTCTT	2890		
Db	601	TGKTTKTKTGKGGKGGGTGKGTGGGGKGGKTKTKGTGKGTGKTKTKTKKKKKTKKK	660		
Qy	2891	CTATGTTTAACTCCAGTGCAGCATCTCTTTTGGGACTGACTCTAGGGTTAGGGCCCAT	2950		
Db	661	KKKKG-TGKGGKGGKGTG---KKKKKKGGTKTKTKTTTKTTTTTKTGTGKKKTGGK	716		
Qy	2951	AGAATGTTGGGTCTCGGAAGTGTCACTGCTTGGTATTCTCATATGTTCTTTAAGTTT	3010		
Db	717	GGKGGTGKGGKGTGGGGGGKGGKTKTKTKTGKGGKTKTKTKTKGTGKGGTKGGK	776		
Qy	3011	TTCCCTCTAGTGTTTGGTGGAAATGGTGTGTTTTTCTATAAGCACTTGCATGGATGTC	3070		
Db	777	TGTGKGTGKGGTKGGTKGGKGGKGGKTKTKTKTGTGKGGGGKTKKKKKGKKT	836		
Qy	3071	TTGCCTAATGATTTG	3086		
Db	837	TKKKGGTKKKKTKK	852		

RESIST 10

CNS0047J/c	947 bp	DNA	linear	GSS 03-JUN-1999
LOCUS				
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR09023 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
VERSION	AL066360.1	GI:4943005		
KEYWORDS	GSS.			
SOURCE	Drosophila melanogaster (fruit fly)			
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
REFERENCE	1 (bases 1 to 947)			
AUTHORS	Genoscope.			
TITLE	Direct Submission			
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secre@genoscope.cns.fr)			
COMMENT	- Web : www.genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ooeogawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .			
FEATURES	Location/Qualifiers			
source	1..947 /organism="Drosophila melanogaster"			

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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR09023"
/clone_lib="RPCI-98"
/notes="end : TET3"

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ORIGIN

Query Match	0.5%	Score 46;	DB 9;	Length 947;
Best Local Similarity	36.8%;	Pred. No. 0.41;		
Matches 93;	Conservative 41;	Mismatches 119;	Indels 0;	Gaps 0;
Qy	2188	GGCCGGTGGTCTAATCTCTGTGGGGTTGTGTGGCAGCAAGTATCTATTTTAGCCTACCT	2247	
Db	592	GSCTKTTTTTKTKTKYTTTTTTTGGTTTTTSCSBSGSVTCBYTTTTTTTTTTTTTTTTTTTTTTTT	533	
Qy	2248	CTGTTACTTGTCCTTGTGTTGGGCGGCTTCTGGTACCCTTGGCTCCTGTGCTCCC	2307	
Db	532	TTTTTTTTTTTTTGTGTTSTNNNTGTMNKKTTTTTKTTTSYKTTTTYKSCBTSTTTTTKCC	473	
Qy	2308	ATCCCACTCGTATCTCCAAGCTGGCTGGGATGTTTTGTCTAAAGCTCAAGTAGCTCCTTT	2367	
Db	472	GTVYCGGCTCTGTTKTTTTTKTTTTTTTTTTTTTTTTTTGGGTCTCKBTGGSTTTGGKGTGC	413	
Qy	2368	TGCTTTGATTTTCTTCATCTGTTTGCTATCTCCGCTGCAGCGTACGTTATGCTGCCCCTTT	2427	
Db	412	TGYCTTTTTTTTTSSSSGTSITTTTGTCKYTTTTYTKKCKSKTGTTTTTTTTTTBTSTTTTTBT	353	
Qy	2428	AGGGTTTGTGCC	2440	
Db	352	TTTTTTTTTTBTG	340	

RESULT 11
AG484307

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AC484307      841 bp      DNA      linear      GSS 04-JUN-2004
LOCUS         Mus musculus molossinus DNA, clone:MSMg01-379M10.T7, genomic survey
DEFINITION    sequence.
ACCESSION     AG484307
VERSION       AG484307.1  GI:48191537
KEYWORDS      GSS.
SOURCE        Mus musculus molossinus
ORGANISM      Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
2 (bases 1 to 841)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. .841
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"

FEATURES
source

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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-379M10.17"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match      0.5%; Score 45.4; DB 9; Length 841;
Best Local Similarity 51.8%; Pred. No. 0.6;
Matches 127; Conservative 0; Mismatches 116; Indels 2; Gaps 1;

Qy 2226 AGTATCTATTATAGCTACCTCTGTTACTGTCCTTTGTTGGGGCGCTTCTGTT 2285
Db 512 ACTTCTCTTTTTCCTCTTCTCCCTTTCTCCCTTTTTCCTCCCTCTTCTTTT 571
Qy 2286 ACCCTTTGGCGTCGTGCTCCATCCAGTCGTATCTCCAGCTGGCTGGGATGTTTGT 2345
Db 572 TTCCTT--CCTTTTTCCTCTCGATCCCTTTTACCTTCCCTGCTCCCTCTTTT 629
Qy 2346 CTAAGCTCAAGTAGCTCTTTTGTCTTTGATTTTCTTCATCTGTTGCTATCTCCGCTGCA 2405
Db 630 TTACTTTTCCCTCTTTTTCATATCTTTTTCCTCCCTTTTCTTATTCATCCTT 689
Qy 2406 GGTACGTTATGTCCTTTTGGGTTTGGCCATGCTGCGGCTTGCCCTAACTT 2465
Db 690 CTCCTACCACTTACACCTTTCTTTGTTCTTCTTTTCTTTTCTGCTCTCCACTATGTT 749
Qy 2466 TCTTT 2470
Db 750 TCTTT 754

RESULT 12
CNS006S5      919 bp      DNA      linear      GSS 03-JUN-1999
LOCUS      Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION      BACR14J09 of RPCI-98 library from Drosophila melanogaster (fruit
                fly), genomic survey sequence.
ACCESSION      AL065856
VERSION      AL065856.1 GI:4944824
KEYWORDS      GSS.
ORGANISM      Drosophila melanogaster (fruit fly)
                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 919)
AUTHORS      Genoscope.
TITLE      Direct Submission
JOURNAL      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
                collaboration with the Berkeley Drosophila Genome Project (BDGP).
                The BDGP is constructing a physical map of the Drosophila
                melanogaster genome using these BACs. For further information
                please see http://www.fruitfly.org The BDGP Drosophila
                melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                Aaron Mammos in Pieter de Jong's laboratory in the Department of
                Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                NY. The library is named RPCI-98 and was constructed by partial
                ECORI digestion of Drosophila DNA provided by the BDGP from the
                isogenic strain v2; cn bw sp, the same strain used for the BDGP's
                p1 and EST libraries. A more detailed description of the library
                and how to order individual BAC clones, the entire library, or
                filters for hybridization from the BACPAC Resource Center can be
                found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES      Location/Qualifiers
                source      1..919
                /organism="Drosophila melanogaster"
                /mol_type="genomic DNA"
                /db_xref="taxon:7227"
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/clone="BACR14J09"
/clone_lib="RPCI-98"
/notes="end : T7"

ORIGIN
Query Match      0.5%; Score 45; DB 9; Length 919;
Best Local Similarity 21.9%; Pred. No. 0.82; 178; Indels 4; Gaps 1;
Matches 93; Conservative 150; Mismatches 178; Indels 4; Gaps 1;

Qy 2173 GGGAGTTACCACCAAGCCGCTGCTAAATCTGTTGGGTTGTCGACCAAGTATCT 2232
Db 493 GGTSTHMHMTWSTCGCGTGWYKTYCTTCTTGTTCCKTGGYTYTYSTY 552
Qy 2233 TATTTAGCTACTCTGTTACTTGTCCCTTTGTTTGGGCGGCTTCTGTTACCCCTT 2292
Db 553 TYVTHTYCTTCTCTCCCTTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
Qy 2293 GCGTCTGCTCTCCATCCAGTCGTATCTCCAGCTGGCTGGGATGTTTGTCTAAAGC 2352
Db 613 BTCTTSBTSYGGYCTCGTYGCTCTCTCVCBGCSTKSGSYGGBTSYGT---GG 668
Qy 2353 TCAAGTAGCTCTCTTTGCTTTGATTTTCTTCATCTGTTGCTATCTCCGCTGACGCTACG 2412
Db 669 KCKKGBTTCTGBTSKCTGTBTGYSKCTGKCTYSTYTCTTKTYTCTCTTYTYTYST 728
Qy 2413 TTATGCTGCCCTTTTAGGTTTGTGCCATGCTGCGGCTTGCCCTAACTTCTTTTGT 2472
Db 729 TTTTSTVBTYTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTK 788
Qy 2473 TGCAGCAGCTGCTGCCCAACAGATTATGACTGGTGGTGGGCTGCTAGTGGCAGGTT 2532
Db 789 BSYSSKSTBVSBSSTSTBSSYSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 848
Qy 2533 AGTTTGTGGCGCGCGCTAACCGTGTGCTACCGCATAGCTCTGCTTAGCTCTCTGCCC 2592
Db 849 SSTSSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 908
Qy 2593 TCTGG 2597
Db 909 TBSB 913

RESULT 13
CNS0164Y      1201 bp      DNA      linear      GSS 26-JUL-1999
LOCUS      Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION      BACN15M04 of DrosBAC library from Drosophila melanogaster (fruit
                fly), genomic survey sequence.
ACCESSION      AL106300
VERSION      AL106300.1 GI:5621234
KEYWORDS      GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM      Drosophila melanogaster
                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 1201)
AUTHORS      Genoscope.
TITLE      Direct Submission
JOURNAL      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
                collaboration with the European Drosophila Genome Project (EDGP) -
                http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
                library (Dros BAC) was made by Alain Billaut at CEPH (Centre
                d'Etude du Polymorphisme Humain) with funding provided by a MRC
                project grant. The DNA was prepared from embryos by Alain Bucheton
                and Genevieve Payan. It has been constructed in the vector
                pBelobAC11.

FEATURES      Location/Qualifiers
                source      1..1201
                /organism="Drosophila melanogaster"
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN15M04"
/clone_lib="DrosBAC"
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/note="end : T7"

ORIGIN

Query Match 0.5%; Score 45; DB 9; Length 1201;

Best Local Similarity 41.6%; Pred. No. 0.91;

Matches 57; Conservative 33; Mismatches 47; Indels 0; Gaps 0;

QY 8954 AGAAGATTGCAGAGTCTCTGTGAAGTATTGGCTGTCAATGTTTTCCTAGGGCTC 9013

DB 671 AGAGAGCTCTTGTGTCAGAGCTATATKTDWDGRATATWVHHYHHHHYHY 730

QY 9014 ATGCTGTGGATTAGCATCAGTGAACCCCAAAATTCAAAATTAACACAGTTTTTT 9073

DB 731 YVTVYBGCTAATWTHYHAAARAATACTWGRWMDAAAAAATAAAAAATADTKTT 790

QY 9074 TTTTITTTTTTTTTTTT 9090

DB 791 TTWKTITTTTTTTTTTTT 807

RESULT 14

CNS0091P/c

LOCUS

Drosophila melanogaster genome survey sequence TET3 end of BAC #

BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

ACCESSION AL053013

VERSION AL053013.1 GI:4934461

KEYWORDS

ORGANISM

Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 925)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw ep, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

1..925

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="BACR19D16"

/clone_lib="RPCI-98"

/note="end : TET3"

ORIGIN

Query Match

Best Local Similarity

Matches

66; Conservative

164; Mismatches

222; Indels

0; Gaps

0;

QY 40 CTCCTGGAGCACCCCTAGCAGGGCGTGGGGATTTCCTCTGCCCTCTGCAGAGGG 99

DB 924 SBSCSGCSBSCSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 865

QY 100 TGGAGCCAAACCACTTAGTATGTAGGGCGGGGACTCATGACGCTCGCGTGATGACAAGC 159

DB 864 SGTSSACVKNASSSSCGCCGMAACMCWCSSSSSSCGSASARGVKVRASGGAGKRGSSG 805

QY 160 GCCAAGCTTGATCTGGATGGCCCTGATGGGGCTTCATGGGTTGCGTGTGTTGGCGCTT 219

DB 804 GASASHSSSSACBSSSSSSSCASWSASSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 745

QY 220 AGGAGCGCTCCACGCCACCACTCCAGATAGAGCGCGGCACCTGTAGGGAAGACCGGG 279

DB 744 SAGSVSSASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 685

QY 280 GACCGGTCACTACCAAGACGACGACGACCTCTTTTGGTATATCACGCTCCGGAAGTAGT 339

DB 684 SWSCSSTASMSAARSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 625

QY 340 GCGAAGCCCACTATATGTGTTGGATGGTGGGTTAGCCATCATACCTACTGCTG 399

DB 624 MSGGGSGSVSASSGMSVSSGGRSGSGGGGSGSGSGSGSGSGSGSGSGSGSVCS 565

QY 400 ATAGGTCCTTGGCGGGGATCTGGAGTCTCGTAGACCGTAGCACATGCTGTATTTC 459

DB 564 GCMCRCSSSAAAAAASCAAASGCMGCKSKSGCTNNNTNTNTNTNTNTNTNTNTNT 505

QY 460 TACTCAACAAAGTCTGTACTCGGCCAGAA 491

DB 504 TAATAANNNTNTATNTNNNNNNNNNNANAA 473

RESULT 15

CNS006QP

LOCUS

Drosophila melanogaster genome survey sequence TET3 end of BAC #

BACR14J09 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

ACCESSION AL065804

VERSION AL065804.1 GI:4944772

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 902)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw ep, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

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Job time : 17787 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 06:47:36 ; Search time 1443 Seconds

(without alignments)
9609.733 Million cell updates/sec

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1068	61.2	3.6	718	18	US-10-027-632-17789	Sequence 17789, A	1141	51.2	3.0	1981	21	US-10-425-115-178086	Sequence 178086,
1069	60	3.6	60	10	US-09-908-975-13736	Sequence 13736, A	1142	51.2	3.0	2286	22	US-10-887-553A-930	Sequence 930, App
1070	57.2	3.4	248	20	US-10-021-323-9953	Sequence 9953, Ap	1143	51	3.0	498	21	US-10-425-115-27352	Sequence 27352, A
1071	56.6	3.4	399	9	US-09-960-352-12773	Sequence 12773, A	1144	51	3.0	517	20	US-10-021-323-11054	Sequence 11054, A
1072	55.8	3.3	665	20	US-10-767-701-20328	Sequence 20328, A	1145	51	3.0	1495	19	US-10-424-599-36589	Sequence 36589, A
1073	55.6	3.3	247	21	US-10-357-930-56798	Sequence 56798, A	1146	50.8	3.0	409	20	US-10-437-963-93518	Sequence 93518, A
1074	55.4	3.3	3569	20	US-10-767-701-14981	Sequence 14981, A	1147	50.8	3.0	540	21	US-10-425-115-117119	Sequence 117119,
1075	55	3.3	440	21	US-10-425-115-140282	Sequence 140282, A	1148	50.8	3.0	553	21	US-10-425-115-112028	Sequence 112028,
1076	55	3.3	563	21	US-10-425-115-96437	Sequence 96437, A	1149	50.8	3.0	597	21	US-10-425-115-35417	Sequence 35417, A
1077	55	3.3	6359	18	US-10-257-166-26	Sequence 26, Appl	1150	50.8	3.0	643	15	US-10-198-846-8987	Sequence 8987, Ap
1078	54.8	3.2	1199	21	US-10-425-115-36465	Sequence 36465, A	1151	50.8	3.0	845	21	US-10-425-115-76939	Sequence 60939, A
1079	54.4	3.2	514	10	US-09-918-995-2447	Sequence 2447, Ap	1152	50.8	3.0	1004	21	US-10-425-115-75154	Sequence 75154, A
1080	54.4	3.2	6171	16	US-10-311-455-761	Sequence 761, App	1153	50.8	3.0	1026	18	US-10-242-535A-53529	Sequence 53529, A
1081	53.8	3.2	489	21	US-10-425-115-14467	Sequence 14467, A	1154	50.8	3.0	1026	19	US-10-085-783A-53529	Sequence 53529, A

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1156	50.8	3.0	1985	19	US-10-424-599-67834	Sequence 67834, A	1229	49.8	3.0	506	10	US-09-918-995-10197	Sequence 10195, A
1157	50.8	3.0	2646	21	US-10-425-115-31139	Sequence 31139, A	1230	49.8	3.0	534	21	US-10-425-115-10197	Sequence 10497, A
1158	50.6	3.0	336	19	US-10-424-599-100526	Sequence 100526,	1231	49.8	3.0	543	21	US-10-357-930-56504	Sequence 56504, A
1159	50.6	3.0	393	21	US-09-814-353-15254	Sequence 15254, A	1232	49.8	3.0	571	20	US-10-021-323-8505	Sequence 8505, Ap
1160	50.6	3.0	395	21	US-10-425-115-135930	Sequence 135930,	1233	49.8	3.0	600	22	US-10-956-157-5858	Sequence 5858, Ap
1161	50.6	3.0	496	19	US-10-424-599-74788	Sequence 74788, A	1234	49.8	3.0	600	22	US-10-956-157-5858	Sequence 11555, A
1162	50.6	3.0	538	19	US-10-424-599-51250	Sequence 51250, A	1235	49.8	3.0	689	21	US-10-425-115-118276	Sequence 118276, A
1163	50.6	3.0	600	24	US-10-972-079-78376	Sequence 78376, A	1236	49.8	3.0	1048	19	US-10-351-334-38	Sequence 38, Appl
1164	50.6	3.0	856	9	US-09-770-445-613	Sequence 613, App	1237	49.8	3.0	1833	19	US-10-231-956A-76	Sequence 76, Appl
1165	50.6	3.0	1226	19	US-10-424-599-43121	Sequence 43121, A	1238	49.8	3.0	1833	21	US-10-684-423-254	Sequence 254, App
1166	50.6	3.0	2270	19	US-10-424-599-44604	Sequence 44604, A	1239	49.8	3.0	1833	22	US-10-489-740-65	Sequence 65, Appl
1167	50.6	3.0	2924	16	US-10-205-219-103	Sequence 103, App	1240	49.8	3.0	1833	22	US-10-956-157-623	Sequence 623, App
1168	50.6	3.0	4990	21	US-10-357-930-24994	Sequence 24994, A	1241	49.8	3.0	1837	18	US-10-439-703-75	Sequence 75, Appl
1169	50.6	3.0	4990	21	US-10-357-930-25389	Sequence 25389, A	1242	49.8	3.0	2044	9	US-09-925-302-315	Sequence 315, App
1170	50.6	3.0	5001	15	US-10-198-846-11011	Sequence 11011, A	1243	49.8	3.0	2044	10	US-09-925-302-315	Sequence 2, Appl
1171	50.6	3.0	6029	19	US-10-240-5890-66	Sequence 66, Appl	1244	49.8	3.0	2045	15	US-10-013-477-2	Sequence 2, Appl
1172	50.6	3.0	3673778	17	US-10-312-841-1	Sequence 1, Appl	1245	49.8	3.0	2045	16	US-10-106-698-349	Sequence 349, App
1173	50.4	3.0	272	9	US-09-960-352-696	Sequence 696, Ap	1246	49.8	3.0	2496	9	US-09-745-763-101	Sequence 101, App
1174	50.4	3.0	319	18	US-10-442-535A-15028	Sequence 15028, A	1247	49.8	3.0	2496	19	US-10-463-260-3	Sequence 3, Appl
1175	50.4	3.0	319	19	US-10-085-783A-15028	Sequence 15028, A	1248	49.8	3.0	3436	9	US-09-789-561-12	Sequence 12, Appl
1176	50.4	3.0	590	21	US-10-425-115-102850	Sequence 102850,	1249	49.8	3.0	3436	9	US-09-790-622-3	Sequence 3, Appl
1177	50.4	3.0	1340	21	US-10-425-115-9974	Sequence 9974, Ap	1250	49.8	3.0	3436	16	US-10-141-953-3	Sequence 3, Appl
1178	50.4	3.0	3687	21	US-10-602-494-233	Sequence 233, App	1251	49.8	3.0	3436	22	US-10-883-936-12	Sequence 12, Appl
1179	50.4	3.0	6668	16	US-10-311-455-1669	Sequence 1669, Ap	1252	49.8	3.0	4080	19	US-10-424-599-115754	Sequence 115754,
1180	50.2	3.0	201	21	US-10-357-930-19029	Sequence 19029, A	1253	49.8	3.0	7346	16	US-10-311-455-318	Sequence 318, App
1181	50.2	3.0	383	21	US-10-357-930-34078	Sequence 34078, A	1254	49.8	3.0	353	20	US-10-437-963-1102	Sequence 1102, Ap
1182	50.2	3.0	383	21	US-10-357-930-42946	Sequence 42946, A	1255	49.6	3.0	378	21	US-10-425-115-44608	Sequence 44608, A
1183	50.2	3.0	384	21	US-09-814-353-2534	Sequence 2534, Ap	1256	49.6	3.0	414	21	US-10-425-115-3585	Sequence 3585, Ap
1184	50.2	3.0	384	10	US-09-814-353-8870	Sequence 8870, Ap	1257	49.6	3.0	481	20	US-10-021-323-14917	Sequence 14917, A
1185	50.2	3.0	384	21	US-10-357-930-18971	Sequence 18971, A	1258	49.6	3.0	543	21	US-10-425-115-117433	Sequence 117433, A
1186	50.2	3.0	418	20	US-10-437-963-79114	Sequence 79114, A	1259	49.6	3.0	613	21	US-10-425-115-82545	Sequence 82545, A
1187	50.2	3.0	433	21	US-10-425-115-119917	Sequence 119917, A	1260	49.6	3.0	660	19	US-10-424-599-24054	Sequence 24054, A
1188	50.2	3.0	448	21	US-10-357-930-48836	Sequence 48836, A	1261	49.6	3.0	665	21	US-10-425-115-180319	Sequence 180319, A
1189	50.2	3.0	462	21	US-10-425-115-111572	Sequence 111572,	1262	49.6	3.0	687	19	US-10-424-599-115631	Sequence 115631,
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1192	50.2	3.0	567	21	US-10-425-115-88563	Sequence 88563, A	1265	49.6	3.0	1486	21	US-10-723-860-5536	Sequence 5536, Ap
1193	50.2	3.0	574	21	US-10-425-115-179039	Sequence 179039,	1266	49.6	3.0	1590	21	US-10-425-115-128137	Sequence 128137,
1194	50.2	3.0	575	19	US-10-424-599-59730	Sequence 59730, A	1267	49.6	3.0	1743	19	US-10-424-599-56660	Sequence 56660, A
1195	50.2	3.0	577	21	US-10-425-115-98308	Sequence 98308, A	1268	49.6	3.0	1977	20	US-10-437-963-98224	Sequence 98224, A
1196	50.2	3.0	629	20	US-10-437-963-61015	Sequence 61015, A	1269	49.6	3.0	2161	10	US-09-814-353-21598	Sequence 21598, A
1197	50.2	3.0	732	20	US-10-437-963-101250	Sequence 101250,	1270	49.6	3.0	5520	16	US-10-311-455-1491	Sequence 1491, Ap
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1199	50.2	3.0	1460	19	US-10-424-599-142655	Sequence 142655,	1272	49.6	3.0	3673778	17	US-10-312-841-2	Sequence 2, Appl
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1202	50	3.0	325	21	US-10-357-930-59036	Sequence 59036, A	1275	49.4	2.9	464	20	US-10-437-963-42827	Sequence 42827, A
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1204	50	3.0	464	21	US-10-357-930-50950	Sequence 50950, A	1277	49.4	2.9	541	21	US-10-425-115-53974	Sequence 53974, A
1205	50	3.0	471	21	US-10-357-930-54342	Sequence 54342, A	1278	49.4	2.9	561	10	US-09-918-995-12358	Sequence 12358, A
1206	50	3.0	520	10	US-09-918-995-32839	Sequence 32839, A	1279	49.4	2.9	579	21	US-10-357-930-58709	Sequence 58709, A
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1209	50	3.0	870	21	US-10-613-076-12	Sequence 12, Appl	1282	49.4	2.9	788	16	US-10-106-698-2095	Sequence 2095, Ap
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1216	50	3.0	21537	16	US-10-311-455-1972	Sequence 1972, Ap	1289	49.4	2.9	1603	21	US-10-357-930-22091	Sequence 22091, A
1217	49.8	3.0	263	18	US-10-425-115-108400	Sequence 108400,	1290	49.4	2.9	1603	21	US-10-357-930-23103	Sequence 23103, A
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1219	49.8	3.0	270	18	US-10-424-535A-707	Sequence 707, App	1292	49.4	2.9	1603	21	US-10-357-930-28971	Sequence 28971, A
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1222	49.8	3.0	367	21	US-10-425-115-108400	Sequence 108400,	1295	49.4	2.9	2645	15	US-10-125-540-76	Sequence 76, Appl
1223	49.8	3.0	376	21	US-10-357-930-57923	Sequence 57923, A	1296	49.4	2.9	3480	21	US-10-723-860-6047	Sequence 6047, Ap
1224	49.8	3.0	380	20	US-10-437-963-20205	Sequence 20205, A	1297	49.4	2.9	3480	21	US-10-723-860-7357	Sequence 7357, Ap
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1227	49.8	3.0	465	10	US-09-918-995-26264	Sequence 26264, A	1300	49.2	2.9	377	21	US-10-425-115-8515	Sequence 8515, Ap

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1303	49.2	2.9	442	21	US-10-357-930-58546	Sequence 58546, A	1376	49	2.9	2947	19	US-10-424-599-49805	Sequence 49805, A
1304	49.2	2.9	448	10	US-09-918-995-12373	Sequence 12373, A	1377	49	2.9	3044	18	US-10-264-049-555	Sequence 555, App
1305	49.2	2.9	463	21	US-10-425-115-166559	Sequence 166559, A	1378	49	2.9	5845	16	US-10-311-455-1635	Sequence 1635, Ap
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1307	49.2	2.9	472	21	US-10-425-115-115781	Sequence 115781, A	1380	49	2.9	6012	16	US-10-311-455-2031	Sequence 2031, Ap
1308	49.2	2.9	486	19	US-10-424-599-57535	Sequence 57535, A	1381	49	2.9	6161	16	US-10-311-455-384	Sequence 384, App
1309	49.2	2.9	494	20	US-10-437-963-35520	Sequence 35520, A	1382	49	2.9	6211	16	US-10-311-455-779	Sequence 779, App
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1312	49.2	2.9	539	21	US-10-357-930-58859	Sequence 58859, A	1385	49	2.9	11416	18	US-10-321-613-19	Sequence 19, Appl
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1314	49.2	2.9	547	20	US-10-437-963-20806	Sequence 20806, A	1387	48.8	2.9	289	21	US-10-425-115-100902	Sequence 100902, A
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1316	49.2	2.9	575	21	US-10-357-930-58433	Sequence 58433, A	1389	48.8	2.9	299	10	US-09-814-353-11141	Sequence 11141, A
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1321	49.2	2.9	717	21	US-10-425-115-120791	Sequence 120791, A	1394	48.8	2.9	340	21	US-10-425-115-38438	Sequence 38438, A
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1326	49.2	2.9	1576	21	US-10-723-860-5808	Sequence 5808, Ap	1399	48.8	2.9	446	21	US-10-357-930-19597	Sequence 19597, A
1327	49.2	2.9	2408	21	US-10-723-860-6245	Sequence 6245, Ap	1400	48.8	2.9	463	21	US-10-425-115-117603	Sequence 117603, A
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1331	49.2	2.9	7058	18	US-10-257-166-133	Sequence 133, App	1404	48.8	2.9	489	21	US-10-357-930-29580	Sequence 29580, A
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Db 2641 TTTTGTATCCGAGATAATTGAGGGCTGACAAATACCACTGTAGTACATTTAGTTGTCAT 2700
Qy 2701 GTCTCGTTTGGCTCTTTGCTCACTGTGTTACCTCGTGTGCTTTAGTTAACTCCTATCT 2760
Db 2701 GTCTCGTTTGGCTCTTTGCTCACTGTGTTACCTCGTGTGCTTTAGTTAACTCCTATCT 2760
Qy 2761 TTGCAAGCTTGGAGAAATGGTTTGGAACTTACATAAGACCGGAGGTTTTCCT 2820
Db 2761 TTGCAAGCTTGGAGAAATGGTTTGGAACTTACATAAGACCGGAGGTTTTCCT 2820
Qy 2821 TGTCTGTTTGGTTTCCCGGTGGACATATGACCGCTGTGACTTCTGTGTGTGTCA 2880
Db 2821 TGTCTGTTTGGTTTCCCGGTGGACATATGACCGCTGTGACTTCTGTGTGTGTCA 2880
Qy 2881 CGTAGCTCTCTATGTTTAAATCCAGTGCAGCATCGTCTTTGGGACTGACTCTAGGGT 2940
Db 2881 CGTAGCTCTCTATGTTTAAATCCAGTGCAGCATCGTCTTTGGGACTGACTCTAGGGT 2940
Qy 2941 TAGGGCCATAGAAATGTTGGTGGCTCTCGGAAAGTGTGCTGTTATTTCTCATTTATGT 3000
Db 2941 TAGGGCCATAGAAATGTTGGTGGCTCTCGGAAAGTGTGCTGTTATTTCTCATTTATGT 3000
Qy 3001 TCTTAAAGTTTTCCTCTTGTGTTTGGTGAATGGTGTGTTTCTATAGCACTTGCA 3060
Db 3001 TCTTAAAGTTTTCCTCTTGTGTTTGGTGAATGGTGTGTTTCTATAGCACTTGCA 3060
Qy 3061 TGGTGATGCTTGTGCTAATGATTTTGCCTCGAAACTACATTGCAAGACCAATTTTCCC 3120
Db 3061 TGGTGATGCTTGTGCTAATGATTTTGCCTCGAAACTACATTGCAAGACCAATTTTCCC 3120
Qy 3121 TTTTGAAGGCAAGGCAAGGCTCTATAGGAATGAAGGAAGACGCTTGGCTGTGGGACAC 3180
Db 3121 TTTTGAAGGCAAGGCAAGGCTCTATAGGAATGAAGGAAGACGCTTGGCTGTGGGACAC 3180
Qy 3181 GGTGTGATGTTTGGCTGTGTCGCTCGGCGCTTGTGCTGCTGCTGCTGCTGCTGCTAT 3240
Db 3181 GGTGTGATGTTTGGCTGTGTCGCTCGGCGCTTGTGCTGCTGCTGCTGCTGCTGCTAT 3240
Qy 3241 GCCGCCAGATGGGTGGGCAATTAACGACCTTTTACGCTGAGTGTCTCTCGAACGTGG 3300
Db 3241 GCCGCCAGATGGGTGGGCAATTAACGACCTTTTACGCTGAGTGTCTCTCGAACGTGG 3300
Qy 3301 CACGCTGTACGCGATGGCAGTGGTATGACTGTTAGACCCCGAACTTGGATCGGAAC 3360
Db 3301 CACGCTGTACGCGATGGCAGTGGTATGACTGTTAGACCCCGAACTTGGATCGGAAC 3360

Db 3361 CAGCCTGTACGCGATGGCACTGTGCTATGACTGTGTATAGACCCCGAACTTGGACTTGGAAAC 3360
Qy 3361 TATCTTCAGATTTAGGATCTCTGGCCACTAGTACTATGGGATTTTGTGTGCAACAGTGT 3420
Db 3361 TATCTTCAGATTTAGGATCTCTGGCCACTAGTACTATGGGATTTTGTGTGCAACAGTGT 3420
Qy 3421 GTATATCTGTCTACATGGCAGCAAGGGCGCGGTTGGCTCATCCACAGGCTCTATACA 3480
Db 3421 GTATATCTGTCTACATGGCAGCAAGGGCGCGGTTGGCTCATCCACAGGCTCTATACA 3480
Qy 3481 CCCAATAACCGTTGACCGGCTATGACAGGACATCTATCAACACCATGTGAGCTGG 3540
Db 3481 CCCAATAACCGTTGACCGGCTATGACAGGACATCTATCAACACCATGTGAGCTGG 3540
Qy 3541 GTCCCTTTACTCGGTGCTCTTTGCGGGAGACCAAGGGGTATCTGGTAAACAGACTGGGTC 3600
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Qy 3601 ATTGGTTGAGGTCAACAAATCCGATGACCTTATTTGGTGTGTGTCGGGGCCCTTCCCAT 3660
Db 3601 ATTGGTTGAGGTCAACAAATCCGATGACCTTATTTGGTGTGTGTCGGGGCCCTTCCCAT 3660
Qy 3661 GGCTGTTGCAAGGGTTCTTCAGGTGCGCGATTTCTGTCTCTCCGGGCATGTTATTGG 3720
Db 3661 GGCTGTTGCAAGGGTTCTTCAGGTGCGCGATTTCTGTCTCTCCGGGCATGTTATTGG 3720
Qy 3721 GATGTTCAACCGCTGCTAGAAATTTCTGGCGGTTTCAGTCAAGTCAAGATTAGGGTTAGGCCGTT 3780
Db 3721 GATGTTCAACCGCTGCTAGAAATTTCTGGCGGTTTCAGTCAAGTCAAGATTAGGGTTAGGCCGTT 3780
Qy 3781 GGTGTGTGCTGGATACATCCCGATGACAGACATGCGCACTCTTGATATAAAACCTTAC 3840
Db 3781 GGTGTGTGCTGGATACATCCCGATGACAGACATGCGCACTCTTGATATAAAACCTTAC 3840
Qy 3841 TGTGCTTAAACGAGTATTCAGTGCAGAAATTTTAAATTTGCCCACTGGCAGCGCAAGTCAAC 3900
Db 3841 TGTGCTTAAACGAGTATTCAGTGCAGAAATTTTAAATTTGCCCACTGGCAGCGCAAGTCAAC 3900
Qy 3901 CAAATTAACCACTTTCTTACATGACGAGAAAGTATGAGTCTTGGTCTCTTAAATCCAGTGT 3960
Db 3901 CAAATTAACCACTTTCTTACATGACGAGAAAGTATGAGTCTTGGTCTCTTAAATCCAGTGT 3960
Qy 3961 GGCTACAAACAGCATCAATGCGCAAGTACATGCGCGACGCTACGCGCTGGAATCCAAATG 4020
Db 3961 GGCTACAAACAGCATCAATGCGCAAGTACATGCGCGACGCTACGCGCTGGAATCCAAATG 4020
Qy 4021 CTATTTTAAATGGCAAAATGTACCAACACAGGGGCTTCACTTACGTACAGCATATGGCAT 4080
Db 4021 CTATTTTAAATGGCAAAATGTACCAACACAGGGGCTTCACTTACGTACAGCATATGGCAT 4080
Qy 4081 GTACCTGACCGGAGCATGTTCCCGAACTATGATGTAATCATTTTGTGACGAATGCCATGC 4140
Db 4081 GTACCTGACCGGAGCATGTTCCCGAACTATGAGTCTCATTTTGTGACGAATGCCATGC 4140
Qy 4141 TACCGATGCAACCAACCGTGTGGGATGGAAGGCTCTTAAACCGAAGCTCCATCCAAAAA 4200
Db 4141 TACCGATGCAACCAACCGTGTGGGATGGAAGGCTCTTAAACCGAAGCTCCATCCAAAAA 4200
Qy 4201 TGTTAGGCTAGTGTGTTCTTCCCGGCTACCCCGCTGGAGTAATCCCTACACCATGTC 4260
Db 4201 TGTTAGGCTAGTGTGTTCTTCCCGGCTACCCCGCTGGAGTAATCCCTACACCATGTC 4260
Qy 4261 CAACATACTGAGATTCAATTTAAACCGATGAAGGACATATCCCTTTTATGAAAAAAGAT 4320
Db 4261 CAACATACTGAGATTCAATTTAAACCGATGAAGGACATATCCCTTTTATGAAAAAAGAT 4320
Qy 4321 TAAGGAGGAAAAATCTGAAGAAAGGAGACACCTTTATCTTTGAGGCTACCAAAAAACCTG 4380
Db 4321 TAAGGAGGAAAAATCTGAAGAAAGGAGACACCTTTATCTTTGAGGCTACCAAAAAACCTG 4380
Qy 4381 TGATGAGCTTGTCTAACGAGTTAGCTCGAAAGGGAATAACAGCTGCTCTTACTATAGGG 4440
Db 4381 TGATGAGCTTGTCTAACGAGTTAGCTCGAAAGGGAATAACAGCTGCTCTTACTATAGGG 4440

QY	4441	ATGTGACATCTCABAAATCCCTGAGGGACGTGTGTAGTAGTTGCCACTGATGCGCTTGTG	4500
Db	4441		
QY	4501	TACAGGGTACACTGGTGAGCTTTGATTCGGTGATGACTGCGAGCCTCATGGTAGAAGGCAC	4560
Db	4501		
QY	4561	ATGCCATGTTGACCTTGACCCCTACTTTTCCATGCGGTGTTCTGTGTGCGGGGTTTCAGC	4620
Db	4561		
QY	4621	AATAGTTAAAGCCAGCGTAGGGCGGCACAGGCGGTGGAGAGCTGGCATATACTACTA	4680
Db	4621		
QY	4681	TGTAGACGGGAGTTGTACCCCTTCGGGTATGTTCTGAAATGCAACATTTGTTGAAGCCTT	4740
Db	4681		
QY	4741	CGAGCCAGCAAGGATGGTATGGTTTGTTCATCAACAGAGCTCAAACTATTTCTGGACAC	4800
Db	4741		
QY	4801	CTATCGCACCCAACTCTGGGTTACCTGCGATAGGAGCAAAATTTGGACGAGTGGGCTGATCT	4860
Db	4801		
QY	4861	CTTTTCTATGTTCAACCCCGAACTTTCTCAATTTGTCAATCTGCAAAAGAACTGCTGACAA	4920
Db	4861		
QY	4921	TTATGTTTGTGACTGAGGCCCACTACTGATGTCATGATGAGTATGCTGCTGCC	4980
Db	4921		
QY	4981	CAATCAGCACCACCGTGGGAGGCGCGCTTGGGAAAAACCTTGTGGGGTCTGTG	5040
Db	4981		
QY	5041	GCGCTTGGACGGCGTGAAGTCAATCTTCTGGGACAGCGCGAATCTGCTGTTGGGTTGAGT	5100
Db	5041		
QY	5101	ATGTGCTTCACTGAAGTCAATCTTCTGGGACAGCGCGAATCTGCTGTTGGGTTGAGT	5160
Db	5101		
QY	5161	GGCTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACTTGTGTGCGCGTTGCTGGTC	5220
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QY	5221	TATTACATCAGTCCCTACCGGTCTACTGTGCGCCAGTGGTTGACGAAGAAGAAATCGT	5280
Db	5221		
QY	5281	GGAGAGTGTGATCATTTCAATCCCTTGGAGGCCATGGTTGCTGCAATTTGACAAAGCTGAA	5340
Db	5281		
QY	5341	GAGTACAAATCACCAACTAGTCCCTTTCATTTGGAACCGCCCTTGAAGAACTTTAAACAC	5400
Db	5341		
QY	5401	CTTTCTGGGCTCATGACGCTACAATCCTTCTATCATAGAGTATGTGCTGGTTTAGT	5460
Db	5401		
QY	5461	CACTTTACCTGACAAATCCCTTTGCAATCATGCGTGTGTGCTTTCATTTGCGGGTATTACTAC	5520
Db	5461		

QY	5521	CCCACTACCTCAAGATCAAAATGTTCTCTGTCAATTTTGGAGGCGCAATTTGCGTCCAA	5580
Db	5521		
QY	5581	GCTTACAGACGCTAGAGCGCACTGGCGGTTTCAATGATGCGGGGCTGCGGGAACAGCTCT	5640
Db	5581		
QY	5641	TGTTACATGGAATCGGTGGGTTTGTCTTTTGACATGCTAGCGGCTATGCTGCCGCTC	5700
Db	5641		
QY	5701	ATCCACTCTCTTGTGACATTTAAATGCTTCAATGGGTGAGTGGCCCACTATGGATCAGCT	5760
Db	5701		
QY	5761	TGCTGGTTTGTCTACTCCGGTTTCAATCCGCGCGCAGAGTTGTGGCGCTCTTGTGACG	5820
Db	5761		
QY	5821	TTGTGCAATGTTTCTTTTGACAAAGAGGCGCCAGATCCTGSCCCCAACAGACTTCTTTAC	5880
Db	5821		
QY	5881	TATGCTTCTAGGAGCAACACTGTATGTAATGAGTACTTTTATTGGCACTCGTGACATCCG	5940
Db	5881		
QY	5941	CAGGAAGATATCGGCAATTTCTGGAGGCATCTACCCCTGGAGTGTCTATCAGCTTGCAT	6000
Db	5941		
QY	6001	CGTTTGGCTTCCACCCCGAGGAGATGATTTGGCGGCTCATTTGCTGGGGTCTAGAGAT	6060
Db	6001		
QY	6061	TTGGCAGTATGTGTCAATTTCTTTGTGATTTGCTTTTAAATGCTTAAAGCTGGAGTTCA	6120
Db	6061		
QY	6121	GAGCATGTTTAACTTCTCTGTGTCTTTTCTACAGCTGCGAGAGGGGTCAAGGGGCC	6180
Db	6121		
QY	6181	CTGGATTGGATCAGGTATGCTTCCAAAGCACGCTGTCCATGCGGTGCTGAATCATCTTTTC	6240
Db	6181		
QY	6241	TGTTGAGAAATGTTTGGCAAACTTTACAAAGGACCCAGAACTTCTTCAAATTTACTGGAG	6300
Db	6241		
QY	6301	AGGGGCTGTTCAAGTCAACGCTAGGCTGTGTGGTGGCTAGACCGGACCCCACTGATTG	6360
Db	6301		
QY	6361	GACTAGTCTTCTCGTCAATTTAGGCTTACGCTGTAATAATATGAGAAATCGGAGA	6420
Db	6361		
QY	6421	TCATAATTTTGTGACAGAGTATCTCTCCAAATGCTGTGTTTACCCAGGTCGCCCCCAAC	6480
Db	6421		
QY	6481	CTTGAGAGCTCAGTGGCGGTGGACGGGTACAGGTTTCAAGTGTATCTAGGTGAGCCCA	6540
Db	6481		
QY	6541	AACCTCTTGGACGACATCTGCTTGTAGCGTCTGACCGGTAGGGTAAACCTGTTAA	6600
Db	6541		
QY	6601	GCTTCCCTTCCGCGTTGACGGTCAACACCTGGTGTGCGCATGCAACTTAAATTTGCGTGA	6660
Db	6601		

[illegible]

7681	DB	AGTTCCAAAGGAGGAGGTCTTGCTGAAGACCCCCAGAAAACCAACAAAGAAAACCCCAAG	7744
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7741	DB	GCATTATCTCGTACCCCAACCTTTGAAATGAGATGTGTTGAGAAAGATGTACTACGGTCAGGT	7800
7801	QY	TGCTCCTGACGTAGTTAAAGCTGTCTATGGGAGATGCGTACGGGTTTGTAAGATCCACGTAC	7860
7801	DB	TGCTCCTGACGTAGTTAAAGCTGTCTATGGGAGATGCGTACGGGTTTGTAAGATCCACGTAC	7860
7861	QY	CCGTGTCAAGCGTCTGTGTTCGATGTGTCACCCGATGCAGTCCGAGCCACATGCCATAC	7920
7861	DB	CCGTGTCAAGCGTCTGTGTTCGATGTGTCACCCGATGCAGTCCGAGCCACATGCCATAC	7920
7921	QY	AGTGTGTTTGGACAGTACCATCACACCCGAGGATATCATGTGGGAGACAGACATCTACTC	7980
7921	DB	AGTGTGTTTGGACAGTACCATCACACCCGAGGATATCATGTGGGAGACAGACATCTACTC	7980
7981	QY	AGCAGCTAAACTCAGTGAACCAACCCAGCTGSCATTCACACCATTTGCGAGGCGAGTTATA	8040
7981	DB	AGCAGCTAAACTCAGTGAACCAACCCAGCTGSCATTCACACCATTTGCGAGGCGAGTTATA	8040
8041	QY	CGCTGGAGGACCGATCGATCGCTTATCATGCGCGAGAGATCGGATATCTGTAAGTGTAGGTC	8100
8041	DB	CGCTGGAGGACCGATCGATCGCTTATCATGCGCGAGAGATCGGATATCTGTAAGTGTAGGTC	8100
8101	QY	TTCCGGCGTCTATACTACCTCAAGTTTCCAAACAGTTTGACCTGCTGGCTCGAAGGTAATGC	8160
8101	DB	TTCCGGCGTCTATACTACCTCAAGTTTCCAAACAGTTTGACCTGCTGGCTCGAAGGTAATGC	8160
8161	QY	TGCAGCGCAACAGGCTGGCAATGAAGAACCTCTGCTCTTATTTTGGCGCGATGATTCGAC	8220
8161	DB	TGCAGCGCAACAGGCTGGCAATGAAGAACCTCTGCTCTTATTTTGGCGCGATGATTCGAC	8220
8221	QY	CGTAAATTTGGAAGCGCGGAGCAGATCGACAAACAAAGCAATCGGTGCTCTTCTGCTAG	8280
8221	DB	CGTAAATTTGGAAGCGCGGAGCAGATCGACAAACAAAGCAATCGGTGCTCTTCTGCTAG	8280
8281	QY	CTGGATGAAGGTGATGGGTGCACCAAGATTGTGTGCCTCAACCCCAAAATACAGTTTGGTA	8340
8281	DB	CTGGATGAAGGTGATGGGTGCACCAAGATTGTGTGCCTCAACCCCAAAATACAGTTTGGTA	8340
8341	QY	AGAATTAACATCATGCTCATCAAAATGTTACCTCTGGAATTCACAAAGTGGCAAGCCTTA	8400
8341	DB	AGAATTAACATCATGCTCATCAAAATGTTACCTCTGGAATTCACAAAGTGGCAAGCCTTA	8400
8401	QY	CTACTTTCTTACAAGAGATCCTGATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
8401	DB	CTACTTTCTTACAAGAGATCCTGATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
8461	QY	ATACAAACCCAGTGCTCGGTGGATTGGGTATCTAATACATCACTACCCATGTTTGTGGGT	8520
8461	DB	ATACAAACCCAGTGCTCGGTGGATTGGGTATCTAATACATCACTACCCATGTTTGTGGGT	8520
8521	QY	TAGCCGTGTGTGGCTGTCCATTTTCATGGAGCAGATGCTCTTTGAGGACAAACTCTCCCGA	8580
8521	DB	TAGCCGTGTGTGGCTGTCCATTTTCATGGAGCAGATGCTCTTTGAGGACAAACTCTCCCGA	8580
8581	QY	GACTGTGACCTTTGACTGTGATGGGAAAAATTAACGGTGCCTGTAGAGATCTGCCCCAG	8640
8581	DB	GACTGTGACCTTTGACTGTGATGGGAAAAATTAACGGTGCCTGTAGAGATCTGCCCCAG	8640
8641	QY	CATCATTTCTGTGTGTGCAGGTATTCAGGCTTTCTCGGTGGTGCCTGTACACCAACGCTGA	8700
8641	DB	CATCATTTCTGTGTGTGCAGGTATTCAGGCTTTCTCGGTGGTGCCTGTACACCAACGCTGA	8700
8701	QY	GATCCTCAGAGTTTCCCAATCACTAACAGACATGACCATGCCCCCCCTCGAGCCTGGCG	8760
8701	DB	GATCCTCAGAGTTTCCCAATCACTAACAGACATGACCATGCCCCCCCTCGAGCCTGGCG	8760
8761	QY	AAAGAAAGCAGGGCGGTCTTCGCCACGCGCAAGAGCGGTGGCGGAGACACACGCAAAAT	8820
8761	DB	AAAGAAAGCAGGGCGGTCTTCGCCACGCGCAAGAGCGGTGGCGGAGACACACGCAAAAT	8820

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QY 8821 GGCTCGCTTCTCTCGCATGCTACATCTAGACCTCTACAGATTTGGATAAGACGAG 8880
D 8821 GGCTCGCTTCTCTCGCATGCTACATCTAGACCTCTACAGATTTGGATAAGACGAG 8880
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D 8881 CGTGGCTCGGTACACCACTTTCAATTAATTTGATGTTTACTCCCGAGGGGGATGTTT 8940
QY 8941 TATTACACACAGAGAAGATTGCAGAAGTTCCTGTAAGTATTTGGCTGTCATTTGTTT 9000
D 8941 TATTACACACAGAGAAGATTGCAGAAGTTCCTGTAAGTATTTGGCTGTCATTTGTTT 9000
QY 9001 TGCCCTAGGGCTCATTTGTTGGATTAGCCATCAGCTGAACCCCAAAATTCAAAATTTAA 9060
D 9001 TGCCCTAGGGCTCATTTGTTGGATTAGCCATCAGCTGAACCCCAAAATTCAAAATTTAA 9060
QY 9061 CTAACAG-----TTTTTTTTTTTTTTTTTTTTTTTATAGGAGCGGGCAACAGGGGAGACCCC 9116
D 9061 TTAACAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGGAGCGGGCAACAGGGGAGACCCC 9120
QY 9117 GGGCTTAACGACCCCGC 9133
D 9121 GGGCTTAACGACCCCGC 9137
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RESULT 2

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US-08-469-260A-390
; Sequence 390, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BULJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 390:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9143 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-260A-390

Query Match          96.4%; Score 9059.8; DB 3; Length 9143;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 9096; Conservative 0; Mismatches 37; Indels 4; Gaps 1;

QY 1 ACCACAAACATCCAGTTTGTACACTCCGTAGGAATGCTCTGGAGACACCCCTCTAG 60
D 1 ACCACAAACATCCAGTTTGTACACTCCGTAGGAATGCTCTGGAGACACCCCTCTAG 60
QY 61 CAGGCGTGGGGGATTTCCCTCCGCTCAGAGAGGTGGAGCAACACCACTTAGTAT 120
D 61 CAGGCGTGGGGGATTTCCCTCCGCTCAGAGAGGTGGAGCAACACCACTTAGTAT 120
QY 121 GTAGCGCGGGGACTCATGACGCTCGGTGATGACAAGCCAAAGCTTTGACTTTGATGGC 180
D 121 GTAGCGCGGGGACTCATGACGCTCGGTGATGACAAGCCAAAGCTTTGACTTTGATGGC 180
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D 301 CAGACCTCTTTTGGATATCAGCCTCCGGAAGTAGTTGGGCAAGCCACCTATATGTGT 360
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D 361 TGGATGGTTGGGTTAGCCATCATACCTGACTGCTCGCTAGTAGGGTCTCTGGAGGGAT 420
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D 421 CTGGAGTCTCGTAGACCGTAGACATGCTGTTATTTCTACTCAAAAGTCTCTGTACC 480
QY 481 TGGCCCCAGAACCGCAAGAAACAAGCAGACGCGAGCTTCATATCTGTGTCATTAAAC 540
D 481 TGGCCCCAGAACCGCAAGAAACAAGCAGACGCGAGCTTCATATCTGTGTCATTAAAC 540
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D 541 ATCTGTTGAAAGGGGACAAACAGCAAGCGCAAGTCCAGCGCGATGCTCGGCTCTGTAA 600
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D 601 TTACAAAATTGCTGTATTCATGATGGCTTCAGACATTTGGCTCAGGTCTTTTCCAGC 660
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D 661 TCATGTTGGGAGCGCAAGACCCCTCGCATTAAGTCTCGCAATCTTGGAACTCTTCTGGA 720
QY 721 TTACCCCTTTGGGTTGGATTGGTGTATTTACAACTCACACACCTCTAGTAGGCCCCCTGT 780
D 721 TTACCCCTTTGGGTTGGATTGGTGTATTTACAACTCACACACCTCTAGTAGGCCCCCTGT 780
QY 781 GGCAGGAGCGGTCTGTTCCAGCTCGCAGATAGTAGCTTGTCTGGAGGATGGAGTCAA 840
D 781 GGCAGGAGCGGTCTGTTCCAGCTCGCAGATAGTAGCTTGTCTGGAGGATGGAGTCAA 840
QY 841 CTGGGCTACTGGTTGGTTCCGTTCCACCTTTTGTGTGTATGTCTGTCTATCTTTGGCCTG 900
D 841 CTGGGCTACTGGTTGGTTCCGTTCCACCTTTTGTGTGTATGTCTGTCTATCTTTGGCCTG 900
QY 901 TCCCTGTAGTGGGCGCGGGTCACTGACCCAGACAAATACCAACCTCTGACCAATTTG 960
D 901 TCCCTGTAGTGGGCGCGGGTCACTGACCCAGACAAATACCAACCTCTGACCAATTTG 960
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Qy 961 CTGCCAGCGTAATCAGGTTAFTCTATTGTTCTCTTCCATTGCCCTACACGAGCCTGGTTG 1020
Db 961 CTGCCAGCGTAATCAGGTTAFTCTATTGTTCTCTTCCATTGCCCTACACGAGCCTGGTTG 1020
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Qy 1081 TTGACTGGCAGCGACTCTCTTTGGCTGACCAATTGATTTTGTATGGCGGCTCTTGT 1140
Db 1081 TTGACTGGCAGCGACTCTCTTTGGCTGACCAATTGATTTTGTATGGCGGCTCTTGT 1140
Qy 1141 GACCTGTGACGCCCTTGACATTGTTGAGTGTGTGGTGGTGTGATTTAGTGGGTGACTG 1200
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Db 1261 AGTCCCACTGGAATAGATCTGGTTCCTAGGGTTTATCGGTTGGATGGCGGCAAGGT 1320
Qy 1321 CGAGGCTGTCTATCTTCTTGACCAAACTGGCTTCAAGTAGTACCATACGCTATTGCGACTAT 1380
Db 1321 CGAGGCTGTCTATCTTCTTGACCAAACTGGCTTCAAGTAGTACCATACGCTATTGCGACTAT 1380
Qy 1381 GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGGCTCTCGGGGCA 1440
Db 1381 GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGGCTCTCGGGGCA 1440
Qy 1441 GTGGTATCAGTTGCTCTAGGCTTATGCTTTTACATAGACGACCTCTGGAACCCCTAT 1500
Db 1441 GTGGTATCAGTTGCTCTAGGCTTATGCTTTTACATAGACGACCTCTGGAACCCCTAT 1500
Qy 1501 CAGGGTGCCCACTGGATGCTCAATAGCTAGTGGTGGCTTTGCTCGCTTTGATGATPACCATGTCC 1560
Db 1501 CAGGGTGCCCACTGGATGCTCAATAGCTAGTGGTGGCTTTGCTCGCTTTGATGATPACCATGTCC 1560
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Qy 1981 TTCCACTCTCTACCCGAGAGTGGGCTAGGTTGCCCGGTACCCACCTGTGGTACG 2040
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Db ATACAAACCCGAGTGGTGGATGGGTATCTAATACATCACTACCCATGTTCTGGGT 8520
Qy TAGCCGTGTGTTGGCTGCTCAATTTATGAGGAGAGATGCTCTTTGAGGCAAACTTCCCGA 8580
Db TAGCCGTGTGTTGGCTGCTCAATTTATGAGGAGAGATGCTCTTTGAGGCAAACTTCCCGA 8580
Qy GACTGTGACCTTTGATGTTGGGAAATATACGGTGCCTGTAGAAAGATCTGCCGAG 8640

Db 8581 GACTGTGACCTTTGACTGTATGGGAAAAATATATACGGTGCCTGTAGAAAGATCTGCCGAG 8640
Qy CATCATTTGCTGTGTGACCGGTATTTAGGCTTTCTCGTGTGTGCTGTACACAAACGCTGA 8700
Db CATCATTTGCTGTGTGACCGGTATTTAGGCTTTCTCGTGTGTGCTGTACACAAACGCTGA 8700
Qy GATCCTCAGAGTTCCTCAATCATAACAGACATGACCATGCCCCCTGCGAGCCTGCGG 8760
Db GATCCTCAGAGTTCCTCAATCATAACAGACATGACCATGCCCCCTGCGAGCCTGCGG 8760
Qy AAAGAAAGCCAGGCGGTCTCCGCCAGGCCAAGAGCGGTGGCGAGCACACGCAAAATTT 8820
Db AAAGAAAGCCAGGCGGTCTCCGCCAGGCCAAGAGCGGTGGCGAGCACACGCAAAATTT 8820
Qy GGCTCGCTTCTCTCTGGCATGTACATCTAGACCTCTACAGATTTGGATTAAGACGAG 8880
Db GGCTCGCTTCTCTCTGGCATGTACATCTAGACCTCTACAGATTTGGATTAAGACGAG 8880
Qy CGTGGCTCGGTACACCACTTTCAATTTATTTGATGTTTACTCCCGGAGGGGATGTTT 8940
Db CGTGGCTCGGTACACCACTTTCAATTTATTTGATGTTTACTCCCGGAGGGGATGTTT 8940
Qy TATTACACCACAGAGAGATTGCAAGATTTCTTGTGAAGTATTTGGCTGTCTATTTT 9000
Db TATTACACCACAGAGAGATTGCAAGATTTCTTGTGAAGTATTTGGCTGTCTATTTT 9000
Qy TGCCCTAGGGCTCATTTGCTGTGATAGCCATCAGCTGAACCCCAAAATTCAAAATTA 9060
Db TGCCCTAGGGCTCATTTGCTGTGATAGCCATCAGCTGAACCCCAAAATTCAAAATTA 9060
Qy CTAACAG---TTTTTTTTTTTTTTTTTTTTTTTTTTAGGCGAGCGCAACAGGGGAGACCCC 9116
Db TTAACAGTTTTTTTTTTTTTTTTTTTTTTTTTTAGGCGAGCGCAACAGGGGAGACCCC 9120
Qy 9117 GGGCTTAACGACCCCGC 9133
Db 9121 GGGCTTAACGACCCCGC 9137

RESULT 3
US-08-469-260A-393
; Sequence 393, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MURAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 393:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9143 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..445
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 446..9037
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 9038..9143
US-08-469-260A-393

Query Match 96.4%; Score 9059.8; DB 3; Length 9143;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 9096; Conservative 0; Mismatches 37; Indels 4; Gaps 1;

Qy	1	ACCAACAACATCCAGTTTGTACATCCCGCTAGGAATGCTCTCGGAGCACCCCCCTAG	60
Db	1	ACCAACAACATCCAGTTTGTACATCCCGCTAGGAATGCTCTCGGAGCACCCCCCTAG	60
Qy	61	CAGGGCGTGGGGATTTCCCTCGCCGCTCGAAGAGGGTGGAGCCAAACACCTTAGTAT	120
Db	61	CAGGGCGTGGGGATTTCCCTCGCCGCTCGAAGAGGGTGGAGCCAAACACCTTAGTAT	120
Qy	121	GTAGCGCGGAGCTCATGACGCTCGGTGATGACAGCGGCAAGCTTGACTTGGATGGC	180
Db	121	GTAGCGCGGAGCTCATGACGCTCGGTGATGACAGCGGCAAGCTTGACTTGGATGGC	180
Qy	181	CCTGATGGCGCTTCATGGGTTTCCGTTGGTGGTGGCTTTAGGAGAGCTTCCAGCCCA	240
Db	181	CCTGATGGCGCTTCATGGGTTTCCGTTGGTGGTGGCTTTAGGAGAGCTTCCAGCCCA	240
Qy	241	CCTCCAGATAGACGGCGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACG	300
Db	241	CCTCCAGATAGACGGCGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACG	300
Qy	301	CAGACCTTTTTCAGTATCAGGCTCCGGAAGTAGTTGGGCAAGCCACCTATATGTT	360
Db	301	CAGACCTTTTTCAGTATCAGGCTCCGGAAGTAGTTGGGCAAGCCACCTATATGTT	360
Qy	361	TGGGATGTTGGGTTAGCCATCATACCTGCTGCTGATAGGCTTCTTCGAGGGGAT	420
Db	361	TGGGATGTTGGGTTAGCCATCATACCTGCTGCTGATAGGCTTCTTCGAGGGGAT	420
Qy	421	CTGGAGTCTCGTAGCGTAGCAGCATGCTGTTATTTCTACTCAAAACAGTCTGTACC	480
Db	421	CTGGAGTCTCGTAGCGTAGCAGCATGCTGTTATTTCTACTCAAAACAGTCTGTACC	480
Qy	481	TGGCCCAAGACCGGCAAGAACAGCAGACCGAGGCTTCATATCTGTGTCATTAAC	540
Db	481	TGGCCCAAGACCGGCAAGAACAGCAGACCGAGGCTTCATATCTGTGTCATTAAC	540
Qy	541	ATCTGTTCAAAAGGGGACAAACAGCAAGCGCAAGTCCAGGCGCATGCTCGGCTCGTAA	600
Db	541	ATCTGTTCAAAAGGGGACAAACAGCAAGCGCAAGTCCAGGCGCATGCTCGGCTCGTAA	600
Qy	601	TTACAAAATTGCTGGTATCCATATGCTTGCAGACATTTGGCTCAGGCTGCTTGGCCAGC	660

Db	601	TTACAAAATTGCTGGTATCCATATGCTTGCAGACATTTGGCTCAGGCTGCTTGGCCAGC	660
Qy	661	TCATGGTTGGGAGCGCCAGACCCCTCGCCATAAGTCTCGCAATCTTGGAAATCCCTTCTGGA	720
Db	661	TCATGGTTGGGAGCGCCAGACCCCTCGCCATAAGTCTCGCAATCTTGGAAATCCCTTCTGGA	720
Qy	721	TTACCCCTTTGGGTTGGATGATGATTAACAATCACACACCTTAGTAGGCCCCGCTGGT	780
Db	721	TTACCCCTTTGGGTTGGATGATGATTAACAATCACACACCTTAGTAGGCCCCGCTGGT	780
Qy	781	GGCAGGAGCGGTCGTTCCAGACGCTCTGCCAGATAGTAGCTGCTGAGGATGAGTCAA	840
Db	781	GGCAGGAGCGGTCGTTCCAGACGCTCTGCCAGATAGTAGCTGCTGAGGATGAGTCAA	840
Qy	841	CTGGGCTACTGGTTGGTTCCGCTGTCACCTTTTGTGGTATGTCTGCTATCTTTGGGCTG	900
Db	841	CTGGGCTACTGGTTGGTTCCGCTGTCACCTTTTGTGGTATGTCTGCTATCTTTGGGCTG	900
Qy	901	TCCTGTAGTGGGCGCGGCTCACTGACCCAGACACAAATACCAAAATCCTGACCAATTTG	960
Db	901	TCCTGTAGTGGGCGCGGCTCACTGACCCAGACACAAATACCAAAATCCTGACCAATTTG	960
Qy	961	CTGCCAGCGTAATCAGGTTATCTATTGTTCTCTTCCACTTGCCTACACGAGCCCTGGT	1020
Db	961	CTGCCAGCGTAATCAGGTTATCTATTGTTCTCTTCCACTTGCCTACACGAGCCCTGGT	1020
Qy	1021	TGTGATCTGTGGGAGCGGCTTCCGCAATCCGCTACATCTCACACCCCTTCCAA	1080
Db	1021	TGTGATCTGTGGGAGCGGCTTCCGCAATCCGCTACATCTCACACCCCTTCCAA	1080
Qy	1081	TTGAGCTGGCAGCGGACTCTTCTTGGCTGACCAATTTGTTATGGGCGCTCTTGT	1140
Db	1081	TTGAGCTGGCAGCGGACTCTTCTTGGCTGACCAATTTGTTATGGGCGCTCTTGT	1140
Qy	1141	GACCTGTAGCGCCCTTGCATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	1200
Db	1141	GACCTGTAGCGCCCTTGCATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	1200
Qy	1201	GCTTGTGAGCGCCTTGCATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	1260
Db	1201	GCTTGTGAGCGCCTTGCATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	1260
Qy	1261	AGTGCCCACTGGATAGATCCTGGTTCCTAGGGTTTATCGGTTGGATGGCGGCAAGGT	1320
Db	1261	AGTGCCCACTGGATAGATCCTGGTTCCTAGGGTTTATCGGTTGGATGGCGGCAAGGT	1320
Qy	1321	CGAGGCTGTATCTTTGACCAAACTGGCTTCAAGTACCATACGCTATTGGGACTAT	1380
Db	1321	CGAGGCTGTATCTTTGACCAAACTGGCTTCAAGTACCATACGCTATTGGGACTAT	1380
Qy	1381	GTTTGTAGCAGTGTACACTACCTGGCGTTGGCGCTCTGATCTACTATGCTCTCGGGGCA	1440
Db	1381	GTTTGTAGCAGTGTACACTACCTGGCGTTGGCGCTCTGATCTACTATGCTCTCGGGGCA	1440
Qy	1441	GTGGTATCAGTGTCTCTAGCGCTTATGCTTTACATAGAGCGACCTCTGGAACCCCAT	1500
Db	1441	GTGGTATCAGTGTCTCTAGCGCTTATGCTTTACATAGAGCGACCTCTGGAACCCCAT	1500
Qy	1501	CAGGGTCCCACTGGATGCTCAATAGCTGAGTTTGTCTCGGCTTTGATGATACCATGTCC	1560
Db	1501	CAGGGTCCCACTGGATGCTCAATAGCTGAGTTTGTCTCGGCTTTGATGATACCATGTCC	1560
Qy	1561	TTGCCACTCTTATTTGAGTGAATGTCAGAAATGTCATTTGTTACAGTCCAAAGTGGAC	1620
Db	1561	TTGCCACTCTTATTTGAGTGAATGTCAGAAATGTCATTTGTTACAGTCCAAAGTGGAC	1620
Qy	1621	CAGGCTTATCAGCTAGAGTATAACAACTCCATATCTTGGTACCCCTATACAATCCCTGG	1680
Db	1621	CAGGCTTATCAGCTAGAGTATAACAACTCCATATCTTGGTACCCCTATACAATCCCTGG	1680
Qy	1681	TGCAGGGGATGATGTTAAATTCAAAATTAACATAGGCTTGGCTGCGCTATTCGCA	1740

QY	3901	CAAAATTACCACTTTCTTACATGCGAGGAGAAAGTATGAGGTCTTGTGCTCTTAAATCCCACTGT	3960
DB	3901	CAAAATTACCACTTTCTTACATGCGAGGAGAAAGTATGAGGTCTTGTGCTCTTAAATCCCACTGT	3960
QY	3961	GGCTACCAACAGCATCAATGCGCAAAAGTACATGCGACGCGAGCTACCGCGTGAATCCAAATG	4020
DB	3961	GGCTACCAACAGCATCAATGCGCAAAAGTACATGCGACGCGAGCTACCGCGTGAATCCAAATG	4020
QY	4021	CTATTTTAAATGGCAAAATGTACCAACACAGGGGCTTTCACCTTACGTACAGCACATATGGCAT	4080
DB	4021	CTATTTTAAATGGCAAAATGTACCAACACAGGGGCTTTCACCTTACGTACAGCACATATGGCAT	4080
QY	4081	GTACTGTACCGGAGCATGTTCCCGGAACTATGAGGTCACTATTTGTGACGAAATGCCATGC	4140
DB	4081	GTACTGTACCGGAGCATGTTCCCGGAACTATGAGGTCACTATTTGTGACGAAATGCCATGC	4140
QY	4141	TACCGATGCAACACCGGTGTTGGCATTTGGAAAGGTCTTAACCGAAGCTCCATCCRAAAA	4200
DB	4141	TACCGATGCAACACCGGTGTTGGCATTTGGAAAGGTCTTAACCGAAGCTCCATCCRAAAA	4200
QY	4201	TGTTAGGCTAGTGGTTCCTTGCCACAGGCTACCCCCCTGGAGTAATCCCTACACCATATGC	4260
DB	4201	TGTTAGGCTAGTGGTTCCTTGCCACAGGCTACCCCCCTGGAGTAATCCCTACACCATATGC	4260
QY	4261	CAACATAACTGAGATTCAATTTAAACCGATGAAGGCACATATCCCTTTTATGGAATAAAGAT	4320
DB	4261	CAACATAACTGAGATTCAATTTAAACCGATGAAGGCACATATCCCTTTTATGGAATAAAGAT	4320
QY	4321	TAAAGGAGGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
DB	4321	TAAAGGAGGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
QY	4381	TGATTGAGCTTCTCTAAACGAGTTAGCTCGAAAGGGGAAATAACAGCTGCTCTTACTATAGGG	4440
DB	4381	TGATTGAGCTTCTCTAAACGAGTTAGCTCGAAAGGGGAAATAACAGCTGCTCTTACTATAGGG	4440
QY	4441	ATGTGACATCTCAAAAAATCCCTGAGGGCGACTGTGTAGTACTGCTTGTG	4500
DB	4441	ATGTGACATCTCAAAAAATCCCTGAGGGCGACTGTGTAGTACTGCTTGTG	4500
QY	4501	TACAGGGTACACTGGTGACTTTGATTCCGTGTATGACTGACAGCTCATGTTAGAAGGCAC	4560
DB	4501	TACAGGGTACACTGGTGACTTTGATTCCGTGTATGACTGACAGCTCATGTTAGAAGGCAC	4560
QY	4561	ATGCCATGTTCACTTGACCTTACTTTTCCACCATGGTGTTCGTGTGTCGGGGTTTCAGC	4620
DB	4561	ATGCCATGTTCACTTGACCTTACTTTTCCACCATGGTGTTCGTGTGTCGGGGTTTCAGC	4620
QY	4621	AATAGTTAAAGGCCAGCGTAGGGCCGCGACAGGCCGTGGGAGAGCTGGCATATACTACTA	4680
DB	4621	AATAGTTAAAGGCCAGCGTAGGGCCGCGACAGGCCGTGGGAGAGCTGGCATATACTACTA	4680
QY	4681	TGTAGACGGGAGTTGTACCCCTTCGGGTATGGTTCTGGAATGCAACATTTGTTGAAGCCTT	4740
DB	4681	TGTAGACGGGAGTTGTACCCCTTCGGGTATGGTTCTGGAATGCAACATTTGTTGAAGCCTT	4740
QY	4741	CGACGACGCAAGGCATGGTATGTTTGTCTCATCAACAGAGCTCAAACTATTTCTGGACAC	4800
DB	4741	CGACGACGCAAGGCATGGTATGTTTGTCTCATCAACAGAGCTCAAACTATTTCTGGACAC	4800
QY	4801	CTATCGCACCCAAACCTGGGTTTACCTTCGATAGGAGCAAAATTTGGACGAGTGGGCTGATCT	4860
DB	4801	CTATCGCACCCAAACCTGGGTTTACCTTCGATAGGAGCAAAATTTGGACGAGTGGGCTGATCT	4860
QY	4861	CTTTTCTATGTTCAACCCCGAAACCTTCAATTTGTCAATACTGCAAAAAAGAACTGCTGACAA	4920
DB	4861	CTTTTCTATGTTCAACCCCGAAACCTTCAATTTGTCAATACTGCAAAAAAGAACTGCTGACAA	4920
QY	4921	TTATGTTTTTGTGACTGCAGCCCCAACTACAACCTGTGTCATCAGTATGCTATGCTGCTCC	4980
DB	4921	TTATGTTTTTGTGACTGCAGCCCCAACTACAACCTGTGTCATCAGTATGCTATGCTGCTCC	4980
QY	4981	CAATGACGCAACCAAGGTGGCAGGGAGCCCGCTTTGGGAAAAAAACCTTTGTGGGGTCTGTG	5040

	Db		CAATGACGACCA	CGGTGGCAGGAGCCGGCTTGGGAAAAAACCTTGTGGGGTTCTGTG	5040
4981	Qy		GGCGTTGGACGGCGCTGACGCCCTGTCTCTGCGCCAGAGAGCCAGCGAGGTGACCAATACCA	5100	
	Db		GGCGTTGGACGGCGCTGACGCCCTGTCTGCGCCAGAGAGCCAGCGAGGTGACCAATACCA	5100	
5041	Qy		AATGTGCTTCACATGAAGTCAATATCTCTGGACAGCCGCACTCGCTGTTGGCGTTGGAGT	5160	
	Db		AATGTGCTTCACATGAAGTCAATATCTCTGGACAGCCGCACTCGCTGTTGGCGTTGGAGT	5160	
5101	Qy		GGCTATGGCTTATCTAGCCATTCACACTTTTGGGCCACTTGTGTGGCGGTGCTCGGTC	5220	
	Db		GGCTATGGCTTATCTAGCCATTCACACTTTTGGGCCACTTGTGTGGCGGTGCTCGGTC	5220	
5161	Qy		TATTACATCAGTCCCTACCGGTGCTACTGTGCGCCCACTGGTTGACGAAGAAGAAATCGT	5280	
	Db		TATTACATCAGTCCCTACCGGTGCTACTGTGCGCCCACTGGTTGACGAAGAAGAAATCGT	5280	
5221	Qy		GGAGGAGTGTGCATCAATTCATCCCTTGGAGGCCATGGTTGCTGCAATTGACAAGCTGAA	5340	
	Db		GGAGGAGTGTGCATCAATTCATCCCTTGGAGGCCATGGTTGCTGCAATTGACAAGCTGAA	5340	
5281	Qy		GAGTACAATCACCAAACTAGTCCCTTTCACATTTGGAAAAACGCCCTTGAAAAACTTAACAC	5400	
	Db		GAGTACAATTAACCAAACTAGTCCCTTTCACATTTGGAAAAACGCCCTTGAAAAACTTAACAC	5400	
5341	Qy		CTTTCTTGGGCTCATGACGCTCAATCCCTTGCTATCATAGAGTATTGCTGTGCTTTAGT	5460	
	Db		CTTTCTTGGGCTCATGACGCTCAATCCCTTGCTATCATAGAGTATTGCTGTGCTTTAGT	5460	
5401	Qy		CACTTTACCTGACAAATCCCTTTGCATCATGCGTGTGTTGCTTTCAATGCGGGTATTACTAC	5520	
	Db		CACTTTACCTGACAAATCCCTTTGCATCATGCGTGTGTTGCTTTCAATGCGGGTATTACTAC	5520	
5461	Qy		CCCACTACCTCACAGATCAAAAATGTTCCCTGTCAATTAATTTGGAGGCCCAATTGGCTCCAA	5580	
	Db		CCCACTACCTCACAGATCAAAAATGTTCCCTGTCAATTAATTTGGAGGCCCAATTGGCTCCAA	5580	
5521	Qy		GCTTTACAGCGCTAGAGCGCACCTGGCGGTTTCATGTCGCGGGCTCGGGGAACAGCTCT	5640	
	Db		GCTTTACAGCGCTAGAGCGCACCTGGCGGTTTCATGTCGCGGGCTCGGGGAACAGCTCT	5640	
5581	Qy		TGTTACATGACATCGGTGGGTTTGTCTTTTGACATCTAGGCGGGCTATGCTGCGCGCTC	5700	
	Db		TGTTACATGACATCGGTGGGTTTGTCTTTTGACATCTAGGCGGGCTATGCTGCGCGCTC	5700	
5641	Qy		ATCCACTGCTTGTGTGACATTTAAATGCTTGTATGGGTGAGTGGGCCACTATGGATCAGCT	5760	
	Db		ATCCACTGCTTGTGTGACATTTAAATGCTTGTATGGGTGAGTGGGCCACTATGGATCAGCT	5760	
5701	Qy		TGCTGGTTTATGCTACTCCGGTTCATCCGGCCGACAGGAGTTGTGTGGCGCTTTGTGAGC	5820	
	Db		TGCTGGTTTATGCTACTCCGGTTCATCCGGCCGACAGGAGTTGTGTGGCGCTTTGTGAGC	5820	
5761	Qy		TTGTGCAATGTTTGTCTTTTGACACAGCAGAGCCAGATCACTGGGCCCAACAGACTTCTTTAC	5880	
	Db		TTGTGCAATGTTTGTCTTTTGACACAGCAGAGCCAGATCACTGGGCCCAACAGACTTCTTTAC	5880	
5821	Qy		TATGCTTGTAGGAGCAACACTGTATGTATAGTACTTTTATTGGCCACTCGTGTGACATCCG	5940	
	Db		TATGCTTGTAGGAGCAACACTGTATGTATAGTACTTTTATTGGCCACTCGTGTGACATCCG	5940	
5881	Qy		CAGGAGATACTGGGCATTCGGAGGCATCTACCCCTGGAGTGTATATCAGCTTCGAT	6000	
	Db		CAGGAGATACTGGGCATTCGGAGGCATCTACCCCTGGAGTGTATATCAGCTTCGAT	6000	
5941	Qy		CCGTTGGCTCCACACCCCGACGGAGATGATTGCGGCTCATTTGCTTTGGGGTCTAGAGAT	6060	
	Db		CCGTTGGCTCCACACCCCGACGGAGATGATTGCGGCTCATTTGCTTTGGGGTCTAGAGAT	6060	
6001	Qy		TTGGCAGTATGTGTGCAATTTCTTTTGTAATTTGCTTTAATGTCTTAAAGCTTGAGTTCA	6120	

Db 6061 TTGGCAGTATGTGCAATTTCTTTGTGATTGTCTTTAATGTCTTTAAAGCTGGAGTTCA 6120
QY 6121 GAGCATGTTAACTTCCTGTTGTCCTTTCTACAGCTGCCAGAGGGGTACAAGGGCCC 6180
Db 6121 GAGCATGTTAACTTCCTGTTGTCCTTTCTACAGCTGCCAGAGGGGTACAAGGGCCC 6180
QY 6181 CTGGATTGGATCAGGTATGCTCCAAAGCACGCTGCTCCATGCGGTGCTGAACTCATCTTTTC 6240
Db 6181 CTGGATTGGATCAGGTATGCTCCAAAGCACGCTGCTCCATGCGGTGCTGAACTCATCTTTTC 6240
QY 6241 TGTTCAGAAATGTTTTGCAAACTTTTACAAGGACCCAGAACTTGTTCAAATTACTGGAG 6300
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QY 6301 AGGGCTGTTCCAGTCAAGCTAGGCTGTGTGGGTGGCTAGACCGGACCCCACTGATTG 6360
Db 6301 AGGGCTGTTCCAGTCAAGCTAGGCTGTGTGGGTGGCTAGACCGGACCCCACTGATTG 6360
QY 6361 GACTAGTCTTGTGCTCAATTTATGGGCTTAGGGACTACTGTAATATGAGAAATGGGAGA 6420
Db 6361 GACTAGTCTTGTGCTCAATTTATGGGCTTAGGGACTACTGTAATATGAGAAATGGGAGA 6420
QY 6421 TCACATTTTGTGTTACAGAGTATCTCTCCAAATGTCTGTTTTCACCCAGGTGCCCCCAAC 6480
Db 6421 TCACATTTTGTGTTACAGAGTATCTCTCCAAATGTCTGTTTTCACCCAGGTGCCCCCAAC 6480
QY 6481 CTTGAGAGCTGAGTGGCGGTGGAAGGGCTGAGGTTCAGTGTGTTATCTAGGTGAGCCCAA 6540
Db 6481 CTTGAGAGCTGAGTGGCGGTGGAAGGGCTGAGGTTCAGTGTGTTATCTAGGTGAGCCCAA 6540
QY 6541 AACTCCTTTGGACGACATCTGCTGTGTTTACCGTCTGACCGTAAAGGGTAAACTGTTAA 6600
Db 6541 AACTCCTTTGGACGACATCTGCTGTGTTTACCGTCTGCGACGGTAAAGGGTAAACTGTTAA 6600
QY 6601 GCTTCCCTTCCCGTTGACGGTCAACACTGCTGGTGGCGATGCAACTTAATTTGCGTGA 6660
Db 6601 GCTTCCCTTCCCGTTGACGGTCAACACTGCTGGTGGCGATGCAACTTAATTTGCGTGA 6660
QY 6661 TGCACCTTGAGCAAAATGACTGTAAATTCACAAACACACTCCTAGTGTAAAGCCGCACT 6720
Db 6661 TGCACCTTGAGCAAAATGACTGTAAATTCACAAACACACTCCTAGTGTAAAGCCGCACT 6720
QY 6721 GTCCGCTCTTGTGTTTCAAAAGGAGTTGCGGGTACAAACCAATTTGCTTAGGCAATTTTC 6780
Db 6721 GTCCGCTCTTGTGTTTCAAAAGGAGTTGCGGGTACAAACCAATTTGCTTAGGCAATTTTC 6780
QY 6781 AGCTGGGTTGACACACAAACTGCGCAGCCCTTCCATCGAAGAGGTAGTGGTAAGAAA 6840
Db 6781 AGCTGGGTTGACACACAAACTGCGCAGCCCTTCCATCGAAGAGGTAGTGGTAAGAAA 6840
QY 6841 GCGCAGTTCCGGGCAAGAACTGTTGCTTACCTTGTGCTCCCTCCGAGATCCGTCCC 6900
Db 6841 GCGCAGTTCCGGGCAAGAACTGTTGCTTACCTTGTGCTCCCTCCGAGATCCGTCCC 6900
QY 6901 AGGAGTGTCACTGCTGAAAGCTGCAACGAAAGTGACCCGTTAGAAGGTCTTCAAACT 6960
Db 6901 AGGAGTGTCACTGCTGAAAGCTGCAACGAAAGTGACCCGTTAGAAGGTCTTCAAACT 6960
QY 6961 CCTCTTTCACCACTGTTCTACAGTTGGCCATGCGGATGCCCTTGTGGAGACGGGTGA 7020
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QY 7141 GGCTTCAACCGCTTCCAGCTACGTTACTGGCCCCCGGTACCTTAAGATACGGGGAAAGGA 7200
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QY 7201 TTCCACTCAGTCAGCCCCGCCAAACCGSCCTTACAAAAAGAAAGTTGGAAAAAGAGTGAGTT 7260
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QY 7261 TTGCTGACGATGAGCTACACTCGGACCGAGCTGATTAGCTTCAAAACTGCTTCTAAAGT 7320
Db 7261 TTGCTGACGATGAGCTACACTCGGACCGAGCTGATTAGCTTCAAAACTGCTTCTAAAGT 7320
QY 7321 TCTGTCTGCAACTCGGGCCATCACTAGTGGTTTCTCAAAACAAAGATCATTTGGTGTATGT 7380
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QY 7501 CGGTGTCACTGTTGGGACTATGATGAAGTAGAGCTCACACGCCCTCTAAGTCTGCTAAGTC 7560
Db 7501 CGGTGTCACTGTTGGGACTATGATGAAGTAGAGCTCACACGCCCTCTAAGTCTGCTAAGTC 7560
QY 7561 CCACATCACTGCTGCGGCACTGATGTTGTTCTGGAGCAGCCCGCAAGGCTGTTCT 7620
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[illegible]

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1  APPLICANT: JAMES C. ERKER
2  APPLICANT: SHERI L. BUIJK
3  APPLICANT: ISA K. MUSHAWAR
4  TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
5  TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
6  NUMBER OF SEQUENCES: 716
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
9  STREET: 100 ABBOTT PARK ROAD
10 CITY: ABBOTT PARK
11 STATE: IL
12 COUNTRY: USA
13 ZIP: 60064-3500
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/488,446
21 FILING DATE:
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US/08/424,550
25 FILING DATE:
26 ATTORNEY/AGENT INFORMATION:
27 NAME: POREMBSKI, PRISCILLA E.
28 REGISTRATION NUMBER: 33,207
29 REFERENCE/DOCKET NUMBER: 5527.PC.01
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 708-937-6365
32 TELEFAX: 708-938-2623
33 INFORMATION FOR SEQ ID NO: 390:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 9143 base pairs
36 TYPE: nucleic acid
37 STRANDEDNESS: double
38 TOPOLOGY: linear
39 MOLECULE TYPE: DNA (genomic)
40 US-08-488-446-390

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Query Match 96.4%; Score 9059.8; DB 4; Length 9143;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 9096: Conservative 0; Mismatches 37; Indels 4;

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Db	361	TGGGATGGTTGGGGT	TAGCCATACATACCGTAC	CTGCTGTAGGGTCC	TTCTCGAGGGGAT			420

RESULT 4
US-08-488-446-390
; Sequence 390, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MARIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF

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[illegible]

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RESULT 5
US-08-488-446-393
; Sequence 393, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATTIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 393:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9143 base pairs
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QY 4621 AATAGTTAAAGGCCAGGTAGGGGCCGCAAGGGCGTGGAGAGCTGGCATATATACTACTA 4680
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QY 4681 TGTAGACGGGAGTTGTACCCCTTCGGGTATGTTTCTGTAATGCAACATTTGTTGAAGCCTT 4740
Db 4681 TGTAGACGGGAGTTGTACCCCTTCGGGTATGTTTCTGTAATGCAACATTTGTTGAAGCCTT 4740
QY 4741 CGACGACGCCAAGGCATGGTATGTTTGTCAATCAACAGAAGCTCAAACTATTTCTGGACAC 4800
Db 4741 CGACGACGCCAAGGCATGGTATGTTTGTCAATCAACAGAAGCTCAAACTATTTCTGGACAC 4800
QY 4801 CTATCGCACCCCAACTGGGTTTACCTGCGATAGGAGCAAAATTTGGACAGAGTGGGCTGATCT 4860
Db 4801 CTATCGCACCCCAACTGGGTTTACCTGCGATAGGAGCAAAATTTGGACAGAGTGGGCTGATCT 4860
QY 4861 CTTTTCTATGTTGATGACTGAGCCCACTTCAATTTGTCAATACTGCAAAAGAACTGCTGACAA 4920
Db 4861 CTTTTCTATGTTGATGACTGAGCCCACTTCAATTTGTCAATACTGCAAAAGAACTGCTGACAA 4920
QY 4921 TTATGTTTTGTTGATGACTGAGCCCACTCAACTGTTGTCATCAGTATGCTATGCTGCTCC 4980
Db 4921 TTATGTTTTGTTGATGACTGAGCCCACTCAACTGTTGTCATCAGTATGCTATGCTGCTCC 4980
QY 4981 CAATGACGACCAACGTTGGAGAGCCCGCTTGGGAAAAAACTTGTGGGGTTCTGTG 5040
Db 4981 CAATGACGACCAACGTTGGAGAGCCCGCTTGGGAAAAAACTTGTGGGGTTCTGTG 5040
QY 5041 GCGCTTTGACGGCGCTGACGCGCTGCTGGCCAGAGCCAGCGAGTGACAGATACCA 5100
Db 5041 GCGCTTTGACGGCGCTGACGCGCTGCTGGCCAGAGCCAGCGAGTGACAGATACCA 5100
QY 5101 AATGTGCTTCACTGAAGTCAATCTCTTGGGACAGCCGCACTCGCTGTTGGCGTTGGAGT 5160
Db 5101 AATGTGCTTCACTGAAGTCAATCTCTTGGGACAGCCGCACTCGCTGTTGGCGTTGGAGT 5160
QY 5161 GGCTATGGCTTATAGGCATTTGACACTTTTGGGCCCACTTGTGTGCGCGCTTGTGCTGTC 5220
Db 5161 GGCTATGGCTTATAGGCATTTGACACTTTTGGGCCCACTTGTGTGCGCGCTTGTGCTGTC 5220
QY 5221 TATTACATCAGTCCCTACCGGTGCTACTGTCGCCCGCTGTTGACGAAGAAGAAATCGT 5280
Db 5221 TATTACATCAGTCCCTACCGGTGCTACTGTCGCCCGCTGTTGACGAAGAAGAAATCGT 5280
QY 5281 GGAGGAGTGTGCATCATTTCCCTTTGGAGGCCATGGTGTCTGCAATTTGAACAGCTGAA 5340
Db 5281 GGAGGAGTGTGCATCATTTCCCTTTGGAGGCCATGGTGTCTGCAATTCGATTAAGCTGAA 5340
QY 5341 GAGTACAATACCAACACTAGTCTCTTTCAATTGGAAACCCGCCCTTGAAGAACTTTAACAC 5400
Db 5341 GAGTACAATACCAACACTAGTCTCTTTCAATTGGAAACCCGCCCTTGAAGAACTTTAACAC 5400
QY 5401 CTTTTCTTGGGCTCATGAGCTACAACTCTTGTATCATAGAGTATTCCTGTGGTTTAGT 5460
Db 5401 CTTTTCTTGGGCTCATGAGCTACAACTCTTGTATCATAGAGTATTCCTGTGGCTTAGT 5460
QY 5461 CACTTTACCTGACAATCCCTTTGTCATCATGCTGTTGCTTTTCAATTTGCGGGTATTACTAC 5520
Db 5461 CACTTTACCTGACAATCCCTTTGTCATCATGCTGTTGCTTTTCAATTTGCGGGTATTACTAC 5520
QY 5521 CCCACTACCTCAAGATCAAAAATGTTCTGTCAATTTTGGAGGGCAATTTGGCGTCCAA 5580
Db 5521 CCCACTACCTCAAGATCAAAAATGTTCTGTCAATTTTGGAGGGCAATTTGGCGTCCAA 5580

Qy	5581	GCTTACAGACGCTAGAGCGCACTGGCGTTTCATGATGGCCGGGGCTGCGGGAA	CAGCTCT	5640
Db	5581	GCTTACAGACGCTAGAGCGCACTGGCGTTTCATGATGGCCGGGGCTGCGGGAA	CAGCTCT	5640
Qy	5641	TGGTACATGACATCGGTGGGTTTGTCTTTGATGCTAGGCGGCTATGCTCGCGCTC		5700
Db	5641	TGGTACATGACATCGGTGGGTTTGTCTTTGATGCTAGGCGGCTATGCTCGCGCTC		5700
Qy	5701	ATCCACTGCTTGTCTTGACATTTAAATGCTTGAATGGGTGAGTGGCCCACTATGATCAGCT		5760
Db	5701	ATCCACTGCTTGTCTTGACATTTAAATGCTTGAATGGGTGAGTGGCCCACTATGATCAGCT		5760
Qy	5761	TGCTGGTTTATGCTTACTCCGCTTCAATCCGGCCGACAGAGTTGTGGCGCTTTGTGCAGC		5820
Db	5761	TGCTGGTTTATGCTTACTCCGCTTCAATCCGGCCGACAGAGTTGTGGCGCTTTGTGCAGC		5820
Qy	5821	TTGTGCAATGTTTGTCTTTGACACAGCAGAGGCGCAGATCACTGGCCCAACAGACTTCTTAC		5880
Db	5821	TTGTGCAATGTTTGTCTTTGACACAGCAGAGGCGCAGATCACTGGCCCAACAGACTTCTTAC		5880
Qy	5881	TATGCTTGTCTAGAGCAACACTGATGTAATGAGTACTTTATTGGCACTCGTGACATCCG		5940
Db	5881	TATGCTTGTCTAGAGCAACACTGATGTAATGAGTACTTTATTGGCACTCGTGACATCCG		5940
Qy	5941	CAGGAAGATACTGGGCATTTCTGGAGGCATCTACCCCTGGAGTGTCTATATCAGCTTGCAT		6000
Db	5941	CAGGAAGATACTGGGCATTTCTGGAGGCATCTACCCCTGGAGTGTCTATATCAGCTTGCAT		6000
Qy	6001	CGTGTGGCTCCACACCCCGACGAGGATGATGCGGCTCATTTGCTGGGGTCTAGAGAT		6060
Db	6001	CGTGTGGCTCCACACCCCGACGAGGATGATGCGGCTCATTTGCTGGGGTCTAGAGAT		6060
Qy	6061	TTGGCAGTATGCTGCAATTTCTTTGTGATTTGCTTTAAATGTCCTTAAAGCTGGAGTTCA		6120
Db	6061	TTGGCAGTATGCTGCAATTTCTTTGTGATTTGCTTTAAATGTCCTTAAAGCTGGAGTTCA		6120
Qy	6121	GAGCATGGTTAAACATTCCTGGTTGTCTTCTACAGCTGCCAGAGGGGTACAAGGGCCCC		6180
Db	6121	GAGCATGGTTAAACATTCCTGGTTGTCTTCTACAGCTGCCAGAGGGGTACAAGGGCCCC		6180
Qy	6181	CTGGATTTGATACAGGTATGCTCAAGCAACGCTGTCCATGCGGTGTGAATCTCATCTTTTC		6240
Db	6181	CTGGATTTGATACAGGTATGCTCAAGCAACGCTGTCCATGCGGTGTGAATCTCATCTTTTC		6240
Qy	6241	TGTTGAGAAATGGTTTTCGCAAACTTTTACAAGGACCCAGAACTTGTTCAAATTACTGGAG		6300
Db	6241	TGTTGAGAAATGGTTTTCGCAAACTTTTACAAGGACCCAGAACTTGTTCAAATTACTGGAG		6300
Qy	6301	AGGGCTGTTTCCAGTCAACGCTAGGCTGTGTGGTGGCTAGACCGGACCCCACTGATTG		6360
Db	6301	AGGGCTGTTTCCAGTCAACGCTAGGCTGTGTGGTGGCTAGACCGGACCCCACTGATTG		6360
Qy	6361	GACTAGTCTTGTGCTCAATTTATGGCGTTAGGACTACTGTAAATATGAGAAATTTGGAGA		6420
Db	6361	GACTAGTCTTGTGCTCAATTTATGGCGTTAGGACTACTGTAAATATGAGAAATTTGGAGA		6420
Qy	6421	TCACATTTTGTATACAGCAGTATCCCTCTCAAATGCTCTGTTTACCAGAGTGCCCCCAAC		6480
Db	6421	TCACATTTTGTATACAGCAGTATCCCTCTCAAATGCTCTGTTTACCAGAGTGCCCCCAAC		6480
Qy	6481	CTTTGAGAGCTGCAGTGGCCGTGGACCGGTACAGGTTTCACTGTTTATCTAGTGGAGCCCA		6540
Db	6481	CTTTGAGAGCTGCAGTGGCCGTGGACCGGTACAGGTTTCACTGTTTATCTAGTGGAGCCCA		6540
Qy	6541	AACTCCTTTGACGACATCTGCTTGTACGGTCCGGAACGTTAAGGGTAAACTGTTAA		6600
Db	6541	AACTCCTTTGACGACATCTGCTTGTGTACGGTCCGGAACGTTAAGGGTAAACTGTTAA		6600
Qy	6601	GCTTCCCTTCGGGTTGACGGTTCACACCTGTGTGCGGATGCAACTTAATTTTGGTGA		6660
Db	6601	GCTTCCCTTCGGGTTGACGGTTCACACCTGTGTGCGGATGCAACTTAATTTTGGTGA		6660

Qy	6661	TGCACTTGAGACAATAAGTACTGTAAATTTCCAAACAAACAACTCCTCTAGTGATGAAGACCGCAGT	6720
Db	6661	TGCACITTGAGACAAATGACTGTAAATTTCCAAACAAACAACTCCTCTAGTGATGAAGACCGCAGT	6720
Qy	6721	GTCCGCTCTTTGTTTTTCAAACAGAGAGTTGCGGGTACAAACCAATTCGTTTGAGGCAATTTTC	6780
Db	6721	GTCCGCTCTTTGTTTTTCAAACAGAGAGTTGCGGGTACAAACCAATTCGTTTGAGGCAATTTTC	6780
Qy	6781	AGCTGGCGTTTGACACCAACCTGCGAGCCCTCCATCGAAGAGGTAGTGGTAAGAAA	6840
Db	6781	AGCTGGCGTTTGACACCAACCTGCGAGCCCTCCATCGAAGAGGTAGTGGTAAGAAA	6840
Qy	6841	GGCGCAGTTCCGGGGAAGAACTGGTTTCGCTTACCTTTGCCCTCCCGCTCCGAGATCCGTCGCC	6900
Db	6841	GGCGCAGTTCCGGGGAAGAACTGGTTTCGCTTACCTTTGCCCTCCCGCTCCGAGATCCGTCGCC	6900
Qy	6901	AGAGTGTCTATGTCCTGAAGCCTGCAACGAAGTACCCTGTAGAAGAGTCTTCAAACCT	6960
Db	6901	AGAGTGTCTATGTCCTGAAGCCTGCAACGAAGTACCCTGTAGAAGAGTCTTCAAACCT	6960
Qy	6961	CCCTCTCTTCAACCACCTGTTCTACAGTTGGCCATGCCGATGCCCTGTTGGGAGCGGGTGA	7020
Db	6961	CCCTCTCTTCAACCACCTGTTCTACAGTTGGCCATGCCGATGCCCTGTTGGGAGCGGGTGA	7020
Qy	7021	GTGTAAACCTTTTCACTGCAATTTGATGTGCAATGACCGGAGAGGCGGCTGATGA	7080
Db	7021	GTGTAAACCTTTTCACTGCAATTTGATGTGCAATGACCGGAGAGGCGGCTGATGA	7080
Qy	7081	TTTTACCCAGTTACCCCTCCCAAAAGAGAGTCTCTGAAATGGTCTGAGAGTGGTCAAC	7140
Db	7081	TTTTACCCAGTTACCCCTCCCAAAAGAGAGTCTCTGAAATGGTCTGAGAGTGGTCAAC	7140
Qy	7141	GGCTTACAACCGCTTCCAGCTACGTTTACTGGCCCCCGTACCCTTAAGATACGGGGAAAGGA	7200
Db	7141	GACTACAACCGCTTCCAGCTACGTTTACTGGCCCCCGTACCCTTAAGATACGGGGAAAGGA	7200
Qy	7201	TTCCACTCAGTCAAGCCCCCGCCAAACGGGCTTACAAAAAGAGTTGGGAAAGAGTGAGTT	7260
Db	7201	TTCCACTCAGTCAAGCCCCCGCCAAACGGGCTTACAAAAAGAGTTGGGAAAGAGTGAGTT	7260
Qy	7261	TTGCTGCGCATGAGCTACACCTGGACCGACGTGATTAGCTTCAAACTGCTTCTAAAGT	7320
Db	7261	TTGCTGCGCATGAGCTACACCTGGACCGACGTGATTAGCTTCAAACTGCTTCTAAAGT	7320
Qy	7321	TCTGTCTGCAACTCGGGCCACTCACTAGTGGTTTCTTCAAAAGAGATCAATGGTGATGT	7380
Db	7321	TCTGTCTGCAACTCGGGCCACTCACTAGTGGTTTCTTCAAAAGAGATCAATGGTGATGT	7380
Qy	7381	GACTGAGCCGCGGGATGCGGAGCTTAGAAAAAAGAGTCACTTAAATAGACAACCTCT	7440
Db	7381	GACTGAGCCGCGGGATGCGGAGCTTAGAAAAAAGAGTCACTTAAATAGACAACCTCT	7440
Qy	7441	GTTCCTCCCATCATACCAAGCAAGTGAGATTGGCTTAAGGAAAAAGCTTCAAAAGTTGT	7500
Db	7441	GTTCCTCCCATCATACCAAGCAAGTGAGATTGGCTTAAGGAAAAAGCTTCAAAAGTTGT	7500
Qy	7501	CGGTGTCATGTGGGACTATGATCAAGTACAGCTCACAGCCCTCTAAGTCTGCTAAGTC	7560
Db	7501	CGGTGTCATGTGGGACTATGATCAAGTACAGCTCACAGCCCTCTAAGTCTGCTAAGTC	7560
Qy	7561	CCACATCACTGGCTCTCGGGGCACTGATGTTGTTCTGGAGCAGCCCGAAGGCTGTTCT	7620
Db	7561	CCACATCACTGGCTCTCGGGGCACTGATGTTGTTCTGGAGCAGCCCGAAGGCTGTTCT	7620
Qy	7621	GGACTTCGAGAAGTGTGTCGAGCGAGTGAGATACCGAGTCAATTAATCGGCAAACTGTGAT	7680
Db	7621	GGACTTCGAGAAGTGTGTCGAGCGAGTGAGATACCGAGTCAATTAATCGGCAAACTGTGAT	7680
Qy	7681	AGTTCCAAAGGAGGAGTCTTCTGTGAAGACCCCGCCAGAACCAACAAAGAAACCCCAAG	7740
Db	7681	AGTTCCAAAGGAGGAGTCTTCTGTGAAGACCCCGCCAGAACCAACAAAGAAACCCCAAG	7740
Qy	7741	GCTTATCTCCGTACCCCACTTGGAAATGAGATGTGTTGAGAAGATGCTACTACGGTCAGGT	7800

MOLECULE TYPE: DNA (genomic)									
SEQUENCE DESCRIPTION: SEQ ID NO: 390;									
US-08-467-344A-390									
Query Match 96.4%; Score 9059.8; DB 4; Length 9143;									
Best Local Similarity 99.6%; Pred. No. 0;									
Matches 9096; Conservative 0; Mismatches 37; Indels 4; Gaps 1;									
Qy	1	ACCAACAACACTCCAGTTTGTACACTCCGCTAGGAATGCTCTGGAGCACCCCCCTAG	60						
Db	1	ACCAACAACACTCCAGTTTGTACACTCCGCTAGGAATGCTCTGGAGCACCCCCCTAG	60						
Qy	61	CAGGGCTGGGGATTTCCCTCGCCGCTCTGCAGAGGTGGAGCCAAACCACTTAGTAT	120						
Db	61	CAGGGCTGGGGATTTCCCTCGCCGCTCTGCAGAGGTGGAGCCAAACCACTTAGTAT	120						
Qy	121	GTAGCGCGGGGACTCATAGCGCTCGGTGATGACAGCGCAAGCTTGACTTCGATGGC	180						
Db	121	GTAGCGCGGGGACTCATAGCGCTCGGTGATGACAGCGCAAGCTTGACTTCGATGGC	180						
Qy	181	CCTGATGGCGCTTCATGGGTTCCGTTGGTGGTGGCGCTTTAGGCGAGCCTCCACGCCACCA	240						
Db	181	CCTGATGGCGCTTCATGGGTTCCGTTGGTGGTGGCGCTTTAGGCGAGCCTCCACGCCACCA	240						
Qy	241	CCTCCAGATAGAGCGCGGCACTGTAGGGAAGACCGGGAGCCCGGTCACTACCAAGGAGC	300						
Db	241	CCTCCAGATAGAGCGCGGCACTGTAGGGAAGACCGGGAGCCCGGTCACTACCAAGGAGC	300						
Qy	301	CAGACCTCTTTTTCAGTATCACGCTCCGGAAGTATGGCAAGCCCACTATATGTT	360						
Db	301	CAGACCTCTTTTTCAGTATCACGCTCCGGAAGTATGGCAAGCCCACTATATGTT	360						
Qy	361	TGGGATGGTTGGGTTAGCCATCATACCGTACTGCTGTAGGCTCTTCGAGGGGAT	420						
Db	361	TGGGATGGTTGGGTTAGCCATCATACCGTACTGCTGTAGGCTCTTCGAGGGGAT	420						
Qy	421	CTGGGAGTCTCGTAGACGCTAGCACATGCTGTTATTTCTACTCAACCAAGTCTGTACC	480						
Db	421	CTGGGAGTCTCGTAGACGCTAGCACATGCTGTTATTTCTACTCAACCAAGTCTGTACC	480						
Qy	481	TGCGCCAGACGCGCAAGACACAGCAGACGCGCTTCATCTCTGCTCCATTAAAC	540						
Db	481	TGCGCCAGACGCGCAAGACACAGCAGACGCGCTTCATCTCTGCTCCATTAAAC	540						
Qy	541	ATCTGTTGAAAGGGGACAAACAGCAAGCGCAAGTCCAGCGGATGCTCGGCTCGTAA	600						
Db	541	ATCTGTTGAAAGGGGACAAACAGCAAGCGCAAGTCCAGCGGATGCTCGGCTCGTAA	600						
Qy	601	TTACAAAATTGCTGGTATCCATGATGGCTTGACAGACATGGCTCAGGCTGTTGCCAGC	660						
Db	601	TTACAAAATTGCTGGTATCCATGATGGCTTGACAGACATGGCTCAGGCTGTTGCCAGC	660						
Qy	661	TCATGGTTGGGAGCCAGACCTCGCCATAGTCTCGCAATCTTGGATCCCTCTGGA	720						
Db	661	TCATGGTTGGGAGCCAGACCTCGCCATAGTCTCGCAATCTTGGATCCCTCTGGA	720						
Qy	721	TTACCCCTTTGGGGTGGATTTGGTATGTTTCAACTCACACACTCTAGTAGGCCCGCTGGT	780						
Db	721	TTACCCCTTTGGGGTGGATTTGGTATGTTTCAACTCACACACTCTAGTAGGCCCGCTGGT	780						
Qy	781	GGCAGGAGCGGTCGTTGCAACAGTCTGCCAGATAGTACGCTTGTGGAGGATGAGTCAA	840						
Db	781	GGCAGGAGCGGTCGTTGCAACAGTCTGCCAGATAGTACGCTTGTGGAGGATGAGTCAA	840						
Qy	841	CTGGGCTACTGGTTGGTTCGGTGTCCACCTTTTGTGGTATGTCGTATCTTTGGCCTG	900						
Db	841	CTGGGCTACTGGTTGGTTCGGTGTCCACCTTTTGTGGTATGTCGTATCTTTGGCCTG	900						
Qy	901	TCCCTGTAGTGGGCGGGGTCACTGACCCAGACAAATACCAATCTCTGACCAATTG	960						
Db	901	TCCCTGTAGTGGGCGGGGTCACTGACCCAGACAAATACCAATCTCTGACCAATTG	960						
Qy	961	CTGCCAGCGTAATCAGGTTATCTATTGTTCTCTCCACTTGCCTACACGAGCCTGGTTG	1020						

961	CTGCCAGCGTAATCAGGTTATCTATTGTTCTCTCTTCCACTTGCCTACACGAGCCTGGTTG	1020
1021	TGTGATCTGTGCGGACGAGTGTGGGTTCCGCAATCCGTACATCTCAACACCCCTTCCAA	1080
1021	TGTGATCTGTGCGGACGAGTGTGGGTTCCGCAATCCGTACATCTCAACACCCCTTCCAA	1080
1081	TTGGAATGGGACCGGACTCTTCTTTGGCTGACCAATTTGATTTTGTATGGGCGCTCTGT	1140
1081	TTGGAATGGGACCGGACTCTTCTTTGGCTGACCAATTTGATTTTGTATGGGCGCTCTGT	1140
1141	GACTGTGACGCGCTTCACATTTGGTGGTGTGTGGTGGTGTGATTTAGTTCGGTGACTG	1200
1141	GACTGTGACGCGCTTCACATTTGGTGGTGTGTGGTGGTGTGATTTAGTTCGGTGACTG	1200
1201	GCTTGTGAGGCACTGGCTTATTCACATAGACCTCAATGAATCAATGTAACCTGTTTACCTGGA	1260
1201	GCTTGTGAGGCACTGGCTTATTCACATAGACCTCAATGAATCAATGTAACCTGTTTACCTGGA	1260
1261	AGTGCCCACTGGAAATAGATCCTGGGTTCTTAGGGTTTATCGGGTGGATGGCCGCAAGGT	1320
1261	AGTGCCCACTGGAAATAGATCCTGGGTTCTTAGGGTTTATCGGGTGGATGGCCGCAAGGT	1320
1321	CGAGGCTGTCTCTTTTGACCAAACTGGCTTCACAAGTACCATACGCTATTGCGACTAT	1380
1321	CGAGGCTGTCTCTTTTGACCAAACTGGCTTCACAAGTACCATACGCTATTGCGACTAT	1380
1381	GTTTAGCAGTGTACACTTCTTGGCGGTTGGCGCTCTGATCTACTATGCTCTCGGGGCAA	1440
1381	GTTTAGCAGTGTACACTTCTTGGCGGTTGGCGCTCTGATCTACTATGCTCTCGGGGCAA	1440
1441	GTGGTATCAGTGTCTCTAGCGCTTATGCTTTACATAGAACGACCTCTGGAACCCCAT	1500
1441	GTGGTATCAGTGTCTCTAGCGCTTATGCTTTACATAGAACGACCTCTGGAACCCCAT	1500
1501	CAGGGTCCCACTGGGATGCTCAATAGCTGATGTTTGTCTCGCTTTGATGATACCATGTC	1560
1501	CAGGGTCCCACTGGGATGCTCAATAGCTGATGTTTGTCTCGCTTTGATGATACCATGTC	1560
1561	TTGGCACTCTTATTTGAGTGAGATGTCAGAACTCATTTGTTTACAGTCCAAAGTGGAC	1620
1561	TTGGCACTCTTATTTGAGTGAGATGTCAGAACTCATTTGTTTACAGTCCAAAGTGGAC	1620
1621	CAGGCTTATCCTCTAGAGTATAACAACTCCATATCTTGGTACCCCTATACAATCCCTGG	1680
1621	CAGGCTTATCCTCTAGAGTATAACAACTCCATATCTTGGTACCCCTATACAATCCCTGG	1680
1681	TGCGAGGGATGATGGTTAAATTTCAAAAATAACACATGGGGTTGCTGCGGTATTCGCA	1740
1681	TGCGAGGGATGATGGTTAAATTTCAAAAATAACACATGGGGTTGCTGCGGTATTCGCA	1740
1741	TGTGCCATCTGCTGCACTATGGGCTGATGAGTGTGAAACGACACTCGCAACACTTA	1800
1741	TGTGCCATCTGCTGCACTATGGGCTGATGAGTGTGAAACGACACTCGCAACACTTA	1800
1801	CGAAGCATCGGCTGTAAACCATGGCTTAACACCGCATGGCATAACCGGCTCAGCCCTGAA	1860
1801	CGAAGCATCGGCTGTAAACCATGGCTTAACACCGCATGGCATAACCGGCTCAGCCCTGAA	1860
1861	ATTGGCTATTATTACCAATACCCCTGGGCTAAAGAAATGTTTAAACCTCATATTTGGATGTC	1920
1861	ATTGGCTATTATTACCAATACCCCTGGGCTAAAGAAATGTTTAAACCTCATATTTGGATGTC	1920
1921	AGGCCATTTGTTATTTTGGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAA	1980
1921	AGGCCATTTGTTATTTTGGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAA	1980
1981	TTCCACTCTCTTACCACCGGAGAGGTGGGCTAGGTTGCCGGTACCCACCTGTGGTACG	2040
1981	TTCCACTCTCTTACCACCGGAGAGGTGGGCTAGGTTGCCGGTACCCACCTGTGGTACG	2040
2041	TGGTCTTGGTTACAGGTTCCGCAAGGGTTTACAGTGTGTAAGACACTTAGCCACAGG	2100

Db 2041 TGGTTCTTGGTTACAGGTTCCGAAAGGTTTTTACAGTGATGTGAAAGACCTAGCCACAGG 2100
Qy 2101 ATTGATCAACCAAGCAAGCCTGGAATAATATCAGGCTTATATTCGCGCACCGGGTGC 2160
Db 2101 ATTGATCAACCAAGCAAGCCTGGAATAATATCAGGCTTATATTCGCGCACCGGGTGC 2160
Qy 2161 TTTGTCTCTTACGGGAGTTACCAACAGGCCGTGTGCTAAATCTGTGTTGGGTTGTGTGG 2220
Db 2161 TTTGTCTCTTACGGGAGTTACCAACAGGCCGTGTGCTAAATCTGTGTTGGGTTGTGTGG 2220
Qy 2221 CAGCAAGTATCTTATTTAGCCTACCTCTGTGTAATTGTGTCCTTTGTTTGGCGCGCTTC 2280
Db 2221 CAGCAAGTATCTTATTTAGCCTACCTCTGTGTAATTGTGTCCTTTGTTTGGCGCGCTTC 2280
Qy 2281 TGGTTACCCTTTGGCTCGTGTGCCCATCCAGTCGATCTCCAAGCTGGCTGGGATGT 2340
Db 2281 TGGTTACCCTTTGGCTCGTGTGCCCATCCAGTCGATCTCCAAGCTGGCTGGGATGT 2340
Qy 2341 TTTGTCTAAAGCTCAAGTAGCTCCTTTTGTGTTGATTTTCTTCACTGTGTGTAFTCTCCG 2400
Db 2341 TTTGTCTAAAGCTCAAGTAGCTCCTTTTGTGTTGATTTTCTTCACTGTGTGTAFTCTCCG 2400
Qy 2401 CTGCAAGCTACGTTATGTCGCCCTTTTAGGGTTTGTGCCATAGGTGCGGGCTTGCCCT 2460
Db 2401 CTGCAAGCTACGTTATGTCGCCCTTTTAGGGTTTGTGCCATAGGTGCGGGCTTGCCCT 2460
Qy 2461 AACTTTCTTTGTCAGCAGCTGTGCCCAACCAAGATATGACTGGTGGTGGCACTGCT 2520
Db 2461 AACTTTCTTTGTCAGCAGCTGTGCCCAACCAAGATATGACTGGTGGTGGCACTGCT 2520
Qy 2521 AGTGGCAGGGTAGTTTTTGTGGCGCGCGTAAACCGTGGTCACCGCATAGCTCTGCTTGT 2580
Db 2521 AGTGGCAGGGTAGTTTTTGTGGCGCGCGTAAACCGTGGTCACCGCATAGCTCTGCTTGT 2580
Qy 2581 AGGTCTTGGGCTCTGGTAGGCTTTTAAACCTCTTGGCATTTGGTTAGCCCTGCTTACG 2640
Db 2581 AGGTCTTGGGCTCTGGTAGGCTTTTAAACCTCTTGGCATTTGGTTAGCCCTGCTTACG 2640
Qy 2641 TTTTGATACCGAGATAATTGGAGGGCTGACATACCACCTGTAGTACGATTAGTTGTCTAT 2700
Db 2641 TTTTGATACCGAGATAATTGGAGGGCTGACATACCACCTGTAGTACGATTAGTTGTCTAT 2700
Qy 2701 GTCTGGTTTGGCTCTTTTGTCTCACTGTGTACCTCGCTGTGCTTTAGTTAACTCCTATCT 2760
Db 2701 GTCTGGTTTGGCTCTTTTGTCTCACTGTGTACCTCGCTGTGCTTTAGTTAACTCCTATCT 2760
Qy 2761 TTGGCAACGTTGGGAGAAATGGTTTTTGGAAACGTTACCTAACACCGGAGAGGTTTTTCT 2820
Db 2761 TTGGCAACGTTGGGAGAAATGGTTTTTGGAAACGTTACCTAACACCGGAGAGGTTTTTCT 2820
Qy 2821 TGTGCTGTTTTGTTTCCCGGTGGACATATGACCGCTGTGTGCTTCTGTGTGTGTCA 2880
Db 2821 TGTGCTGTTTTGTTTCCCGGTGGACATATGACCGCTGTGTGCTTCTGTGTGTGTCA 2880
Qy 2881 CGTAGCTCTTCTATGTTTAAACATCCAGTGCAGCATCGTTCTTTTGGGACTGACTAGGGT 2940
Db 2881 CGTAGCTCTTCTATGTTTAAACATCCAGTGCAGCATCGTTCTTTTGGGACTGACTAGGGT 2940
Qy 2941 TAGGGCCCATAGATTTGGTGGCTCTCGGAAAGTGTCAATGCTTGGTATTTCTATATATGT 3000
Db 2941 TAGGGCCCATAGATTTGGTGGCTCTCGGAAAGTGTCAATGCTTGGTATTTCTATATATGT 3000
Qy 3001 TCTTAAGTTTTTCTCTTAGTGTGTGGTGAATCGTGTGTTTCTATAGCACTTGCA 3060
Db 3001 TCTTAAGTTTTTCTCTTAGTGTGTGGTGAATCGTGTGTTTCTATAGCACTTGCA 3060
Qy 3061 TGGTGATGCTTGTCCCTAATGTTTTGCTCTCGAAACTACCATTTGCAAGAGCCATTTTCCC 3120
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Qy 3121 TTTTGAAGGCAAGGCAAGGCTCTATAGGAAATGAAGGAAGACGCTTGGGCTGTGGGACAC 3180
Db 3121 TTTTGAAGGCAAGGCAAGGCTCTATAGGAAATGAAGGAAGACGCTTGGGCTGTGGGACAC 3180

Qy 3181 GGTGTATGGTTTGGCCGTTGTGTGGCGCTCTCGGCAACCTTGTGTTTTCGCAGGGTTGGCTAT 3240
Db 3181 GGTGTATGGTTTGGCCGTTGTGTGGCGCTCTCGGCAACCTTGTGTTTTCGCAGGGTTAGCTAT 3240
Qy 3241 GCGCCAGATGGGTGGGCCATTACCGCACTTTTACGCTGCAGTGTCTCTCTGAACGTGG 3300
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Qy 3301 CACGCTGTACGCGATGGCAGTGGTTCATGACTGGTATAGACCCCGMACTTGACCTGGAAAC 3360
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Qy 3361 TATCTTACAGATTAGGATCTCTGGGCCATTAGCTACATGGGATTTGTGTTGTGACACGCTGT 3420
Db 3361 TATCTTACAGATTAGGATCTCTGGGCCATTAGCTACATGGGATTTGTGTTGTGACACGCTGT 3420
Qy 3421 GTATACCTGCTCACATGGCAGAGGGCGCGGTTGGCTCATCCACAGAGCTCTATACA 3480
Db 3421 GTATACCTGCTCACATGGCAGAGGGCGCGGTTGGCTCATCCACAGGCTCCATACA 3480
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Qy 3541 GTCCCTTACTCGGTGCTCTTGGCGGGAGACCAAGGGGTATCTGGTAAACACGACTGGGCTC 3600
Db 3541 GTCCCTTACTCGGTGCTCTTGGCGGGAGACCAAGGGGTATCTGGTAAACACGACTGGGCTC 3600
Qy 3601 ATTGGTTGAGGTCAACAAATCCGATGACCCCTTATTTGGTGTGTGCGGGGCCCTTCCAT 3660
Db 3601 ATTGGTTGAGGTCAACAAATCCGATGACCCCTTATTTGGTGTGTGCGGGGCCCTTCCAT 3660
Qy 3661 GGCTTTGGCCAAAGGGTTCTTCAGTGGCCCGATTTCTGTCTCTCCGGGCATGTTATGG 3720
Db 3661 GGCTTTGGCCAAAGGGTTCTTCAGTGGCCCGATTTCTGTCTCTCCGGGCATGTTATGG 3720
Qy 3721 GATGTTTACCGCTGTAGAAATTTCTGGCGGTTCTAGTCAGTCAAGTATAGGGTTAGGCCGTT 3780
Db 3721 GATGTTTACCGCTGTAGAAATTTCTGGCGGTTCTAGTCAAGTATAGGGTTAGGCCGTT 3780
Qy 3781 GGTGTGTCTGGATACCATCCAGTACACAGCATGCCACTCTTGATACAAAACCTAC 3840
Db 3781 GGTGTGTCTGGATACCATCCAGTACACAGCATGCCACTCTTGATACAAAACCTAC 3840
Qy 3841 TGTGCCTAACGAGTATTTCAAGTGCATAATTTTAAATTTGCCCCCACTGGCAGCGCAAGTCAAC 3900
Db 3841 TGTGCCTAACGAGTATTTCAAGTGCATAATTTTAAATTTGCCCCCACTGGCAGCGCAAGTCAAC 3900
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Db 3901 CAAATTTACCACTTTCTTACATGCAGGAGAACTATGAGGTCTTGGTCTTAAATCCAGTGT 3960
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Db 3961 GGCTACAAACAGCATCAATGCGCAAGTACATGCGCGAGCTACGGCGTGAATCCAAATG 4020
Qy 4021 CTATTTTAAATGGCAATGTACCAACAGGGGCTTCACTTACGTACAGCATATGGCAT 4080
Db 4021 CTATTTTAAATGGCAATGTACCAACAGGGGCTTCACTTACGTACAGCATATGGCAT 4080
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Db 4081 GTACTGTACCGGAGCATGTTCCCGAACTATGATGTAAATCATTTGTGTGACGAATGCCATGC 4140
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Db 4141 TACCATGCAACCAACCGTGTGGCATTTGGAAGGTCTTAAACGAGTCCATCCATAAAAA 4200
Qy 4201 TGTTAGGCTAGTGTCTTGTGCAAGGCTACCCCGCTGGAGTAAATCCCTACACCATGC 4260
Db 4201 TGTTAGGCTAGTGTCTTGTGCAAGGCTACCCCGCTGGAGTAAATCCCTACACCATGC 4260

QY 4261 CAACATAA CTGAGATTCAATTAA CCGATGAAGGCATCTATCCCCCTTT CATGGAAAAAAGAT 4320
DB |||||
QY 4261 CAACA TAACTGAGATTCAATTAA CCGATGAAGGCAC TATCCCCCTTT CATGGAAAAAAGAT 4320
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QY 4321 TAAAGGAGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG 4380
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QY 4321 TAAAGGAGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG 4380
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DB |||||
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DB |||||
QY 5461 CACTTTACCTGACAAATCCCTTTGTCATCATCGTGTGTTTTGCTTTCAATCGGGGATTTACTTAC 5520
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QY 5701 ATCCACTGCTTGTGTGACATTTAAATGCTTGA TGGGTGAGTGGGCCCACTATGGATCAGCT 5760
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DB |||||
QY 5821 TTGTGCAATGTTTGTCTTTTGA CAACAGCAGGCGCCAGATCACTTGGCCCAACAGACTTCTTAC 5880
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QY 5881 TATGCTTGTAGAGGAAACACTGTATGTATGAGTACTTTTATTTGCCACTGCTGACATCCG 5940
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QY 5881 TATGCTTGTAGAGGAAACACTGTATGTATGAGTACTTTTATTTGCCACTGCTGACATCCG 5940
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DB |||||
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QY 6121 GAGCATGGTTAA CATTCTCGTTGCTCTTTCTACAGCTGCCAGAGGGGTACAAGGGGCC 6180
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QY 6241 TGTGAGAAATGGTTTTGCAAAA CTTTACAAGGACCCAGAACTTTGTTCAAA TTAATCTGGAG 6300
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QY 6301 AGGGGCTGTTCCAGTCAACGCTAGGCTGTGGGTGCTGAGCCGAGCCCACTGATTG 6360
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QY 6301 AGGGGCTGTTCCAGTCAACGCTAGGCTGTGGGTGCTGAGCCGAGCCCACTGATTG 6360
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QY 6361 GACTAGTCTTGTCTGCTCAATTTATGCGGTTAGGGACTACTGTAAATATGAGAAATTTGGAGA 6420
DB |||||
QY 6361 GACTAGTCTTGTCTGCTCAATTTATGCGGTTAGGGACTACTGTAAATATGAGAAATTTGGAGA 6420
DB |||||
QY 6421 TCACATTTTGTGTACAGAGTATCTCTCTCAAAATGTCTGTTTACCAGGTTGCCCCAC 6480
DB |||||

[illegible]

Qy	7561	CCACATC	ACTGGCGCTTCGGGGCACTGATGTTGCTTCTGAGCAGACCGCGCAAGCGCTGTTCT	7620
Db	7561	CCACATC	ACTGGCGCTTCGGGGCACTGATGTTGCTTCTGGAGCAGACCGCGCAAGCGCTGTTCT	7620
Qy	7621	GGACTTC	GACGAAGTGTGTGCGAGGCAGGTGAGATACCGAGTCAATTATTCGGCAAACTGTGAT	7680
Db	7621	GGACTTC	GACGAAGTGTGTGCGAGGCAGGTGAGATACCGAGTCAATTATTCGGCAAACTGTGAT	7680
Qy	7681	AGTTCCAA	AGGAGGAGGTCTTCTGTGAAGACCCCCCAAGAAACCAACAAAGAAAACCCCAAG	7740
Db	7681	AGTTCCAA	AGGAGGAGGAGTCTTCTGTGAAGACCCCCCAAGAAACCAACAAAGAAAACCCCAAG	7740
Qy	7741	GCTTATCT	CGTACCCCACTTCAAATGAGATGTGTTGAGAAGATGTACTACCGTCAGGT	7800
Db	7741	GCTTATCT	CGTATCTCGTACCCCACTTGAATGAGATGTGTTGAGAAGATGTACTACCGTCAGGT	7800
Qy	7801	TGCTCTCG	AGTGTAAAGCTGTATGGGAGATGCGTACGGGTTTTGTAGATCCACGTAC	7860
Db	7801	TGCTCTCG	AGTGTAAAGCTGTATGGGAGATGCGTACGGGTTTTGTGACCCACGTAC	7860
Qy	7861	CGTGTC	CAAGCGTCTGTTGTGATGTGTCACCCGATGCAGTCCGAGCCACATGCCATAC	7920
Db	7861	CGTGTC	CAAGCGTCTGTTGTGATGTGTCACCCGATGCAGTCCGAGCCACATGCCATAC	7920
Qy	7921	AGTGTGTT	TTTGACAGTACCATCACACCCGAGGATATCATGGTGGAGACAGACATCTACTC	7980
Db	7921	AGTGTGTT	TTTGACAGTACCATCACACCCGAGGATATCATGGTGGAGACAGACATCTACTC	7980
Qy	7981	AGCAGCT	ATAACTCAGTGACCAACACCGAGTGGCATTCACACCATTTGCGAGGCGAGTTATA	8040
Db	7981	AGCAGCT	ATAACTCAGTGACCAACACCGAGTGGCATTCACACCATTTGCGAGGCGAGTTATA	8040
Qy	8041	CGCTGG	AGGACCGATGATCGCTTATGATGCGCAGAGATCGGATATCGTAGGTGTTAGTGC	8100
Db	8041	CGCTGG	AGGACCGATGATCGCTTATGATGCGCAGAGATCGGATATCGTAGGTGTTAGTGC	8100
Qy	8101	TTCCGG	CGCTATACCTCAAAGTTCACACAGTTCGCTGGCTGAAGGTAAATGC	8160
Db	8101	TTCCGG	CGCTATACCTCAAAGTTCACACAGTTCGCTGGCTGAAGGTAAATGC	8160
Qy	8161	TGCAGC	CGCAAGCTGCGATGAAGAACCTCCCTTCCTTATTTGGCGCATGATGTCAC	8220
Db	8161	TGCAGC	CGCAAGCTGCGATGAAGAACCTCCCTTCCTTATTTGGCGCATGATGTCAC	8220
Qy	8221	CGTAA	TTTGAAGCCGCGAGCAGATGAGACAAACAGCAATCGCTCTTTGCTAG	8280
Db	8221	CGTAA	TTTGAAGCCGCGAGCAGATGAGACAAACAGCAATCGCTCTTTGCTAG	8280
Qy	8281	CTGGAT	GAGGTGATGGGTGCAACACAGATGTGTGCTCAACCCCAATACAGTTTGGTA	8340
Db	8281	CTGGAT	GAGGTGATGGGTGCAACACAGATGTGTGCTCAACCCCAATACAGTTTGGTA	8340
Qy	8341	AGAA	TAAACATCATGCTCAAAATGTACCTCTGGAAATACCAAAAGTGGCAAGCCTTA	8400
Db	8341	AGAA	TAAACATCATGCTCAAAATGTACCTCTGGAAATACCAAAAGTGGCAAGCCTTA	8400
Qy	8401	CTACT	TTTCAAGAGATCCTCGTATCCCTTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
Db	8401	CTACT	TTTCAAGAGATCCTCGTATCCCTTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
Qy	8461	ATACAA	CCCCAGTCTCGTGGATTTGGGTATCTAATACATCACTACCCATGTTTGTGGGT	8520
Db	8461	ATACAA	CCCCAGTCTCGTGGATTTGGGTATCTAATACATCACTACCCATGTTTGTGGGT	8520
Qy	8521	TAGCCG	TGTGTGGCTCCATTTCTAGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA	8580
Db	8521	TAGCCG	TGTGTGGCTCCATTTCTAGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA	8580
Qy	8581	GACTGT	GACCTTTGACTGGTATGGGAAAAATATATACCGTGCTGTAGAAAGATCTGCCACG	8640
Db	8581	GACTGT	GACCTTTGACTGGTATGGGAAAAATATATACCGTGCTGTAGAAAGATCTGCCACG	8640

Db 601 TTACAAAATTGCTGGTATCCATGATGGCTTGCGACATTTGGCTCAGGCTGCTTTGCCAGC 660
Qy 661 TCATGGTTGGGAGCCCAAGACCCCTCGCATAGTCTCGCAATCTTGGAACTCTTCTGGA 720
Db 661 TCATGGTTGGGAGCCCAAGACCCCTCGCATAGTCTCGCAATCTTGGAACTCTTCTGGA 720
Qy 721 TTACCCCTTTGGGGTGGATTGGTGAATGTTAACTCACACACCTCTAGTAGGCCCGCTGGT 780
Db 721 TTACCCCTTTGGGGTGGATTGGTGAATGTTAACTCACACACCTCTAGTAGGCCCGCTGGT 780
Qy 781 GGCAGGACGGTCTGTTGCACACAGTCTGCAGATAGTACGCTTCTGGAGGATGGAGTCAA 840
Db 781 GGCAGGACGGTCTGTTGCACACAGTCTGCAGATAGTACGCTTCTGGAGGATGGAGTCAA 840
Qy 841 CTGGCTACTGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGG 900
Db 841 CTGGCTACTGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGG 900
Qy 901 TCCCTGTAGTGGGCGCGGGTCACTGACCCAGACACAAATACCAAACTCCTGACCAATTG 960
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Qy 961 CTGCCAGGCTAATCAGGTTATCTATTGTTCTCTTCCATCCGCTACAGAGCCTGGTTG 1020
Db 961 CTGCCAGGCTAATCAGGTTATCTATTGTTCTCTTCCATCCGCTACAGAGCCTGGTTG 1020
Qy 1021 TGTGATCTGCGGACGAGTCTGGGTTCCGCCCAATCCGTACATCTCACACCTTCCAA 1080
Db 1021 TGTGATCTGCGGACGAGTCTGGGTTCCGCCCAATCCGTACATCTCACACCTTCCAA 1080
Qy 1081 TTGGACTGGCACGGACTCCTTCTTGGCTGACACATTTGTTATGGGCGCTCTTGT 1140
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Qy 1141 GACCTGTACGCCCTTGACATTTGTTGAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1200
Db 1141 GACCTGTACGCCCTTGACATTTGTTGAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1200
Qy 1201 GCTTCTCAGGCACTGGCTTATTCACATAGACTCAATGAACCTGCTACTTGTACTCTGA 1260
Db 1201 GCTTCTCAGGCACTGGCTTATTCACATAGACTCAATGAACCTGCTACTTGTACTCTGA 1260
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Db 1261 AGTGCCCACTGGAATPAGATCTCGGTTCTAGGGTTTATCGGGTGGATGGCGGCAAGGT 1320
Qy 1321 CGAGCTGTCTATCTTCTTGACCAAACTGGCTTCACAGTACCATGCTATTTGCCACTAT 1380
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Qy 1441 GTGGTATCAGTTGCTCTAGCGCTTATGCTTTACATAGAAGGACCTCTGGAACCCCTAT 1500
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Qy 1681 TCCGAGGGGATGATGGTTAAATTCAAAATAAACATGGGGTTGCTGCCGTATTCGCAA 1740
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Qy 1801 CGAAGCATGCGGTTAAACACCATGGCTAAACCGCATGGCAACCGGCTCAGGCTCAGGCTGAA 1860
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Qy 2041 TGGTTCTTGGTTACAGGTTCCGCAAGGGTTTTACAGTATGTGAAAGACCTAGCCACAGG 2100
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Db 2581 AGGTCTTGGCTCTGTTAGCGCTTTTAAACCTCTTGCATTTGGTTAGCGCTTCAGC 2640
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Qy 5401 CTTTCTTGGGCTCATGAGCTACAAATCCTTGCTATCATAGATATTCGTGGTTTGTAGT 5460
Db 5401 CTTTCTTGGGCTCATGAGCTACAAATCCTTGCTATCATAGATATTCGTGGTTTGTAGT 5460
Qy 5461 CACTTTACCTGACAACTCCCTTTGCAATCATGCGTGTTCCTTTTCAATTTGGGGGTATTACTAC 5520
Db 5461 CACTTTACCTGACAACTCCCTTTGCAATCATGCGTGTTCCTTTTCAATTTGGGGGTATTACTAC 5520
Qy 5521 CCCACTACTCACAGATCAAAATGTTCTGTCAATTTATTTGGAGCGCAATTCGCTCAA 5580
Db 5521 CCCACTACTCACAGATCAAAATGTTCTGTCAATTTATTTGGAGCGCAATTTGCGTCAA 5580
Qy 5581 GCTTACAGACGCTAGAGCGCACTGGCGTTCAATGATGCGGGCTTGGGGAAAGAGCTCT 5640
Db 5581 GCTTACAGACGCTAGAGCGCACTGGCGTTCAATGATGCGGGCTTGGGGAAAGAGCTCT 5640
Qy 5641 TGGTACATGGACATCGGTGGGTTTTGTCTTTTGACATGCTAGCGGCTATGCTGCGCGCTC 5700
Db 5641 TGGTACATGGACATCGGTGGGTTTTGTCTTTTGACATGCTAGCGGCTATGCTGCGCGCTC 5700
Qy 5701 ATCCACTGCTTGTCTGACATTTAAATGCTTGAATGGTGAAGTGGCCCACTATGGATCAGCT 5760
Db 5701 ATCCACTGCTTGTCTGACATTTAAATGCTTGAATGGTGAAGTGGCCCACTATGGATCAGCT 5760
Qy 5761 TGCTGGTTTTAGTCTACTCCGCTTCAATCCGCGCCAGAGTTGTGGCGTCTTGTCAAGC 5820
Db 5761 TGCTGGTTTTAGTCTACTCCGCTTCAATCCGCGCCAGAGTTGTGGCGTCTTGTCAAGC 5820
Qy 5821 TTGTGCAATGTTTGTCTTTGACAAAGAGGCGCAGATCACTGGCCCAACAGACTTCTTAC 5880
Db 5821 TTGTGCAATGTTTGTCTTTGACAAAGAGGCGCAGATCACTGGCCCAACAGACTTCTTAC 5880
Qy 5881 TATGCTTGTAGGAGCAACACTGTATGTAAATGAGTACTTTATTTGCACTCGTGAATCCG 5940
Db 5881 TATGCTTGTAGGAGCAACACTGTATGTAAATGAGTACTTTATTTGCACTCGTGAATCCG 5940
Qy 5941 CAGGAAGTACTTGGGCACTTCTGGAGGCATCTACCCCTGGAGTGTCAATCAGCTTGTGAT 6000
Db 5941 CAGGAAGTACTTGGGCACTTCTGGAGGCATCTACCCCTGGAGTGTCAATCAGCTTGTGAT 6000
Qy 6001 CCGTTGGCTTCCACACCCCGACGAGGATGATTTGGCGCTCAATTTGGGGTCTAGAGAT 6060
Db 6001 CCGTTGGCTTCCACACCCCGACGAGGATGATTTGGCGCTCAATTTGGGGTCTAGAGAT 6060
Qy 6061 TTGGCAGTATGTGCAATTTCTTTGTGATTTGCTTTAATGTCCTTAAAGCTGGAGTTCA 6120
Db 6061 TTGGCAGTATGTGCAATTTCTTTGTGATTTGCTTTAATGTCCTTAAAGCTGGAGTTCA 6120

Qy 6121 GAGCATGGTTAAACATTTCTGTGTGTCTTTCTACAGCTGCCAGAGGGGTACAAGGGCCC 6180
Db 6121 GAGCATGGTTAAACATTTCTGTGTGTCTTTCTACAGCTGCCAGAGGGGTACAAGGGCCC 6180
Qy 6181 CTGATTTGGATCAGGTATGCTTCCAAAGCAGCGTGTCCATGCGGTGCTGAACATCTTTTC 6240
Db 6181 CTGATTTGGATCAGGTATGCTTCCAAAGCAGCGTGTCCATGCGGTGCTGAACATCTTTTC 6240
Qy 6241 TGTGAGAAATGGTTTTCGAAACCTTTTACAAAGGACCCAGAACTTGTTCAAAATTAAGTGA 6300
Db 6241 TGTGAGAAATGGTTTTCGAAACCTTTTACAAAGGACCCAGAACTTGTTCAAAATTAAGTGA 6300
Qy 6301 AGGGGCTGTTCAGTCAACGCTAGGCTGTGTGGGTGCGGTAGACCGGACCCCAACTGATTTG 6360
Db 6301 AGGGGCTGTTCAGTCAACGCTAGGCTGTGTGGGTGCGGTAGACCGGACCCCAACTGATTTG 6360
Qy 6361 GACTAGTCTTGTCTGCTCAATTAATGGGTTAGGGAATACTGTAAATATGAGAAATTTGGAGA 6420
Db 6361 GACTAGTCTTGTCTGCTCAATTAATGGGTTAGGGAATACTGTAAATATGAGAAATTTGGAGA 6420
Qy 6421 TCACATTTTGTGTTACGAGTATCCTCTCCTCAAAATGTCTGTTTCAACCGAGGTGCCCCCAAC 6480
Db 6421 TCACATTTTGTGTTACGAGTATCCTCTCCTCAAAATGTCTGTTTCAACCGAGGTGCCCCCAAC 6480
Qy 6481 CTTGAGAGCTCAGTGGCGGTGGAAGCGGTACAGGTTTCAAGTGTATCTAGGTGAGGCCCAA 6540
Db 6481 CTTGAGAGCTCAGTGGCGGTGGAAGCGGTACAGGTTTCAAGTGTATCTAGGTGAGGCCCAA 6540
Qy 6541 AACTCCTTGGACGACATCTGCTGTGTACGGTCTGACCGGTAAAGGGTAAACTGTTTAA 6600
Db 6541 AACTCCTTGGACGACATCTGCTGTGTACGGTCTGACCGGTAAAGGGTAAACTGTTTAA 6600
Qy 6601 GCTTCCCTTCCGCTTGAAGGTCACACCTGCTGCGCATGCAACTTAATTTTTCGCTGA 6660
Db 6601 GCTTCCCTTCCGCTTGAAGGTCACACCTGCTGCGCATGCAACTTAATTTTTCGCTGA 6660
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Db 6661 TGCACCTTGAGACAAATGACTGTAATTTCCACAAAACCACTCTAGTGTAGAGCCGCACT 6720
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Db 6901 AGGAGTGTCTGCTGCTGAAAGCTGCAACGAAGTGAACCGTTAGAGGTCTTCAAACT 6960
Qy 6961 CCCTCTTCAACACTGTTCTACAGTTGGCCATCGGATGCCCTGTTGGGAGCGGTGA 7020
Db 6961 CCCTCTTCAACACTGTTCTACAGTTGGCCATCGGATGCCCTGTTGGGAGCGGTGA 7020
Qy 7021 GTGTAAACCTTTTCACTGCAATTTGGATGTGCAATGACCGAAACAGCGGAGGCCCTGTATGA 7080
Db 7021 GTGTAAACCTTTTCACTGCAATTTGGATGTGCAATGACCGAAACAGCGGAGGCCCTGTATGA 7080
Qy 7081 TTTTACCCAGTTACCTTCCCAAAAAAGGAGGTCTCTGAATGGTCAAGAAAGTTGTCAGAC 7140
Db 7081 TTTTACCCAGTTACCTTCCCAAAAAAGGAGGTCTCTGAATGGTCAAGAAAGTTGTCAGAC 7140
Qy 7141 GGCTACAAACCGCTTCCAGCTACGTTACTTGGCCCCCGGTACCTTAAGATACGGGGAAGGA 7200
Db 7141 GGCTACAAACCGCTTCCAGCTACGTTACTTGGCCCCCGGTACCTTAAGATACGGGGAAGGA 7200

Qy	7201	TTCCACTCAGTCAAGCCCGCCGCAAAACGGCCCTTACAAAAAGAGATTGGGAAAGAGTGAAGTT	7260
Db	7201	TTCCACTCAGTCAAGCCCGCCGCCAAACGGCCCTTACAAAAAGAGATTGGGAAAGAGTGAAGTT	7260
Qy	7261	TTCTGTGAGCAGTGAAGTACACTCTGGACCGACGTCATTAGCTTCAAAACTGCTCTTAAAGT	7320
Db	7261	TTCTGTGAGCAGTGAAGTACACTTGGACCGACGTCATTAGCTTCAAAACTGCTCTTAAAGT	7320
Qy	7321	TCTGTCTGCAACTCGGGCCATCACTAGTGGTTCCTCAAAACAAAGATCATTTGGTGTAATGT	7380
Db	7321	TCTGTCTGCAACTCGGGCCATCACTAGTGGTTCCTCAAAACAAAGATCATTTGGTGTAATGT	7380
Qy	7381	GACTGAGCGCGGATCGGAGCTTTAGAAAACAAAAAGTCACTATTAAATAGACAAACCTCT	7440
Db	7381	GACTGAGCGCGGATCGGAGCTTTAGAAAACAAAAAGTCACTATTAAATAGACAAACCTCT	7440
Qy	7441	GTTCCTCCCTCATATACACACAGCAAGTGAATTCGGCTTAAGGMAAAGCTTCAAAAGTTGT	7500
Db	7441	GTTCCTCCCTCATATACACACAGCAAGTGAATTCGGCTTAAGGMAAAGCTTCAAAAGTTGT	7500
Qy	7501	CGGTGTCTATGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTAAGTCTGCTAAAGTC	7560
Db	7501	CGGTGTCTATGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTAAGTCTGCTAAAGTC	7560
Qy	7561	CCACATCACTGGCCCTTCGGGCGCACTGATGTTCGTCTCGAGCAGCCCGCAAGGCTGTCT	7620
Db	7561	CCACATCACTGGCCCTTCGGGCGCACTGATGTTCGTCTCGAGCAGCCCGCAAGGCTGTCT	7620
Qy	7621	GGACTTCGAGAGTGTGTGCGAGGACGCTGAGATACCGAGTCACTTATCGGCAAACTGTGAT	7680
Db	7621	GGACTTCGAGAGTGTGTGCGAGGACGCTGAGATACCGAGTCACTTATCGGCAAACTGTGAT	7680
Qy	7681	AGTTCCAAAGGAGGAGGTCTTTCGTGAAGACCCCCAGAAAACCAACAAAGAAACCCCCCAAG	7740
Db	7681	AGTTCCAAAGGAGGAGGTCTTTCGTGAAGACCCCCAGAAAACCAACAAAGAAACCCCCCAAG	7740
Qy	7741	GCTTATCTCGTACCCCACTTGAATGAGATGTGTTGAGAGATGTACTACGGTCAAGT	7800
Db	7741	GCTTATCTCGTACCCCACTTGAATGAGATGTGTTGAGAGATGTACTACGGTCAAGT	7800
Qy	7801	TGCTCCTGACGTAGTTAAAGCTGTCACTGGAGATGCGTACGGGTTTCTAGATCCACGTCAC	7860
Db	7801	TGCTCCTGACGTAGTTAAAGCTGTCACTGGAGATGCGGTAACGGGTTTCTGCAACCAAGTAC	7860
Qy	7861	CCGTGTCAAGCGTCTGTGTTCGATGTGGTCAACCCGATGCGAGTCCGAGCCACATCGGATAC	7920
Db	7861	CCGTGTCAAGCGTCTGTGTTCGATGTGGTCAACCCGATGCGAGTCCGAGCCACATCGGATAC	7920
Qy	7921	AGTGTGTTTGAAGTACCATCAACACCGAGGATATCATGGTGGAGACAGACATCTACTC	7980
Db	7921	AGTGTGTTTGAAGTACCATCAACACCGAGGATATCATGGTGGAGACAGACATCTACTC	7980
Qy	7981	AGCAGCTTAACTCAGTACCAACACCGAGTGGCATTCACACCAATTCGGAGGCGAGTTATA	8040
Db	7981	AGCAGCTTAACTCAGTACCAACACCGAGTGGCATTCACACCAATTCGGAGGCGAGTTATA	8040
Qy	8041	CGCTGGAGGACCGATGATCGCTTATGATGGCCGAGAGATCGGATATCGTAGGTCTAGGTC	8100
Db	8041	CGCTGGAGGACCGATGATCGCTTATGATGGCCGAGAGATCGGATATCGTAGGTCTAGGTC	8100
Qy	8101	TTCCGGCTCTTATACTACCTCAAGTTTCCAAAGTTCGCTTCCTTATTTGCGCGCATGATTCGAC	8160
Db	8101	TTCCGGCTCTTATACTACCTCAAGTTTCCAAAGTTCGCTTCGCTTCGCTGAGGTTAAATGC	8160
Qy	8161	TGCAGCCGACAGGCTGGCATGAAGAACCCTCGCTTCCTTATTTGCGCGCATGATTCGAC	8220
Db	8161	TGCAGCCGACAGGCTGGCATGAAGAACCCTCGCTTCCTTATTTGCGCGCATGATTCGAC	8220
Qy	8221	CGTAATTTGGAAGACGCGCGGACAGATGACAGACAAACAAAGCAATGCGTGTCTTTGCTAG	8280
Db	8221	CGTAATTTGGAAGACGCGCGGACAGATGACAGACAAACAAAGCAATGCGTGTCTTTGCTAG	8280
Qy	8281	CTGGATGAAGGTGTATGGGTGCACACCAAGATTTGTGTCCTCAACCCCAAAATACAGTTTGGTA	8340

Db	8281	CTGGATGAAGGTTGATGGGTGCACCAAGATTGTGTGCCTCAACCCAAATACAGTTTGGG	8340
Qy	8341	AGAAATTAACATCATGCTCATCAAAATGTTACTCTCTGGAATTAACAAAGTGGCAAGCCTTA	8400
Db	8341	AGAATTAACATCATGCTCATCAAAATGTTACTCTGGAATTAACCAAAAGTGGCAAGCCTTA	8400
Qy	8401	CTACTTTCTTACAAGAGATCCTCGTATCCCTTTGGCAGGTGCTGTGCCAGAGGTCTGGG	8460
Db	8401	CTACTTTCTTACAAGAGATCCTCGTATCCCTTTGGCAGGTGCTGTGCCAGAGGTCTGGG	8460
Qy	8461	ATACAACCCAGTGTCTGGTGAATCGGTATCTAAATACATCACTACCACATGTTTGTGGGT	8520
Db	8461	ATACAACCCAGTGTCTGGTGAATCGGTATCTAAATACATCACTACCACATGTTTGTGGGT	8520
Qy	8521	TAGCCGTGTGTGGCTGTCTCATTTTCATGGAGCAGATGCTCTTTTGAGGACAAACTTCCCGA	8580
Db	8521	TAGCCGTGTGTGGCTGTCTCATTTTCATGGAGCAGATGCTCTTTTGAGGACAAACTTCCCGA	8580
Qy	8581	GACTGTGACCTTTTGACTGTATGGGAAAAATATATACGGTGCCCTGTAGAAGATCTGCCCGAG	8640
Db	8581	GACTGTGACCTTTTGACTGTATGGGAAAAATATACGGTGCCCTGTAGAAGATCTGCCCGAG	8640
Qy	8641	CATCATTTGCTGTGTGCACCGTATGAGGCTTTCTCGGTGGTGCGCTTACACCAACGCTGA	8700
Db	8641	CATCATTTGCTGTGTGCACCGTATGAGGCTTTCTCGGTGGTGCGCTTACACCAACGCTGA	8700
Qy	8701	GATCCTCAGAGTTTCCCAATCACTAAACAGACATGACCATGCCCCCTCGGAGCCTGGCG	8760
Db	8701	GATCCTCAGAGTTTCCCAATCACTAAACAGACATGACCATGCCCCCTCGGAGCCTGGCG	8760
Qy	8761	AAAGAAAGCAGGGCGGTCTCGCCAGCGCAAGAGCGGTGGCGGAGCAACCGCAAAATT	8820
Db	8761	AAAGAAAGCAGGGCGGTCTCGCCAGCGCAAGAGCGGTGGCGGAGCAACCGCAAAATT	8820
Qy	8821	GGCTCGCTCTCTCTCGGCACTGCTACATCTAGACCTTACACAGATTGTGATAAGACGAG	8880
Db	8821	GGCTCGCTCTCTCTCGGCACTGCTACATCTAGACCTTACACAGATTGTGATAAGACGAG	8880
Qy	8881	CGTGGCTCGGTACACCACTTTCAATTATTGTGATGTTTACTCCCGGAGGGGATGTGTT	8940
Db	8881	CGTGGCTCGGTACACCACTTTCAATTATTGTGATGTTTACTCCCGGAGGGGATGTGTT	8940
Qy	8941	TATTACACACAGAGAGATTGACAGAGTTCCTTGTGAGATTTTGGCTGTCTATTGTTTT	9000
Db	8941	TGTTTACACACAGAGAGATTGACAGAGTTCCTTGTGAGATTTTGGCTGTCTATTGTTTT	9000
Qy	9001	TGCCCTAGGGCTCATTTGCTGTGGATTAGCCATCAGCTGAACCCCAAAATTCAAAATTAA	9060
Db	9001	TGCCCTAGGGCTCATTTGCTGTGGATTAGCCATCAGCTGAACCCCAAAATTCAAAATTAA	9060
Qy	9061	CTAACAG-----TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGGGCAGCGGCAACGAGGAGACCCC	9116
Db	9061	TTAACAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGGGCAGCGGCAACGAGGAGACCCC	9120
Qy	9117	GGGCTTAACGACCCCGC 9133	
Db	9121	GGGCTTAACGACCCCGC 9137	

RESULT 8
US-08-424-550B-390
; Sequence 390, Application us/08424550B
; Patent No. 6720166
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATTIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER

APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESS: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 390:
SEQUENCE CHARACTERISTICS:
LENGTH: 9143 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-424-550B-390

Query Match 96.4%; Score 9059.8; DB 4; Length 9143;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 9096; Conservative 0; Mismatches 37; Indels 4; Gaps 1;
QY 1 ACCACAAACATCCAGTTTGTATACACTCCGCTAGAGAAATGCTCTCGAGACACCCCCCTAG 60
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DB 61 CAGGCGTGGGGATTTCCCTGCCGCTCGAGAGGGTGGAGCCACCCCTTAGTAT 120
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DB 121 GTAGCGCGGGACTCATGACGCTCGCGTGATGACAAGCGCCAAAGCTTGACTTGGATGGC 180
QY 181 CCTGATGGCGTTATGAGTTTCGTTGCGTGGCGCTTTAGGACGCTCCACGCCACCA 240
DB 181 CCTGATGGCGTTATGAGTTTCGTTGCGTGGCGCTTTAGGACGCTCCACGCCACCA 240
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DB 361 TGGGATGTTGGGTTAGCCATCCATACCGTACTGCTGATAGAGTCTTTCGAGGGGAT 420
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QY 481 TCGCCCCAGAACGCGCAAGAACAAAGCAGACGACGCTTCAATCCTGTGTCCATTAATAAC 540
DB 481 TCGCCCCAGAACGCGCAAGAACAAAGCAGACGACGCTTCAATCCTGTGTCCATTAATAAC 540
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DB 541 ATCTGTTGAAAGGGGACAAAGAGCAAGCGAAAGTCCAGCGCATGCTCGGCCCTCGTAA 600
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QY 661 TCATGTTGGGAGCCCAAGACCTCGCCATAAAGTCTCGCAATCTTGGAAATCCTTCTGGA 720
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QY 721 TTACCTTTGGGGTGGATTTGGTATGTTTAACTCAGACCTCTAGTAGGCGCGCTGCT 780
DB 721 TTACCTTTGGGGTGGATTTGGTATGTTTAACTCAGACCTCTAGTAGGCGCGCTGCT 780
QY 781 GGCAGGAGCGTCTGTTGACCAAGTCTGCCAGATAGTACGCTTGTGGAGGATGAGTCAA 840
DB 781 GGCAGGAGCGTCTGTTGACCAAGTCTGCCAGATAGTACGCTTGTGGAGGATGAGTCAA 840
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DB 841 CTGGGCTACTGCTGTTGGTTCGCTGCCACCTTTTGTGGTATGCTGCTATCTTTGGCCTG 900
QY 901 TCCCTGTAGTGGGCGGGTCACTGACCCAGACAAATACCAATCCTTGACCAATG 960
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QY 961 CTGCAGCGTAATCAGGTTATCTATTGTTCTCTTCCACTTGCCTACAGAGCCTGTTG 1020
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QY 1261 AGTGCCCACTGGAATAGATCTCTGGGTTCTAGGTTTATCGGGTGGATGGCGGCAAGGT 1320
DB 1261 AGTGCCCACTGGAATAGATCTCTGGGTTCTAGGTTTATCGGGTGGATGGCGGCAAGGT 1320
QY 1321 CGAGGCTGCTCATCTTTGACCAAACTGGCTTCAAGTACCATCGCTATTGGCACTAT 1380
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QY 1501 CAGGCTGCCACTGGATGCTCAATAGCTGAGTGTGCTCGCTTTGATGATACCATGTC 1560
DB 1501 CAGGCTGCCACTGGATGCTCAATAGCTGAGTGTGCTCGCTTTGATGATACCATGTC 1560
QY 1561 TTGCCACTCTTTATTGAGTGAGAAATGTGTCAAGAGTCAATTTGTTTACAGTCCAAAGTGGAC 1620

Db 1561 |||||TTGCCACTCTTATTTAGAGTGAGAAATGTTGCAGAAAGTCATTTGTTACAGTCCANAAGTGAC 1620
Qy 1621 CAGGCTTACTCTAGAGTATAACAACCTCCATATCTTGGTACCCCTATACAAATCCCTGG 1680
Db 1622 CAGGCTGTCTACTAGAGTATACAACTCCATCTATCTGGTACCCCTATACAAATCCCTGG 1680
Qy 1681 TGCAGGGGATGTATGTTAAATCAAAAAATAACAATGAGGTTGTCGCCGTATTCGCAA 1740
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Qy 1741 TGTGCCATCGTACTGCACTATGGCACTGATGCGAGTGGGAACGACACTCGCAACACTTA 1800
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Qy 1861 ATTGGCTATATACAAATACCTCGGTCTAAAGAAATGTTTAAACCTCATAAATGGATGTC 1920
Db 1862 ATTGGCTATATACAAATACCTCGGTCTAAAGAAATGTTTAAACCTCATAAATGGATGTC 1920
Qy 1921 AGGCCATTTGATTTTGAAGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAA 1980
Db 1922 AGGCCATTTGATTTTGAAGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAA 1980
Qy 1981 TTCCACTCTCTACCAACGAGAGTGGCTGAGTTGCCGTACCCCTACCCCACTGTGGTACG 2040
Db 1982 TTCCACTCTCTACCAACGAGAGTGGCTGAGTTGCCGTACCCCTACCCCACTGTGGTACG 2040
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Qy 2101 ATTGATCAACCAAGACCTTGGAATAATATCAGTCTTATATTCGCGCAACGGTGC 2160
Db 2102 ATTGATCAACCAAGACCTTGGAATAATATCAGTCTTATATTCGCGCAACGGTGC 2160
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Db 2162 TTTGTCTCTACGGGAGTTACCAACAGCGGTGGTGAATCTGTTGGGGTTGTGG 2220
Qy 2221 CAGCAAGTATCTATTTTACGCTACCTCTGTACTGTGTCCTTTGTTGGCGCGCTTC 2280
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Qy 2341 TTTGTCTAAAGCTCAAGTAGCTCTTTTGTGCTTGAATTTTCTCATCTGTTCTATCTCCG 2400
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Qy 2401 CTGAGGCTACGTTATGCTGCCCTTTTAAAGGTTTGTGCCCATGGCTGGGGCTTGCCCTC 2460
Db 2402 CTGAGGCTACGTTATGCTGCCCTTTTAAAGGTTTGTGCCCATGGCTGGGGCTTGCCCTC 2460
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Db 2462 AACTTTCTTTTGTGAGCAGCTGTGTCGCCCAACCAAGATTATGATGGTGGGTGCGACTGCT 2520
Qy 2521 AGTGCAGGGTTAGTTTGTGGCGCGCGGTAAACCGTGGTCAACGATAGCTCTGCTTGT 2580
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DB 3421 GTATACCTCTACCATGGCAGCAAGGGGCGCGGTTGGCTCATCCCAAGGCTCTATACA 3480

QY 3481 CCCAATAACCGTTGACCGGGCTAATGACACGAGCATCTATCAACACCATGTTGAGCTGG 3540
DB 3481 CCCAATAACCGTTGACCGGGCTAATGACACGAGCATCTATCAACACCATGTTGAGCTGG 3540
QY 3541 GTCCCTTACTCGGTGCTCTTGGCGGGAGACCAAGGGGTATCTGTAAACGACTGGGGTC 3600
DB 3541 GTCCCTTACTCGGTGCTCTTGGCGGGAGACCAAGGGGTATCTGTAAACGACTGGGGTC 3600
QY 3601 ATTGTTGAGGTCAACAAATCCGATGACCCCTTATTGTTGTTGTTGCGGGGCCCTTCCCAT 3660
DB 3601 ATTGTTGAGGTCAACAAATCCGATGACCCCTTATTGTTGTTGTTGCGGGGCCCTTCCCAT 3660
QY 3661 GSCCTTTGCCAAGGGTTCTTCAGGTGCCCGAATCTGTGTCTCTCGGGCAATGTTATGG 3720
DB 3661 GSCCTTTGCCAAGGGTTCTTCAGGTGCCCGAATCTGTGTCTCTCGGGCAATGTTATGG 3720
QY 3721 GATGTTCAACCGCTCTAGAAATTTCTGGGGTTTCACTGAGTCAGATCAGATTAGGGTTAGCCGTT 3780
DB 3721 GATGTTCAACCGCTCTAGAAATTTCTGGGGTTTCACTGAGTCAGATCAGATTAGGGTTAGCCGTT 3780
QY 3781 GGTGTGCTGATACCATCCCGAGTACACAGCACATGCCACTCTTGATACAAAACCTTAC 3840
DB 3781 GGTGTGCTGATACCATCCCGAGTACACAGCACATGCCACTCTTGATACAAAACCTTAC 3840
QY 3841 TGTGCTAAACGAGTATTCAGTGCATAATTTTAAATGCCCCACTGTGCAGCGCAAGTCAAC 3900
DB 3841 TGTGCTAAACGAGTATTCAGTGCATAATTTTAAATGCCCCACTGTGCAGCGCAAGTCAAC 3900
QY 3901 CAAATTACCACTTTCTTACATGACGAGGAAGTATGAGTCTTGGTCTTAAATCCAGTGT 3960
DB 3901 CAAATTACCACTTTCTTACATGACGAGGAAGTATGAGTCTTGGTCTTAAATCCAGTGT 3960
QY 3961 GGTACAAACAGCATCAATGCCCCAAAGTATCATGACGCGAGTACGCGGTGAATCCAAATG 4020
DB 3961 GGTACAAACAGCATCAATGCCCCAAAGTATCATGACGCGAGTACGCGGTGAATCCAAATG 4020
QY 4021 CTATTTTAAATGGCAAAATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT 4080
DB 4021 CTATTTTAAATGGCAAAATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT 4080
QY 4081 GTACTGACCGGAGATGTTCCCGAACTATGATGTAATCATTTTGTGACGAATGCCATGC 4140
DB 4081 GTACTGACCGGAGATGTTCCCGAACTATGATGTAATCATTTTGTGACGAATGCCATGC 4140
QY 4141 TACCGATCAACACCGTGTGGGCTTGGAAAGTCTTAAACCGAAGTCTTCAATCCAAAA 4200
DB 4141 TACCGATCAACACCGTGTGGGCTTGGAAAGTCTTAAACCGAAGTCTTCAATCCAAAA 4200
QY 4201 TGTAGGCTAGTGGTTCTTGCACGGCTACCCCGCTGGAGTAAATCCCTACACCATGC 4260
DB 4201 TGTAGGCTAGTGGTTCTTGCACGGCTACCCCGCTGGAGTAAATCCCTACACCATGC 4260
QY 4261 CAAATTAATGAGATTCAATTAACCGATGAAGGCACTATCCCTTTTCAATGNAAGAAAT 4320
DB 4261 CAAATTAATGAGATTCAATTAACCGATGAAGGCACTATCCCTTTTCAATGNAAGAAAT 4320
QY 4321 TAAGGAGAAATCTGAAGAAAGGAGACACTTATCTTTGAGGCTACCAAAAAACACTG 4380
DB 4321 TAAGGAGAAATCTGAAGAAAGGAGACACTTATCTTTGAGGCTACCAAAAAACACTG 4380
QY 4381 TGATGAGCTTGTCTAAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGG 4440
DB 4381 TGATGAGCTTGTCTAAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGG 4440
QY 4441 ATGTGACATCTCAAAAAATCCCTGAGGGGACATGTGTAGTAGTGGCACTGATGCCCTTGT 4500
DB 4441 ATGTGACATCTCAAAAAATCCCTGAGGGGACATGTGTAGTAGTGGCACTGATGCCCTTGT 4500
QY 4501 TACAGGGTACACTGGTGACTTTGATTCGCTGTATGACTGACGCTCATGTGTAAGAGGCAC 4560
DB 4501 TACAGGGTACACTGGTGACTTTGATTCGCTGTATGACTGACGCTCATGTGTAAGAGGCAC 4560
QY 4561 ATGCCATGTTGACCTTGACCTTACTTTTCCATCCATGGGTGTTGTTGTTGCGGGGTTTCAGC 4620

Db	4561		ATGCCATGTTGACCTTGACCTTACTTTTCCACATGGGTGTTGTTGTTGCGGGTCTCAGC	4620
Qy	4621		AATAGTTTAAAGCCAGCGTATGGGCGCCACAGGCGGTGGAGAGCTGGCATATATACTACTA	4680
Db	4621		AATAGTTTAAAGCCAGCGTATGGGCGCCACAGGCGGTGGAGAGCTGGCATATATACTACTA	4680
Qy	4681		TGTAGA CCGGAGTTGTATCCCTTCGGGTATGTTTCTGTAATGCAACATTTGTGAAGCCTT	4740
Db	4681		TGTAGA CCGGAGTTGTATCCCTTCGGGTATGTTTCTGTAATGCAACATTTGTGAAGCCTT	4740
Qy	4741		CGAGCAGCCCAAGCATGTTATGTTTGTCTATCAACAGAGCTCAAACTATTCTGGACAC	4800
Db	4741		CGAGCAGCCCAAGCATGTTATGTTTGTCTATCAACAGAGCTCAAACTATTCTGGACAC	4800
Qy	4801		CTATCGCAACCCAACTCTGGTTTACCTGGGATAGAGAGCAAAATTTGACAGTGGGCTGATCT	4860
Db	4801		CTATCGCAACCCAACTCTGGTTTACCTGGGATAGAGAGCAAAATTTGACAGTGGGCTGATCT	4860
Qy	4861		CTTTTCTATGTTCAACCCGAACTTCAATTTGTCAATACTGCAAAAAGAACTGCTGACAA	4920
Db	4861		CTTTTCTATGTTCAACCCGAACTTCAATTTGTCAATACTGCAAAAAGAACTGCTGACAA	4920
Qy	4921		TTATGTTTGTGTTGACTGAGCCCAACTACAACTGTGTCTATCAGTATGGCTATGCTGCTCC	4980
Db	4921		TTATGTTTGTGTTGACTGAGCCCAACTACAACTGTGTCTATCAGTATGGCTATGCTGCTCC	4980
Qy	4981		CAATGACGACACCGGTGGAGGAGCCCGCTTGGGAAATAAATTTGTGGGGTCTGTGTG	5040
Db	4981		CAATGACGACACCGGTGGAGGAGCCCGCTTGGGAAATAAATTTGTGGGGTCTGTGTG	5040
Qy	5041		CGCCTTGGACGGCGCTCAGCGCTCTGCTGGCCAGAGCCCAAGAGGTGACAGATACCA	5100
Db	5041		CGCCTTGGACGGCGCTCAGCGCTCTGCTGGCCAGAGCCCAAGAGGTGACAGATACCA	5100
Qy	5101		AATGTGCTTCACTGAAGTCAATCTTCTGGAGAGCCGCACTCGCTGTGGCGTTGGAGT	5160
Db	5101		AATGTGCTTCACTGAAGTCAATCTTCTGGAGAGCCGCACTCGCTGTGGCGTTGGAGT	5160
Qy	5161		GGCTATGGCTTATCTAGCCATTGACACTTTTGGGCGCACTTGTGGCGGTCTGCTGTC	5220
Db	5161		GGCTATGGCTTATCTAGCCATTGACACTTTTGGGCGCACTTGTGGCGGTCTGCTGTC	5220
Qy	5221		TATTTACATCAGTCCCTACCGGTGCTACTGTGCCCCAGTGGTTGACGAAGAAGAAATCGT	5280
Db	5221		TATTTACATCAGTCCCTACCGGTGCTACTGTGCCCCAGTGGTTGACGAAGAAGAAATCGT	5280
Qy	5281		GGAGGAGTGCATCATTTCCCTTGGAGGCCATGGTTGCTGCAATTCGATAAGCTGAA	5340
Db	5281		GGAGGAGTGCATCATTTCCCTTGGAGGCCATGGTTGCTGCAATTCGATAAGCTGAA	5340
Qy	5341		GAGTACAATCACCAACTAGTCTTTTACCAATTTGAAACCGCCCTTGAAATAACTTTAACAC	5400
Db	5341		GAGTACAATTAACCAACTAGTCTTTTACCAATTTGAAACCGCCCTTGAAATAACTTTAACAC	5400
Qy	5401		CTTTCTTTGGGCTCATGAGCTCAAACTCTTGTCTATCATAGAGTATTGCTGTGTTTGT	5460
Db	5401		CTTTCTTTGGGCTCATGAGCTCAAACTCTTGTCTATCATAGAGTATTGCTGTGTTTGT	5460
Qy	5461		CACTTTACCTGACAACTCCCTTGGATCATGCGGTGTTGCTTTTCAATGGGGGTATTACTAC	5520
Db	5461		CACTTTACCTGACAACTCCCTTGGATCATGCGGTGTTGCTTTTCAATGGGGGTATTACTAC	5520
Qy	5521		CCCACTACCTCACAAGATCAAAATGTTCTGTCATTTTGGAGGCGCAATTTGGCTCCAA	5580
Db	5521		CCCACTACCTCACAAGATCAAAATGTTCTGTCATTTTGGAGGCGCAATTTGGCTCCAA	5580
Qy	5581		GCTTTACAGACGCTAGAGCGCACTGGGTTTCAATGATGGCGGGGCTGGGAAACAGCTCT	5640
Db	5581		GCTTTACAGACGCTAGAGCGCACTGGGTTTCAATGATGGCGGGGCTGGGAAACAGCTCT	5640
Qy	5641		TGGTACATGGACATCGGTGGGTTTGTCTTTTGA CATGCTAGGCGGCTATGCTGCGGCTC	5700
Db	5641		TGGTACATGGACATCGGTGGGTTTGTCTTTTGA CATGCTAGGCGGCTATGCTGCGGCTC	5700

Db	5641		TGGTACATGGACATCGGTGGGTTTGTCTTTTGACATGCTAGGCGGCTATGCTGCGGCTC	5700
Qy	5701		ATCCACTGCTTGTCTTGACATTTAAATGCTTGAATGGGTGAGTGGCCCACTATGGATCAGCT	5760
Db	5701		ATCCACTGCTTGTCTTGACATTTAAATGCTTGAATGGGTGAGTGGCCCACTATGGATCAGCT	5760
Qy	5761		TGCTGGTTTATGTTCTATCCCGGTTCAATCCGGCGCAGGAGTTGTGGGCGTCTTGTGACG	5820
Db	5761		TGCTGGTTTATGTTCTATCCCGGTTCAATCCGGCGCAGGAGTTGTGGGCGTCTTGTGACG	5820
Qy	5821		TTGTGCAATGTTTGTCTTGTGACACAGCAGGCGCAGATCACTGGGCCCAACAGACTTCTTAC	5880
Db	5821		TTGTGCAATGTTTGTCTTGTGACACAGCAGGCGCAGATCACTGGGCCCAACAGACTTCTTAC	5880
Qy	5881		TATGCTTGTCTAGGAGCAACACTGTGTATGTAATGAGTACTTTTATTTGCCACTCGTGACATCCG	5940
Db	5881		TATGCTTGTCTAGGAGCAACACTGTGTATGTAATGAGTACTTTTATTTGCCACTCGTGACATCCG	5940
Qy	5941		CAGGAGATACTGGGCATTTCTGGAGGCATCTACCCCTGGAGTGTCTATATCAGCTTGCAT	6000
Db	5941		CAGGAGATACTGGGCATTTCTGGAGGCATCTACCCCTGGAGTGTCTATATCAGCTTGCAT	6000
Qy	6001		CCGTTGGCTCCACACCCCGACGGAGGATGATTCGGGCTCATTTGCTTTGGGCTCTAGAGAT	6060
Db	6001		CCGTTGGCTCCACACCCCGACGGAGGATGATTCGGGCTCATTTGCTTTGGGCTCTAGAGAT	6060
Qy	6061		TTGGCAGTATGTGCAAAATTTCTTTGTGATTTTGTCTTTAATGCTCTTAAAGCTGGAGTTCA	6120
Db	6061		TTGGCAGTATGTGCAAAATTTCTTTGTGATTTTGTGATTTGCTTTAATGCTCTTAAAGCTGGAGTTCA	6120
Qy	6121		GAGCATGGTTAAACATTTCTGCTTGTCTTCTACAGCTGCCAGAGGGGTACAAGGGGCC	6180
Db	6121		GAGCATGGTTAAACATTTCTGCTTGTCTTCTACAGCTGCCAGAGGGGTACAAGGGGCC	6180
Qy	6181		CTGATTTGGATCAGTATGCTTCCAAAGCACGCTGTCCATGGGTGCTGCAACTCATCTTTTC	6240
Db	6181		CTGATTTGGATCAGTATGCTTCCAAAGCACGCTGTCCATGGGTGCTGCAACTCATCTTTTC	6240
Qy	6241		TGTTGAGATGGTTTGTGCAAAATTTTACAAGGACCCAGAACTTTGTTCAAAATTAAGTGGAG	6300
Db	6241		TGTTGAGATGGTTTGTGCAAAATTTTACAAGGACCCAGAACTTTGTTCAAAATTAAGTGGAG	6300
Qy	6301		AGGGCTGTTTCCAGTCAACGCTAGGCTGTGTGGGTGCGCTAGACCGGACCCCACTGATTG	6360
Db	6301		AGGGCTGTTTCCAGTCAACGCTAGGCTGTGTGGGTGCGCTAGACCGGACCCCACTGATTG	6360
Qy	6361		GACTAGTCTTGTGTCATTTATGCGTTTGGGACTACTGTAAATATGAGAAATGGGAGA	6420
Db	6361		GACTAGTCTTGTGTCATTTATGCGTTTGGGACTACTGTAAATATGAGAAATGGGAGA	6420
Qy	6421		TCACATTTTGTGTACAGCAGTATCTCTCCAAATGTCTGTTTTCACCCAGGTGCCCCCAAC	6480
Db	6421		TCACATTTTGTGTACAGCAGTATCTCTCCAAATGTCTGTTTTCACCCAGGTGCCCCCAAC	6480
Qy	6481		CTTGAGAGCTGCAAGTGGCGGTGAGCGGCTACAGGTTTCAAGTTTATCTAGGTGAGCCCAA	6540
Db	6481		CTTGAGAGCTGCAAGTGGCGGTGAGCGGCTACAGGTTTCAAGTTTATCTAGGTGAGCCCAA	6540
Qy	6541		AACCTCTTGGACGACATCTGCTTGTGTTACGGTCTCTGACGGTAAGGGTAAACTGTTAA	6600
Db	6541		AACCTCTTGGACGACATCTGCTTGTGTTACGGTCTCTGACGGTAAGGGTAAACTGTTAA	6600
Qy	6601		GCTTCCCTTCCGGGTTGACCGGTACACACCTGTTGTGCGCATGCAACTTAAATTTGCGTGA	6660
Db	6601		GCTTCCCTTCCGGGTTGACCGGTACACACCTGTTGTGCGCATGCAACTTAAATTTGCGTGA	6660
Qy	6661		TGCACTTTGAGCAAAATGACTGTATTTCCACAAACACACTCTCTAGTGTATGAGCGCGAGT	6720
Db	6661		TGCACTTTGAGCAAAATGACTGTATTTCCATAAACAACACTCTCTAGTGTATGAGCGCGAGT	6720
Qy	6721		GTCCGCTCTTGTCTTCAACAGGAGTTTGGCGGTACAAACCAATTTGCTTGGGCAATTTTC	6780
Db	6721		GTCCGCTCTTGTCTTCAACAGGAGTTTGGCGGTACAAACCAATTTGCTTGGGCAATTTTC	6780

Db 1091 AGATCCTGGGTTCTTAGGGTTTATCGGGTGAATGCCGGAAGGTGCGAGGCTGTATCATCTT 1150
QY 1336 CTTGACCAAACTGGCTTACAAAGTACCATAAGCTATTGGGACTATGTTTAGCAGTGTACA 1395
Db 1151 CTTGACCAAACTGGCTTACAAAGTACCATAAGCTATTGGGACTATGTTTAGCAGTGTACA 1210
QY 1396 CTACCTGGCGGTGGCGCTCTGATCTACTATAGCCCTCGGGCAAGTGGTATCAGTTGCT 1455
Db 1211 CTAAGTGGCGGTGGCGCTCTGATCTACTATAGCCCTCTGGGGCAAGTGGTATCAGTTGCT 1270
QY 1456 CCTAGCGCTTATGCTTTACATAGAAAGCAGCCTCTGGAACCCCAATCAGGGGTGCCACTGG 1515
Db 1271 CCTAGCGCTTATGCTTTACATAGAAAGCAGCCTCTGGAACCCCAATCAGGGGTGCCACTGG 1330
QY 1516 ATGCTCAATAGCTGAGTTTGGCTCGCCTTGGATGATACGATGCTCTGGCACTCTTATTT 1575
Db 1331 ATGCTCAATAGCTGAGTTTGGCTCGCCTTGGATGATACGATGCTCTGGCACTCTTATTT 1390
QY 1576 GAGTGAGAAATGTCAGAAAGTCAATTTGTACAGTCCAAAGTGGACAGGCCCTATCACCTCT 1635
Db 1391 GAGTGAGAAATGTCAGAAAGTCAATTTGTACAGTCCAAAGTGGACAGGCCCTGTCACCTCT 1450
QY 1636 AGAGTATAACAACTCCATATCTTGGTACCCCTPATACAATCCCTGGTGGAGGGGATGTAT 1695
Db 1451 AGAGTATAABAACTCCATATCTTGGTACCCCTPATACAATCCCTGGTGGAGGGGATGTAT 1510
QY 1696 GGTAAATTCAAAAATAACACATGAGGTTGCTGCGCG - WMTGCGCAATGTGCCATCGTACTG 1755
Db 1511 GGTAAATTCAAAAATAACACATGAGGTTGCTGCGCG - WMTGCGCAATGTGCCATCGTACTG 1569
QY 1756 CACTATGGGCACTGATGAGTGTGAAGCAGCACTCGCAACACTTACGAAGCATGGGTGT 1815
Db 1570 CACTATGGGCACTGATGAGTGTGAAGSACAGTCCGAACACTTACGAAGCATGGGTGT 1629
QY 1816 AACACCATGGCTAACCAACCGCATGCGACAGCACTCGCAACACTTACGAAGCATGGGTGT 1875
Db 1630 AACACCATGGCTAACCAACCGCATGCGACAGCACTCGCAACACTTACGAAGCATGGGTGT 1689
QY 1876 ATACCTGGGCTAAAGAAATGTTTAAACCTCATAAATGGATGTCAGGGCATTTGTATTT 1935
Db 1690 ATACCTGGGCTAAAGAAATGTTTAAACCTCATAAATGGATGTCAGGGCATTTGTATTT 1749
QY 1936 TGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAATCCACCTCTCCTACC 1995
Db 1750 TGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAATCCACCTCTCCTACC 1809
QY 1996 ACCGAGAGGTGGGTAGGTTGCCCGGTACCCACCTGTGTPACGTGGTTCCTTGGTTACA 2055
Db 1810 ACCGAGAGGTGGGTAGGTTGCCCGGTACCCACCTGTGTPACGTGGTTCCTTGGTTACA 1869
QY 2056 GGTTCGCAAGGGTTTACAGTGTATGTAAGACCTTAGCCACAGGATGATCACCAGAA 2115
Db 1870 GGTTCGCAAGGGTTTACAGTGTATGTAAGACCTTAGCCACAGGATGATCACCAGAA 1928
QY 2116 CAAGCCCTGGAATAATATCAGTCTTATATTCGCCACGGGTGCTTTGCTCTTACCGG 2175
Db 1929 CAAGCCCTGGAATAATATCAGTCTTATATTCGCCACGGGTGCTTTGCTCTTACCGG 1989
QY 2176 AGTTACCAAGGCGGTGGTGTAAATCTGTGTGGGTGTGTGGCAGCAAGTATCTTTAT 2235
Db 1989 AGTTACCAAGGCGGTGGTGTAAATCTGTGTGGGTGTGTGGCAGCAAGTATCTTTAT 2048
QY 2236 TTTAGCCTACCTGTATTACTGTCTTGTGGGCGCGCTTCTGGTACCCCTTTGGG 2295
Db 2049 TTTAGCCTACCTGTATTACTGTCTTGTGGGCGCGCTTCTGGTACCMCTTTGGG 2108
QY 2296 TCCTGTGCTCCCATCCAGTGTATCTCAAGCTGGGTGTTGTTGCTCTAAAGCTCA 2355
Db 2109 TCCTGTGCTCCCATCCAGTGTATCTCAAGCTGGGTGTTGTTGCTCTAAAGCTCA 2168
QY 2356 AGTAGCTCCTTTGCTTTGATTTTCTCATCTGTTGCTATCTCCGCTCAGGCTACGTTA 2415

Db 2169 AGTAGCTCMTTTTTCCTTTGATTTTCTTTCATCTGTGTGCTATCTCCGCTGCAGGCTACGTTA 2228
QY 2416 TGCTGCCCTTTTAGGGTTTGGCCATGGCTTGGCGGCTTGGCCCTAACCTTCTTTTGTGTC 2475
Db 2229 TGCTGCCCTTTTAGGGTTTGGCCATGGCTTGGCGGCTTGGCCCTAACCTTCTTTTGTGTC 2288
QY 2476 AGCAGCTGCTGCCCAACAGATTAAGCTGTGTGGGTGCGACTGTAGTGGCAGGGTATG 2535
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QY 2536 TTTGTGGGCGGCGGTAAACCGTGTACCGATAGCTCTGCTGTGTAGTGTCTTGGCCCTCT 2595
Db 2349 TTTGTGGGCGGCGGTAAACCGTGTACCGATAGCTCTGCTGTGTAGTGTCTTGGCCCTCT 2407
QY 2596 GGTAGCGCTTT - TAAACCTCTTGCATTTGGTTAGCGCTGCTTACGCTTTTGCATATACCGAGA 2654
Db 2408 GGTAGCGCTTTTAAACCCCTTTGCATTTSSPKACGCTGCTT - AGCTTTTGCACCGAGA 2466
QY 2655 TAAATTGGAGGGCTGACCAATACCACTGTAGTAGCAATTAGTTTGTCTCATGTCTCGTTTGGCT 2714
Db 2467 TAAATTGGAGGGCTGACCAATACCACTGTAGTAGCAATTAGTTTGTCTCATGTCTCGTTTGGCT 2526
QY 2715 TCCTTGTCTCACTGTTTACCTCGCTGTGCTTTAGTTTAACTCTCTATCTTTGGCAACGTTGGG 2774
Db 2527 TCCTTGTCTCACTGTTTACCTCGCTGTGCTTTAGTTTAACTCTCTATCTTTGGCAACGTTGGG 2586
QY 2775 AGAATTGGTTTTGGAAAGTTTACACTAAGACCGGAGAGGTTTTCTCTGTGCTGCTGTTGCTT 2834
Db 2587 AGAATTGGTTTTGGAAAGTTTACACTAAGACCGGAGAGGTTTTCTCTGTGCTGCTGTTGCTT 2646
QY 2835 TCCCGGTCGCAATATGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 2894
Db 2647 TCCCGGTCGCAATATGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 2706
QY 2895 GTTTAAACATCCAGTGCAGCATCTCTTTGGGACTGACTTAGGGTTAGGGGCCCATAGAA 2954
Db 2707 GTTTAAACATCCAGTGCAGCATCTCTTTGGGACTGACTTAGGGTTAGGGGCCCATAGAA 2766
QY 2955 TGTTGGTGGCTCGGAAGTGCATGCTGGTATCTCATATTGTTCTTAAAGTTTTTCC 3014
Db 2767 TGTTGGTGGCTCGGAAGTGCATGCTGGTATCTCATATTGTTCTTAAAGTTTTTCC 2826
QY 3015 TCCTTAGTGTGTTGGTGCAGAAATGGTGTGTTTCTATAAGCACTTGCATGGTGTCTTTCG 3074
Db 2827 TCCTTAGTGTGTTGGTGCAGAAATGGTGTGTTTCTAKAAGCACTTGCATGGTGTCTTTCG 2886
QY 3075 CTAAATGATTTTGCCTCGAAACTACATTTGCAAGACCAATTTTCCCTTTTGAAGCAAGG 3134
Db 2887 CTAATGATTTTGCCTCGAAACTACCAATTTGCAAGACCAATTTTCCCTTTTGAAGCAAGG 2946
QY 3135 CAAGGCTCTATAGGAATGAAGGAAGACGCTTGGGCTGTGGGACACGGTTCATGTTGCTTTCG 3194
Db 2947 CAAGGCTCTATAGGAATGAAGGAAGACGCTTGGGCTGTGGGACACGGTTCATGTTGCTTTCG 3006
QY 3195 CCGTTGTTCCGCTCTCGGCGACCTTGTGTTTTCGAGGGTTGGCTATGCGGCCAGATGGGT 3254
Db 3007 SCGTTGTBGGCGCTCTCGGCGACCTTGTGTTTTCGAGGGTGTAGCTATGCGCGCAGATGGT 3066
QY 3255 GGGCCATPACCGCACTTTTACGCTGCAAGTGTCTCTCTGAACGCTGGGCAACGCTGTGAGGGA 3314
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QY 3315 TGGCAGTGGTCACTGCTATAGACCCCGAACTTGGACTGGAACTATCTTCAGATTAG 3374
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QY 3375 GATCTCTGCGCCACTAGCTATACATGGGATTTGTTTGTGAACAGCTGTTGTATCTGCTCACC 3434
Db 3187 GATCTCTGCGCCACTAGCTATACATGGGATTTGTTTGTGAACAGCTGTTGTATCTGCTCACC 3246
QY 3435 ATGGCAGCAAGGGGCGCGGTGGCTCATCCACAGGCTCTATACACCCCAATAACCGTTG 3494
Db 3247 ATGGCAGCAAGGGGCGCGGTGGCTCATCCACAGGCTCCATACACCCCAATAACCGTTG 3306

Qy 3495 ACGGGCTAATGACAGGACATCTATCAACCAACATGTGGAGCTGGGTCCCTTACTCGGT 3554
Db |||||
Qy 3307 ACGGGCTAATGACAGGACATCTATCAACCAACATGTGGAGCTGGGTCCCTTACTCGGT 3366
Db |||||
Qy 3555 GCTCTTGGGGGAGACCAAGGGGTATCTGTGAACAGACTGGGTCAATGGTTGAGGTCA 3614
Db |||||
Qy 3367 GCTCTTGGGGGAGACCAAGGGGTATCTGTGAACAGACTGGGTCAATGGTTGAGGTCA 3426
Db |||||
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Db |||||
Qy 3427 ACAAAATCCGATGACCCCTATTATGGTGTGTGCGGGGCCCTTCCCACTGGCTGTGSCCAAGG 3486
Db |||||
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Db |||||
Qy 3487 GTTCTTCAGGTGCCCGGATCTGTGCTCCTCGGGCAGTGTATTGGGATGTTCAACCGCTG 3546
Db |||||
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Db |||||
Qy 3547 CTAGAAATCTGGGGTTCAGTCCGCGCAGATTAGGGTTAGGCCGTGGTGTGCTGGAT 3606
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Qy 3607 ACCATCCCACTACACAGCAGATGCCACTCTTGATACAAACCTACTGTGCTTAACGAGT 3666
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Qy 3667 ATTCACTGCCAAATTTTAAATGCCCCCACTGGCAGCGGCAAGTCAACCAAAATTTACCACCTT 3726
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Qy 3915 CTTATATGACAGGAGAAGTATGAGTCTTGTGCTTAATCCAGATGCCGTGTGCTTACACAGCAT 3974
Db |||||
Qy 3727 CTTATATGACAGGAGAAGTATGAGTCTTGTGCTTAATCCAGTGTGGCTACACAGCAT 3786
Db |||||
Qy 3975 CAATGCCAAAGTACATGCAGCGACGTACGCGTGAATCCAAATTTGCTATTTTAATGGCA 4034
Db |||||
Qy 3787 CAATGCCAAAGTACATGCAGCGACGTACGCGTGAATCCAAATTTGCTATTTTAATGGCA 3846
Db |||||
Qy 4035 AATGTACCAACACAGGGGCTTCACTTACGTACAGCAGCATATGGCATGTACCTGACCGGAG 4094
Db |||||
Qy 3847 AATGTACCAACACAGGGGCTTCACTTACGTACAGCAGCATATGGCATGTACCTGACCGGAG 3906
Db |||||
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Db |||||
Qy 3907 GATGTTCCGGAACTATGATGAATATTTGTGACGAATGCCATGCTACCGATGCAACCA 3966
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Db |||||
Qy 3967 CCGTGTGGGCAATGGAAAGGTCTTAACCGAAGCTCCATCCAAATTTAGGCTAGTGG 4026
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Qy 4207 ACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGGATGTGACATCTCAA 4266
Db |||||
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RESULT 11
US-08-488-446-11
; Sequence 11, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWHAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8912 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-488-446-11

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RESULT 11
US-08-488-446-11
; Sequence 11, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B
; TITLE OF INVENTION: REAGENTS AND
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESS: ABBOTT LABORATORIES
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIAN TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8912 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-488-446-11

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Qy 3375 GATCTCTGGCCACTAGCTACATGGGATTTGTTGTGCAACGTTGTGTATCTGCTCACC 3434
Db 3187 GATCTCTGGCCACTAGCTACATGGGATTTGTTGTGCAACGTTGTGTATCTGCTCACC 3246
Qy 3435 ATGCGACAGGGGCGCGGTGGCTCATCCACAGGCTCTATACACCCCAATAACCGTTG 3494
Db 3247 ATGCGACAGAGCGGGGCGGTGGCTCATCCACAGGCTCATACACCCCAATAACCGTTG 3306
Qy 3495 ACGCGGCTAATGACAGGACATCTATCAACCAATGTGGAGCTGGGTCCCTTACTCGGT 3554

Db 3307 ACGCGGCTAATACCAAGGACATCTATCAACCACTGTGGAGCTGGGTCCCTTACTCGGT 3366
Qy 3555 GCTCTTTCGGGGAGACCAAGGGGTATCTGTAAACACGACTGGGTCACTTGTGTAGGTCA 3614
Db 3367 GCTCTTTCGGGGAGACCAAGGGGTATCTGTAAACGACTGGGTCACTTGTGTAGGTCA 3426
Qy 3615 ACAAATCCGATGACCCCTTATTTGTGTGTGTGGGGCCCTTCCCATGGCTGTGGCCAAAG 3674
Db 3427 ACAAATCCGATGACCCCTTATTTGTGTGTGTGGGGCCCTTCCCATGGCTGTGGCCAAAG 3486
Qy 3675 GTTCTTCAGTGGCCCGATTTCTGTCTCTCCGGGCATGTTATTTGGGATGTTTCAACCCGTG 3734
Db 3487 GTTCTTCAGTGGCCCGATTTCTGTCTCTCCGGGCATGTTATTTGGGATGTTTCAACCCGTG 3546
Qy 3735 CTAGAAATTTCTGGCGTTTCACTCAGTCAGATTAGGGTTAGGCGGTTGGTGTGTCTGGAT 3794
Db 3547 CTAGAAATTTCTGGCGTTTCACTGCGGCAGATTAGGGTTAGGCGGTTGGTGTGTCTGGAT 3606
Qy 3795 ACCATCCCAGTACACAGCACATGCCACTCTTGATACAAAACCTACTGTGCTTAAACGAGT 3854
Db 3607 ACCATCCCAGTACACAGCACATGCCACTCTTGATACAAAACCTACTGTGCTTAAACGAGT 3666
Qy 3855 ATTCAGTGCATAATTTTAAATTTGCCCCCACTGGCAGCGCAAGTCAACCAAAATTTACCACCTT 3914
Db 3667 ATTCAGTGCATAATTTTAAATTTGCCCCCACTGGCAGCGCAAGTCAACCAAAATTTACCACCTT 3726
Qy 3915 CTTTACATGACGAGGAAGTATGAGGTCTTGGTCTTAAATCCAGTGTGGCTTACACACAGAT 3974
Db 3727 CTTTACATGACGAGGAAGTATGAGGTCTTGGTCTTAAATCCAGTGTGGCTTACACACAGAT 3786
Qy 3975 CAATGCCCCAAAGTACATGACGCGACGTACCGCGTGAATCCAAATTTGCTATTTTAAATGGCA 4034
Db 3787 CAATGCCCCAAAGTACATGACGCGACGTACCGCGTGAATCCAAATTTGCTATTTTAAATGGCA 3846
Qy 4035 AATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGCGCATGCTGACCCGGAG 4094
Db 3847 AATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGCGCATGCTGACCCGGAG 3906
Qy 4095 CATGTTCCCGGAACTATGATGTAATCATTTGTGACGAATGCCATGCTACCGATGCAACCA 4154
Db 3907 GATGTTCCCGGAACTATGATGTAATCATTTGTGACGNAATGCCATGCTACCGATGCAACCA 3966
Qy 4155 CCGTGTGGGCACTTGGAAAGGTCTTAAACGAAGCTCCATCCAAAAATGTTAGGCTAGTGG 4214
Db 3967 CCGTGTGGGCACTTGGAAAGGTCTTAAACGAAGCTCCATCCAAAAATGTTAGGCTAGTGG 4026
Qy 4215 TTTCTTGCACCGCTACCCCGCTGGAGTAATCCCTACACACATGCCCAACATTAACAGTA 4274
Db 4027 TTTCTTGCACCGCTACCCCGCTGGAGTAATCCCTACACACATGCCCAACATTAACAGTA 4086
Qy 4275 TTTCAATTTAACCCGATGAAGGCACTATCCCTTTTCAATGGAATAAGATTAAAGGAGGAAATC 4334
Db 4087 TTTCAATTTAACGATGAAGGCACTATCCCTTTTCAATGGAATAAGATTAAAGGAGGAAATC 4146
Qy 4335 TGAAGAAAGGAGACACCTTATCTTTAGGCTACCAAAACACACTGTGATGAGCTTGTCTA 4394
Db 4147 TGAAGAAAGGAGACACCTTATCTTTAGGCTACCAAAACACACTGTGATGAGCTTGTCTA 4206
Qy 4395 ACAGATTAGCTCGAAGGGAATTAACAGCTCTCTTACTATAGGGGATGACATCTCNA 4454
Db 4207 ACAGATTAGCTCGAAGGGAATTAACAGCTCTCTTACTATAGGGGATGACATCTCNA 4266
Qy 4455 AAATCCCTGAGGCGACTGTGATGTTAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4514
Db 4267 AAATGCTGAGGGGACTGTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4326
Qy 4515 GTGACTTTTGAATCCGTTGATGACTGACGCTCATGGTGAAGGCACATGCCATGTGTGACC 4574
Db 4327 GTGACTTTTGAATCCGTTGATGACTGACGCTCATGGTGAAGGCACATGCCATGTGTGACC 4386
Qy 4575 TTGACCCCTACTTTCACCATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4634
Db 4387 TTGACCCCTACTTTCACCATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4446

QY	4635	AGCTAGGGGCGGCACAGGCCGTGGGAGAGCTGGCATATACTACTATGTAGACGGGAGTT	4694
DB	4447	AGCGTAGGGGCGGCACAGGCCGTGGGAGAGCTGGCATATACTACTATGTAGACGGGAGTT	4506
QY	4695	GTAACCCCTTCGGGTATGGTTCCTGAATGCAACATGTTGAAGCCCTCGACGCAGCCAAAG	4754
DB	4507	GTAACCCCTTCGGGTATGGTTCCTGAATGCAACATGTTGAAGCCCTCGACGCAGCCAAAG	4566
QY	4755	CATGGTATGGTTCGTATCAACAGAGAGCTCAAACTATTCTTGGACACCTATCGCACCCCAAC	4814
DB	4567	CATGGTATGGTTCGTATCAACAGAGAGCTCAAACTATTCTTGGACACCTATCGCACCCCAAC	4626
QY	4815	CTGGGTTACCTGCGATAGGAGCAAAATTTGACGAGTGGGCTGATCTCTTTTCTATGGTCA	4874
DB	4627	CTGGGTTACCTGCGATAGGAGCAAAATTTGACGAGTGGGCTGATCTCTTTTCTATGGTCA	4686
QY	4875	ACCCGGAACCTTCATTTGTCAATCTGCAAAAAGAACTGCTGACAAATATGTTTTGTTGA	4934
DB	4687	ACCCGGAACCTTCATTTGTCAATCTGCAAAAAGAACTGCTGACAAATATGTTTTGTTGA	4746
QY	4935	CTGCAGCCCACTACAACCTGCTGCTATCAGTATGCTATGCTGCTCCCAATGACGACCCAC	4994
DB	4747	CTGCAGCCCACTACAACCTGCTGCTATCAGTATGCTATGCTGCTCCCAATGACGACCCAC	4806
QY	4995	GCTGGCAGGAGCCCGGCTTCGGGAAAAAACTCTGTGGGTTCTGTGGCGCTTGGACGGCG	5054
DB	4807	GCTGGCAGGAGCCCGGCTTCGGGAAAAAACTCTGTGGGTTCTGTGGCGCTTGGACGGCT	4866
QY	5055	CTGACGCGCTGCTCTGGGCCAGAGCCACGAGGTGACAGANATCAAAATGTGCTTCACTG	5114
DB	4867	CTGACGCGCTGCTCTGGGCCAGAGCCACGAGGTGACAGANATCAAAATGTGCTTCACTG	4926
QY	5115	AAGTCAATACCTCTGGGACAGCCCACTCGCTGTGTGGCGTTGGAGTGGCTATGGCTTATC	5174
DB	4927	AAGTCAATACCTCTGGGACAGCCCACTCGCTGTGTGGCGTTGGAGTGGCTATGGCTTATC	4986
QY	5175	TAGCATTTGACACTTTTGGGCCCACTTGTGTGGCGGCTTGCTGTCTATTACATCATGCTCC	5234
DB	4987	TAGCATTTGACACTTTTGGGCCCACTTGTGTGGCGGCTTGCTGTCTATTACATCATGCTCC	5046
QY	5235	CTACCGGTGCTACTGTGTGCCCCAGTGTGTGAAGAAGAAATCGTGGAGGAGTGTGCAT	5294
DB	5047	CTACCGGTGCTACTGTGTGCCCCAGTGTGTGAAGAAGAAATCGTGGAGGAGTGTGCAT	5106
QY	5295	CATTCAATCCCTTGGAGGCCATGTTGCTGCAATTTGACAGCTGAAAGGTACATCACCA	5354
DB	5107	CATTCAATCCCTTGGAGGCCATGTTGCTGCAATTTGACAGCTGAAAGGTACATCACCA	5166
QY	5355	CAACTAGTCCCTTTCACATTGGAACCGCCCTTGAAAAAATCTTACACCTTCTTGGGGCTC	5414
DB	5167	CAACTAGTCCCTTTCACATTGGAACCGCCCTTGAAAAAATCTTACACCTTCTTGGGGCTC	5226
QY	5415	ATGACGCTACAATCCTTGCTATCATAGAGTATGCTGTGGTTTATGTCACCTTTACCTGACA	5474
DB	5227	ATGACGCTACAATCCTTGCTATCATAGAGTATGCTGTGGTTTATGTCACCTTTACCTGACA	5286
QY	5475	ATCCCTTTGCAATATGCGTGTGTTTCAATGCGGGTATTTACTACCCCACTACCTCAACA	5534
DB	5287	ATCCCTTTGCAATATGCGTGTGTTTCAATGCGGGTATTTACTACCCCACTACCTCAACA	5346
QY	5535	AGATCAAAATGTTCTCTGTCATTTATTTGGAGCGCAATTTGGCTCAAGCTTACAGACGCTA	5594
DB	5347	AGATCAAAATGTTCTCTGTCATTTATTTGGAGCGCAATTTGGCTCAAGCTTACAGACGCTA	5406
QY	5595	GAGCGCACTGGCGTTTCATGATGGCCGGGCTGGGGAAACAGCTCTTTGGTACATGGACAT	5654
DB	5407	GAGCGCACTGGCGTTTCATGATGGCCGGGCTGGGGAAACAGCTCTTTGGTACATGGACAT	5466
QY	5655	CGGTGGGTTTGTCTTTTGACATGCTAGCGGCTATGCTGCGGCTCATCCACTGCTTGTCT	5714
DB	5467	CGGTGGGTTTGTCTTTTGACATGCTAGCGGCTATGCTGCGGCTCATCCACTGCTTGTCT	5526

QY	5715	TGACATTTAAATGCTTGATGGGTGAGTGGGCCACTATAGATCAGCTTGTCTGTTTAACTCT	5774
DB	5527	TGACATTTAAATGCTTGATGGGTGAGTGGGCGACTATGAGATCAGCTTGTGTTTAACTCT	5586
QY	5775	ACTCCGGTTTCAATCCGGCCGCGAGGAGTTGTGTGGCGCTCTTGTCAGCTTGTGCAATGTTTG	5834
DB	5587	ACTCCGGTTTCAATCCGGCCGCGAGGAGTTGTGGCGCTCTTGTCAGCTTGTGCAATGTTTG	5646
QY	5835	CTTTTGACAAACAGCAGGGCCAGATCACTGGGCCCAACACAGACTTCTTATCTATGCTTGTCTAGGA	5894
DB	5647	CTTTTGACAAACAGCAGGGCCAGATCACTGGGCCCAACACAGACTTCTTATCTATGCTTGTCTAGGA	5706
QY	5895	GCAACACTGTATGTAAATGAGTACTTTATTATGCCACTCGTGTGACATCCGAGAGAAATACTGG	5954
DB	5707	GCAACACTGTATGTAAATGAGTACTTTATTATGCCACTCGTGTGACATCCGAGAGAAATACTGG	5766
QY	5955	GCATTCTGGAGGCATCTACCCCTGGAGTGTATATCAGCTTGCATCCGTTGCTCCACAC	6014
DB	5767	GCATTCTGGAGGCATCTACCCCTGGAGTGTATATCAGCTTGCATCCGTTGCTCCACAC	5826
QY	6015	CCCCGACGAGGATGATTGGCGGCTCATTTGCTTTGGGCTTAGAGATTTGGCAGTATGTGT	6074
DB	5827	CCCCGACGAGGATGATTGGCGGCTCATTTGCTTTGGGCTTAGAGATTTGGCAGTATGTGT	5886
QY	6075	GCAATTTCTTTGTGATTTGCTTTAAATGTCCTTAAAGCTGAGTTTCAGAGCATGGTTAAACA	6134
DB	5887	GCAATTTCTTTGTGATTTGCTTTAAATGTCCTTAAAGCTGAGTTTCAGAGCATGGTTAAACA	5946
QY	6135	TTCTCTGTTGTCTTTCTACAGCTGCCAGAAAGGGGTACAAGGCCCTCTGGATTTGGATCAG	6194
DB	5947	TTCTCTGTTGTCTTTCTACAGCTGCCAGAAAGGGGTACAAGGCCCTCTGGATTTGGATCAG	6006
QY	6195	GTATGCTCCAAGCACGCTGTCCATGCGGTGCTGCAACTCATCTTTTCTGTTTGAGAAATGGTT	6254
DB	6007	GTATGCTCCAAGCACGCTGTCCATGCGGTGCTGCAACTCATCTTTTCTGTTTGAGAAATGGTT	6066
QY	6255	TTGCAAACTTTTACAAAGACCAGAACTTTGTTCAAATTACTGGAGAGGGGCTGTTCCAG	6314
DB	6067	TTGCAAACTTTTACAAAGACCAGAACTTTGTTCAAATTACTGGAGAGGGGCTGTTCCAG	6126
QY	6315	TCAAACGTAGCTGTGTGGGTGCGGTAGACCGGACCCCACTGATTTGGACTAGTCTTGTCTCG	6374
DB	6127	TCAAACGTAGCTGTGTGGGTGCGGTAGACCGGACCCCACTGATTTGGACTAGTCTTGTCTCG	6186
QY	6375	TCAATTAATGCGTTTAGGACACTCTGTAATAATACAGAAATGGAGAGATCAATTTTGTTA	6434
DB	6187	TCAATTAATGCGTTTAGGACACTCTGTAATAATACAGAAATGGAGAGATCAATTTTGTTA	6246
QY	6435	CAGCAGTATCCTCTCCAATATGTCGTTTACCCAGGTGCCCCCAACTGGAGAGCTGCAG	6494
DB	6247	CAGCAGTATCCTCTCCAATATGTCGTTTACCCAGGTGCCCCCAACTGGAGAGCTGCAG	6306
QY	6495	TGGCCGTGAGCGGGTACAGGTTACAGTTTATCTAGGTGAGGCCCAAACTCCTTGGACGA	6554
DB	6307	TGGCCGTGAGCGGGTACAGGTTACAGTTTATCTAGGTGAGGCCCAAACTCCTTGGACGA	6366
QY	6555	CATCTGCTTCTGTTACGTTACGTTTAAAGGTAAGGTAAGGTTAAAGTTCCTTCCGCG	6614
DB	6367	CATCTGCTTCTGTTACGTTTAAAGGTAAGGTAAGGTTAAAGTTCCTTCCGCG	6426
QY	6615	TTGACGCTCACACACTTGGTGTGCGCATGCAACTTAATTTGCGGTGATGCACTTTGAGACAA	6674
DB	6427	TTGACGACACACACTTGGTGTGCGCATGCAACTTAATTTGCGGTGATGCACTTTGAGGCAA	6486
QY	6675	ATGACTGTAAATCCACAAACACACTCTTAGTATGAAGCCGAGTGTCCGCTCTTGT	6734
DB	6487	ATGACTGTAAATCCATAAAACACACTCTTAGTATGAAGCCGAGTGTCCGCTCTTGT	6546
QY	6735	TCAAACAGGAGTTGCGGCGTACAAACCAATTTGCTTGAGGCAATTTACGCTGGGCTTACAC	6794
DB	6547	TCAAACAGGAGTTGCGGCGTACAAACCAATTTGCTTGAGGCAATTTACGCTGGGCTTACAC	6606
QY	6795	CCACCAACTGCCACGCCCTCC - - - ATCGAAGAGGTAGTGGTGAAGAAACGCCAGTTCC	6851

Db 6607 |||||CCACCAAACTGCCAGCCGCCCCCTCCAGATCGAAGAGGTAGTGGTAAGAAAGCGCCAGTTCC||| 6666
Qy 6852 GGGCAAGAACTGGTTGCTTACCTTGTCTCCCTCCGAGATCGTCCCGAGGAGTGTCAAT||| 6911
Db 6667 GGGCAAGAACTGGTTGCTTACCTTGTCTCCCTCCGAGATCGTCCCGAGGAGTGTCAAT||| 6726
Qy 6912 GTCTGAAAGCTCGCAACGAAGTGAACCGTTGAGAGTTCCTTCAAACTCCCTCTTCAAC||| 6971
Db 6727 GTCTGAAAGCTCGCAACGAAGTGAACCGTTGAGAGTTCCTTCAAMCCTCCCTTCTTCAAC||| 6786
Qy 6972 CACCTGTTCTACAGTTGGCCATGCGGATGCCCTGTTGGGAGCGGTTGAGTGAACCCCTT||| 7031
Db 6787 CACCTGTTCTACAGTTGGCCATGCGGATGCCCTGTTGGGAGCGGTTGAGTGAACCCCTT||| 6846
Qy 7032 TCACCTGCAATTTGGATGTGCAATGACCGAAACGAGCGGAGGCCCTGATGATTTACCCAGATT||| 7091
Db 6847 TCACCTGCAATTTGGATGTGCAATGACCGAAACGAGCGGAGGCCCTGATGATTTACCCAGATT||| 6906
Qy 7092 ACCCTCCAAAAGGAGGTCTCTGAATGGTCAGACGAAGTTGGTCAGCGGCTCAACCG||| 7151
Db 6907 ACCCTCCAAAAGGAGGTCTCTGAATGGTCAGACGAAGTTGGTCAGCGGCTCAACCG||| 6966
Qy 7152 CTTCCAGTAGTTACTGGCCCCCGCTACCTTAAGATACGGGAAAGATTCCACTCAGT||| 7211
Db 6967 CTTCCAGTAGTTACTGGCCCCCGCTACCTTAAGATACGGGAAAGATTCCACTCAGT||| 7026
Qy 7212 CAGCCCCCGCAACCGGCTTCAAAAAGAGTTGGGAAAGAGTGAGTTTTCGTGCAGCA||| 7271
Db 7027 CAGCCACGCGCAACCGGCTTCAAAAAGAGTTGGGAAAGAGTGAGTTTTCGTGCAGCA||| 7086
Qy 7272 TGAGCTACACCTGGACCGACGTGATAGCTTTCAAACTGCTTTCAAAAGTTCTGTCTCAA||| 7331
Db 7087 TGAGCTACACCTGGACCGACGTGATAGCTTTCAAACTGCTTTCAAAAGTTCTGTCTCAA||| 7146
Qy 7332 CTCGGGCCATCAGTAGTGGTTTCTCAAAAGAGATCATTTGGTGTATGTGACTGAGCGC||| 7391
Db 7147 CTCGGGCCATCAGTAGTGGTTTCTCAAAAGAGATCATTTGGTGTATGTGACTGAGCGC||| 7206
Qy 7392 GGGATGGGAGCTTAGAAAAAAGGCTTAAAGTCACTATTAAATAGACAACCTCTGTTCGCCCAT||| 7451
Db 7207 GGGATGGGAGCTTAGAAAAAAGGCTTAAAGTCACTATTAAATAGACAACCTCTGTTCGCCCAT||| 7266
Qy 7452 CATACCAAGCAAGTGAAGTTGGCTTAAGGAAAAAGCTTCAAAAGTTGTGCGTGTCAATG||| 7511
Db 7267 CATACCAAGCAAGTGAAGTTGGCTTAAGGAAAAAGCTTCAAAAGTTGTGCGTGTCAATG||| 7326
Qy 7512 GGGACTATGATGAAGTAGCAGCTCACAGCCCTCTAAGTCTGCTAAGTCCACATCACTG||| 7571
Db 7327 GGGACTATGATGAAGTAGCAGCTCACAGCCCTCTAAGTCTGCTAAGTCCACATCACTG||| 7386
Qy 7572 GCTTTGGGGCAGCTGATGTTGTTCTGGAGCAGCCCGCAAGGCTGTTCTGGACTTGCAGA||| 7631
Db 7387 GCTTTGGGGCAGCTGATGTTGTTCTGGAGCAGCCCGCAAGGCTGTTCTGGACTTGCAGA||| 7446
Qy 7632 AGTGTGTGAGGAGGTGAGATACCGAGTCAATTATCGGCAAACTGTGATAGTTCCAAAGG||| 7691
Db 7447 AGTGTGTGAGGAGGTGAGATACCGAGTCAATTATCGGCAAACTGTGATAGTTCCAAAGG||| 7506
Qy 7692 AGGAGGTCTTCGTGAAGACCCCGCAGAAACCAACAAAGAAACCCCGCAAGGCTTATCTCGT||| 7751
Db 7507 AGGAGGTCTTCGTGAAGACCCCGCAGAAACCAACAAAGAAACCCCGCAAGGCTTATCTCGT||| 7566
Qy 7752 ACCCCCACTTTGAAATGAGATGTGTTGAGAGAGTACTACGGTCAAGTTCCTCTGACG||| 7811
Db 7567 ACCCCCACTTTGAAATGAGATGTGTTGAGAGAGTACTACGGTCAAGTTCCTCTGACG||| 7626
Qy 7812 TAGTTAAAGCTGTGATGGGAGATGCTACCGGTTTGTAGATCCACGTACCGGTGTCAAGC||| 7871
Db 7627 TAGTTAAAGCTGTGATGGGAGATGCTACCGGTTTGTAGATCCACGTACCGGTGTCAAGC||| 7686
Qy 7872 GTCTGTTGTGATGTGTCACCGATGTCAGTTCGAGGCCAATGCGATACAGTGTGTTTG||| 7931

Db 7687 GTCTGTTGTGATGTGTTGTCACCCGATGCGATCGGAGCCACATGCGATACAGTGTGTTTG||| 7746
Qy 7932 ACAGTACCATCACACCCGAGGATATCATGTGGAGACAGACATCTACTCAGCAGCTAAAC||| 7991
Db 7747 ACAGTACCATCACACCCGAGGATATCATGTGGAGACAGACATCTACTCAGCAGCTAAAC||| 7806
Qy 7992 TCAGTGAACCAACCCGAGCTGGCATTCACACCATTTGCGAGGAGATTATACGCTCGAGGAC||| 8051
Db 7807 TCAGTGAACCAACCCGAGCTGGCATTCACACCATTTGCGAGGAGATTATACGCTCGAGGAC||| 7866
Qy 8052 CGATGATCGCTTATGATGGCGGAGAGATCGATATCGTAGGTGAGTCTTCCCGCGTCT||| 8111
Db 7867 CGATGATCGCTTATGATGGCGGAGAGATCGATATCGTAGGTGAGTCTTCCCGCGTCT||| 7926
Qy 8112 ATACTACTCAAGTTTCAACAGATTTCACCTGCTGCTGCTGAAGGTAAATGCTGACGCCGAAC||| 8171
Db 7927 ATACTACTCAAGTTTCAACAGATTTCACCTGCTGCTGCTGAAGGTAAATGCTGACGCCGAAC||| 7986
Qy 8172 AGGCTGCGATGAAGAACCCCTCGCTTCTTATTTGCGGCGGATGATGTCACCGTAAATTTGGA||| 8231
Db 7987 AGGCTGCGATGAAGAACCCCTCGCTTCTTATTTGCGGCGGATGATGTCACCGTAAATTTGGA||| 8046
Qy 8232 AGAGCGCGGAGCAGATGCGAGACAAACAAAGCAATGCGTGTCTTTGCTAGCTGGAATGAAG||| 8291
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Qy 8292 TGATGGGTGACCAAGAGATTGTGCTCAACCCAAATACAGTTTGGAGAAATTAACAT||| 8351
Db 8107 TGATGGGTGACCAAGAGATTGTGCTCAACCCAAATACAGTTTGGAGAAATTAACAT||| 8166
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Db 8167 CATGCTCATCAAAATGTTTACCTCTGGAATTAACAAAGTGGCAAGCTTACTACTTTCTTA||| 8226
Qy 8412 CAAGAGATCCTCGTATCCCTTGGCAGGTGCTCTGCGAGGGTCTCGGATACAAACCCA||| 8471
Db 8227 CAAGAGATCCTCGTATCCCTTGGCAGGTGCTCTGCGAGGGTCTCGGATACAAACCCA||| 8286
Qy 8472 GTGCTGCTGGATTGGGTATCTAATACATCACTACCCATGTTTGTGGTTAGCCGTGTGT||| 8531
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Qy 8532 TGGCTGTCCATTTTCAAGGAGATGCTCTTTGAGGACAAACTTCCCGAGACTGTGACCT||| 8591
Db 8347 TGGCTGTCCATTTTCAAGGAGATGCTCTTTGAGGACAAACTTCCCGAGACTGTGACCT||| 8406
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Db 8407 TTGACTGGTATGGAAAAATATACGGTGTCTGTAGAGATCTGCCAGCATCATTTGCTG||| 8466
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Qy 8772 GGGCGGTCTCGCCAGCGCCCAAGGGCGTGGCGGACACGCAAAATTTGGCTCGCTTCC||| 8831
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Db 8706 ACACCACTTTCAATTTTGTGATTTTACT-CCCGAGGGGAGTGTGTTTATTACACCAAC||| 8764
Qy 8952 AGAGAAATGTCAGAAAGTTCCTTGTGAAGTATTTGGCTGTCAATTTTGGCCCTAGGGC||| 9011
Db 8765 AGAGAAATGTCAGAAAGTTCCTTGTGAAGTATTTGGCTGTCAATTTTGGCCCTAGGGC||| 8824

Db 1151 CTTGACCAAACTGGCTTCACAAGTACCAATAGCGTATTGTGGAGCTAATGTTTATGACAGTGATACA 1210
Qy 1396 CTACCTGGCGGTGGCGCTCTGATCTACTATGATCCCTCTCGGGGCAAGTGGTATCAGTTGCT 1455
Db 1211 CTACCTGGCGGTGGCGCTCTGATCTACTATAGCCTCTCTCGGGCAAGTGGTATCAGTTGCT 1270
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Db 1630 AACACCATGGCTAAACAACCGCATGGGCAACAGCGCTCAGCCCTGAAATGGCTATATTACA 1689
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Db 1690 ATACCTGGGTCTAAGAAATGTTTAAACCTCATAAATGGATGTCAGGCCAATGGTATTT 1749
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Db 1750 TGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAATCCACTCTCCTACC 1809
Qy 1996 ACCGAGAGTGGGTAGTGGTCCCGGTACCCCACTGTGGTACGTGGTCTTGGTTACA 2055
Db 1810 ACCGAGAGTGGGTAGTGGTCCCGGTACCCCACTGTGGTACGTGGTCTTGGTTACA 1869
Qy 2056 GGTTCGCGNAGGTTTTACAGTGTATGTAAGAGCTAGCCACAGGATGATCACAAGA 2115
Db 1870 GGTTCGCGCAA--GGTTTTACAGTGTATGTAAGAGCTAGCCACAGGATGATCACAAGA 1928
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Db 2109 TCCTGTGCTCCCATCCCACTCGTATCTCCAAGCTGGGTGGGATGTTTGTCTAAAGCTCA 2168
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RESULT 13
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; Patent No. 6720166
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; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
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; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
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; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
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; REFERENCE/DOCKET NUMBER: 5527.PC.01
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; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8912 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-424-550B-11
Query Match 92.5%; Score 8692.6; DB 4; Length 8912;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 8781; Conservative 56; Mismatches 52; Indels 10; Gaps 8;
QY 196 TGGGTTCCGGTGGTGGCGCTTTAGGCAGCGCTCCACGCCACACCTCCCCAGATAGAGC 255
DB 11 TGGGTTCCGGTGGTGGCGCTTTAGGCAGCGCTCCACGCCACACCTCCCCAGATAGAGC 70
QY 256 GCGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACGACACCTCTTTTGA 315
DB 71 GCGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACGACACCTCTTTTGA 130
QY 316 GTATCACCCCTCCGGAAGTAGTTGGGCAAGCCACCTATATGTGTGGATGGTTGGGT 375
DB 131 GTATCACCCCTCCGGAAGTAGTTGGGCAAGCCACCTATATGTGTGGATGGTTGGGT 190

QY 376 TAGCCATCCA TACCGTACTGCTGATAGGGTCTTTGCGAGGGGATCTGGGAGTCTCGTAG 435
Db 191 TAGCCATCCATACCGTACTGCTGATAGGGTCTTTGCGAGGGGATCTGGGAGTCTCGTAG 250
QY 436 ACCGTAGCAGATGCTGTATTTCTACTCAACAAGTCTCTGACTGCGGCCAGACGGC 495
Db 251 ACCGTAGCAGATGCTGTATTTCTACTCAACAAGTCTCTGACTGCGGCCAGACGGC 310
QY 496 CAAGAAACAAGCAGACCGCAGGCTTCATATCCTGTGTCCCAATTAACAATCTGTGTGAAGGGG 555
Db 311 CAAGAAACAAGCAGACCGCAGGCTTCATATCCTGTGTCCCAATTAACAATCTGTGTGAAGGGG 370
QY 556 ACAAGCAGAAAGCAGAAAGTCCAGCGGATGCTCGGCTCGTAAATTAACAATTTGCTGG 615
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QY 616 TATCCATGATGGCTTGCAGACATTTGGCTCAGGCTGCTTGGCAGCTCAATGTTGGGAGC 675
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QY 736 GATTGGTGAATGTTACAACTCAACACCTCTAGTAGGCCCCGCTGGTGGCAGGAGCGTCTGT 795
Db 551 GATTGGTGAATGTTACAACTCAACACCTCTAGTAGGCCCCGCTGGTGGCAGGAGCGTCTGT 610
QY 796 TCGACCACTCGCCAGATAGTACGGTCTGCGAGGATGGAGTCAATCGGCTACTGTTG 855
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QY 1396 CTACCTGGGTTGGGCTCTGATCTACTATGCTCTCGGGCAGTGGTATCAGTTGCT 1455
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Db 1630 AACACATGGCTAAACACCGCATGGCAACACCGCTCAGCCCTGAAATTTGGCTATATTACA 1689
QY 1876 ATACCTGGGTCTAAAGAAATGTTTAAACCTCATAAATTTGGATGTCAGGCCATTTGATTT 1935
Db 1690 ATACCTGGGTCTAAAGAAATGTTTAAACCTCATAAATTTGGATGTCAGGCCACTTTGATTT 1749
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Db 1750 TGAGGATCAGATACCCCTATAGTTTACTTTTATGACCTGTGAATTTCCACTCTCTTACC 1809
QY 1996 ACCGAGAGTGGGTAGTGGTCCCGTACCCACCTGTGTGTAAGTGGTCTTGTGGTTACA 2055
Db 1810 ACCGAGAGTGGGTAGTGGTCCCGTACCCACCTGTGTGTAAGTGGTCTTGTGGTTACA 1869
QY 2056 GGTTCGCCAAGGGTTTACAGTGTGTAAGACCTAGCCACACAGATTTGATCACCAGA 2115
Db 1870 GGTTCGCCAAGGGTTTACAGTGTGTAAGACCTAGCCACACAGATTTGATCACCAGA 1928
QY 2116 CAAAGCTCGAAAATTTATCAGTCTTATATTTCCGCCACGGGTCTTTGTCTTTACGGG 2175
Db 1929 CAAAGCTCGAAAATTTATCAGTCTTATATTTCCGCCACGGGTCTTTGTCTTTACGGG 1988
QY 2176 AGTTACCAACAAAGCCGTGTGCTAAATCTGTGGGTGTGTGGCAGCAAGTATCTTAT 2235
Db 1989 AGTTACCAACAAAGCCGTGTGCTAAATCTGTGGGTGTGTGGCAGCAAGTATCTTAT 2048
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Db 2049 TTTAGCCTACTCTGTTACTGTTCCCTTTGTTTGGGCGGCTTCTGGTACMCTTTGG 2108
QY 2296 TCCTGTCTCCATCCCACTCGTATCTCCAAAGCTGGGTGGGATGTTTGTCTTAAAGCTCA 2355
Db 2109 TCCTGTCTCCATCCCACTCGTATCTCCAAAGCTGGGTGGGATGTTTGTCTTAAAGCTCA 2168
QY 2356 AGTAGCTCTTTTGGCTTTGATTTTCTTCTCATCTGTGTCTA TCTCCGCTGACGGTACGTTA 2415
Db 2169 AGTAGCTCTTTTGGCTTTGATTTTCTTCTCATCTGTGTCTA TCTCCGCTGACGGTACGTTA 2228
QY 2416 TGCTGCCCTTTTAGGGTTTGTGCCCATGGCTGCGGCTTGGCCCTTACTTTCTTTGTC 2475
Db 2229 TGCTGCCCTTTTAGGGTTTGTGCCCATGGCTGCGGCTTGGCCCTTACTTTCTTTGTC 2288
QY 2476 AGCAGCTGCTGCCCAACAGATTTATGCTGGTGGGTGCGACTGTAGTGGCAGGTTAGT 2535
Db 2289 AGCAGCTGCTGCCCAACAGATTTATGCTGGTGGGTGCGACTGTAGTGGCAGGTTAGT 2348
QY 2536 TTTGTGGGCGGCGGTAAACCGTGGTCAACCGCATAGCTCTGTGTGTAGTGGTCTTGGCCTCT 2595

[illegible]

Db	3427	ACAAATCCGATGACCCCTTATTGTGTGTGTGTGGCGGGCCCTTCCTCCATGGCTGTGTGCCAAGG	3486
Qy	3675	GTTCTTCAGGTGCCCCGAITTCGTGTCTCCTCCGGGCATGTTATTGGGATGTTTCACCGCTG	3734
Db	3487	GTTCTTCAGGTGCCCCGAITTCGTGTCTCCTCCGGGCATGTTATTGGGATGTTTCACCGCTG	3546
Qy	3735	CTAGAATAATCTGGCGGTTCAGTCAGTCAGATTAAGGTTTAGGCCGTGTGGTGCTGTGGAT	3794
Db	3547	CTAGAATAATCTGGCGGTTCAGTCGGCGCAGATTAGGGTTAGGCCGTGTGTGTGCTGTGGAT	3606
Qy	3795	ACCATCCCAGTACACAGCACATGCCACTCTTGATACAAAACCTACTGTGCTCTAACGAGT	3854
Db	3607	ACCATCCCAGTACACAGCACATGCCACTCTTGATACAAAACCTACTGTGCTCTAACGAGT	3666
Qy	3855	ATTCAAGTGCAAATTTTTAAATGCCCCACTGGCAGCGCAGTCAACCAAATTAACCACTTT	3914
Db	3667	ATTCAAGTGCAAATTTTTAAATGCCCCACTGGCAGCGCAGTCAACCAAATTAACCACTTT	3726
Qy	3915	CTTACATGCAGGAGAAATATGAGGCTTTGGTCTCTAAATCCAGTGTGGCTACAACAGCAT	3974
Db	3727	CTTACATGCAGGAGAAATATGAGGCTTTGGTCTCTAAATCCAGTGTGGCTACAACAGCAT	3786
Qy	3975	CAATGCCAAAGTACATGCACGCGACGTACGGCGTGAATCCAAATTCGCTATTTAATGGCA	4034
Db	3787	CAATGCCAAAGTACATGCACGCGACGTACGGCGTGAATCCAAATTCGCTATTTAATGGCA	3846
Qy	4035	AATGTACCAACACAGGGGCTTCATCTACGTFACAGCACATATGCGCATGTACTGCACCGGAG	4094
Db	3847	AATGTACCAACACAGGGGCTTCATCTACGTFACAGCACATATGCGCATGTACTGCACCGGAG	3906
Qy	4095	CATGTTCCCGAACTATGATGTAATCATTTGTGACGAATGCCATGCTACCGATGCAACCA	4154
Db	3907	GATGTTCCCGAACTATGATGTAATCATTTGTGACGAATGCCATGCTACCGATGCAACCA	3966
Qy	4155	CCGTGTTGGGCAATTGGAAGGTCCTAACCGAGCTCCATCCAAAAATGTTAGGCTAGTGG	4214
Db	3967	CCGTGTTGGGCAATTGGAAGGTCCTAACCGAGCTCCATCCAAAAATGTTAGGCTAGTGG	4026
Qy	4215	TTCCTTGCCACGGCTACCCCTCCGGAGTAATCCCTACACCACATGCCAATAACTAGTA	4274
Db	4027	TTCCTTGCCACGGCTACCCCTCCGGAGTAATCCCTACACCACATGCCAATAACTAGTA	4086
Qy	4275	TTCAATTAACCGATGAAGGCACATATCCCTTTTCATGSAAAAAAGATTAAAGGAGGAAAAATC	4334
Db	4087	TTCAATTAACCGATGAAGGCACATATCCCTTTTCATGSAAAAAAGATTAAAGGAGGAAAAATC	4146
Qy	4335	TGAAGAAAGGAGACACCTTATCTTTAGGCTACCAAAAAACHACTGTGATGAGCTTGCCTA	4394
Db	4147	TGAAGAAAGGAGACACCTTATCTTTAGGCTACCAAAAAACHACTGTGATGAGCTTGCCTA	4206
Qy	4395	ACGAGTTAGCTCGAAAGGGAATAACAGCTGCTCTTACTATAGGGGATGACATCTCAA	4454
Db	4207	ACGAGTTAGCTCGAAAGGGAATAACAGCTGCTCTTACTATAGGGGATGACATCTCAA	4266
Qy	4455	AAATCCCTGAGGGCGACTGTGTAGTAGTTGCCACTGATGCTTGTGTACAGGGGTACACTG	4514
Db	4267	AAATCCCTGAGGGCGACTGTGTAGTAGTTGCCACTGATGCTTGTGTACAGGGGTACACTG	4326
Qy	4515	GTGACTTTGATTCGTGTATGACTGCAGCTCATGTGTAGAGGCAATGTCATGTTTGACC	4574
Db	4327	GTGACTTTGATTCGTGTATGACTGCAGCTCATGTGTAGAGGCAATGTCATGTTTGACC	4386
Qy	4575	TTGACCTTACTTTTACCACATGGGTTCGTGTGTGCGGGGTTTCAGCAATAGTTAAAGGCC	4634
Db	4387	TTGACCTTACTTTTACCACATGGGTTCGTGTGTGCGGGGTTTCAGCAATAGTTAAAGGCC	4446
Qy	4635	AGCGTAGGGGCGCACAGGCGCTGGGAGAGCTGGCATATACTACTATGTAGACGGGAGTT	4694
Db	4447	AGCGTAGGGGCGCACAGGCGCTGGGAGAGCTGGCATATACTACTATGTAGACGGGAGTT	4506
Qy	4695	GTACCCCTTCGGGTPATGGTTCCTGAATGCAACAATGTTGAAGCCTTCGACGCAAGCAAGG	4754
Db	4507	GTACCCCTTCGGGTPATGGTTCCTGAATGCAACAATGTTGAAGCCTTCGACGCAAGCAAGG	4566

Qy 4755 CATGGTATGGTTGTGCATCAACAGAGCTCAAACCTAATCTGGACACCTATCGCACCCAAAC 4814
Db 4567 CATGGTATGGTTGTGCATCAACAGAGCTCAAACTATTCTTGGACACCTATCGCACCCAAAC 4626
Qy 4815 CTGGGTTACCTGGCATAGGAGCAAAATTTGGACGAGTGGGCTGATCTCTTTCTATGTGCA 4874
Db 4627 CTGGGTTACCTGGCATAGGAGCAAAATTTGGACGAGTGGGCTGATCTCTTTCTATGTGCA 4686
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Qy 5175 TAGCCATGACACTTTTGGCCGCACTTGTGTGGCGGCTGTGCTTATTAATCATAGTCC 5234
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Qy 6015 CCCGACGAGGATGATGGGCGCTCATTTGCTTGGGCTCTAGAGATTTGGCAGTATGTT 6074
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Db 6727 GTCTGAAAGCGCTGCAACGAAAGTGACCCGTTAGAAAGGTCCTTCAAMCCTCCCTTCTTCAC 6786
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Db 6787 CACCTGTTCTACAGTGGCCATGCCGATGCCCTCTGTTGGAGCGGTGAGTGTAACCCCTT 6846
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Qy 7452 CATACCAACAGCAAGTGAGATTGGTTAAAGAAAAAGCTTCAAAAGTTGTCGGTGTCATG 7511
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Db 7447 AGTGTGTCGAGCAGGTGAGATACCGAGTCAATTATCGGCAAACTGTGTAGTTCCAAAG 7506
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Db 7507 AGGAGTCTTCGTGAAGACCCCGCAACCAACAAAGAACCCCAAGGCTTATCTCGT 7566
Qy 7752 ACCCCACCTTCAAAATGAGATGTTGTGAAGATGTACTACGGTCAGGTTGCTCCTGACG 7811
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Qy 7932 ACAGTACCATCACCCGAGGATATCATGGTGGAGACAGACATCTACTCAGCAGCTAAAC 7991
Db 7747 ACAGTACCATCACCCGAGGATATCATGGTGGAGACAGACATCTACTCAGCAGCTAAAC 7806
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Search completed: October 30, 2005, 23:28:10

Job time : 991 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 10:18:21 ; Search time 4375 Seconds

(without alignments)
17743.142 Million cell updates/sec

Title: US-10-009-002-1

Perfect score: 9399

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Gapop 10.0 , Gapext 1.0

Searched: 9784742 seqs, 4129495052 residues

Total number of hits satisfying chosen parameters: 19569484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	9386.2	99.9	9399	19 US-10-189-359-2	Sequence 2, Appli
3	9059.8	96.4	9143	8 US-08-424-550B-390	Sequence 390, App
4	9059.8	96.4	9143	8 US-08-424-550B-393	Sequence 393, App
5	8692.6	92.5	8912	8 US-08-424-550B-11	Sequence 11, Appl

6	4159	44.2	4268	8	US-08-424-550B-80	Sequence 80, Appl
7	449.8	4.8	479	8	US-08-424-550B-25	Sequence 25, Appl
8	449.8	4.8	479	8	US-08-424-550B-392	Sequence 392, App
9	319.6	3.4	337	8	US-08-424-550B-29	Sequence 29, Appl
10	319.6	3.4	337	8	US-08-424-550B-159	Sequence 159, App
11	279.4	3.0	281	8	US-08-424-550B-18	Sequence 18, Appl
12	279.4	3.0	281	8	US-08-424-550B-20	Sequence 20, Appl
13	262.4	2.8	5211	17	US-10-328-127-1	Sequence 1, Appl
14	262.4	2.8	5211	17	US-10-328-206-1	Sequence 1, Appl
15	262.4	2.8	5211	26	US-11-140-379-1	Sequence 1, Appl
16	256	2.7	9609	20	US-10-333-449A-33	Sequence 33, Appl
17	254.4	2.7	260	19	US-10-189-359-1	Sequence 1, Appl
18	252.6	2.7	2061	9	US-09-929-955-16	Sequence 16, Appl
19	252.6	2.7	2061	11	US-09-930-591-1	Sequence 1, Appl
20	252.6	2.7	2061	18	US-10-307-047-1	Sequence 1, Appl
21	252.6	2.7	2061	21	US-10-817-591-16	Sequence 16, Appl
22	252.6	2.7	2061	26	US-11-043-808-1	Sequence 1, Appl
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25	250.8	2.7	2058	19	US-10-637-323-1	Sequence 1, Appl
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28	250.8	2.7	2058	21	US-10-899-715-1	Sequence 1, Appl
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36	247.6	2.6	5965	21	US-10-492-178-10	Sequence 10, Appl
37	244.4	2.6	9646	9	US-09-742-659-3	Sequence 3, Appl
38	244	2.6	1893	16	US-10-214-932-77	Sequence 77, Appl
39	243	2.6	9365	10	US-09-827-688-7	Sequence 7, Appl
40	243	2.6	9416	9	US-09-929-955-13	Sequence 13, Appl
41	243	2.6	9416	14	US-10-104-966-13	Sequence 13, Appl
42	243	2.6	9416	19	US-10-719-619-13	Sequence 13, Appl
43	243	2.6	9416	21	US-10-817-591-13	Sequence 13, Appl
44	243	2.6	12980	9	US-09-238-076-5	Sequence 5, Appl
45	243	2.6	12980	10	US-09-995-937-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09742659
; Patent No. US20010034019A1
; GENERAL INFORMATION:
; APPLICANT: Hong, Zhi
; APPLICANT: Butkiewicz, Nancy J.
; APPLICANT: Zhong, Weidong
; APPLICANT: Ingravallo, Paul
; APPLICANT: Wright-Minogue, Jacquelyn
; APPLICANT: Lau, Johnson Y.
; APPLICANT: Lemon, Stanley M.
; TITLE OF INVENTION: Chimeric HCV/GBV-B viruses
; FILE REFERENCE: ID01116
; CURRENT APPLICATION NUMBER: US/09/742,659
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/171,469
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9399
; TYPE: DNA
; ORGANISM: GB virus-B
US-09-742-659-1

Query Match 100.0%; Score 9399; DB 9; Length 9399;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 9399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Ds	181	CCTGATGGCGTTCAATGGTTGCGTGGTGGCGCTTTAGGCAGCCTCCAGCCACCA	240
Qy	241	CCTCCAGATAGAGCGCGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACG	300
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Ds	301	CAGACCTCTTTTGGATATACGCTCCGGAAGTAGTTGGGCAAGCCCACTATATGTGT	360
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Ds	1141	GACCTGTGACGCCCTTGACATTTGGTGTGTTGTGGTGTGTATATTAGTCGGTGACTG	1200
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Qy	4081	GTACCTGACCGG	AGCATGTTCCCGAACTAT	GATGTAATCAATTTGTGACGAATGCCATGC	4140
Db	4081	GTACCTGACCGG	AGCATGTTCCCGAACTAT	GATGTAATCAATTTGTGACGAATGCCATGC	4140
Qy	4141	TACCGATGCAAC	CAACCGTGTGGGCA	TTGGAAAGGCTCTAACCGAAGCTCCATCCAAAA	4200
Db	4141	TACCGATGCAAC	CAACCGTGTGGGCA	TTGGAAAGGCTCTAACCGAAGCTCCATCCAAAA	4200
Qy	4201	TGTTAGGCTAGTGT	CTTGCCACGGCTAC	CCCCCTTGGAGTAAATCCCTACACCATGTC	4260
Db	4201	TGTTAGGCTAGTGT	CTTGCCACGGCTAC	CCCCCTTGGAGTAAATCCCTACACCATGTC	4260
Qy	4261	CAACAATGAGAT	TTCAATTAACCGAT	GAAGGCATATCCCTTTTATGGAATAAGAT	4320
Db	4261	CAACAATGAGAT	TTCAATTAACCGAT	GAAGGCATATCCCTTTTATGGAATAAGAT	4320
Qy	4321	TAAGGAGAAATCT	GAGAAAGGGAGAC	CACTTATCTTTAGGCTTACCAAAAAACACTG	4380

Db 4321 TAAGGAGGAAAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG 4380
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Db 4381 TGATGAGCTTGCTAACGAGTTAGCTCGAAGGGAATAACAGCTGCTCTTACTATAGGG 4440
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Db 4501 TACAGGGTACACTGGTGACTTTGATTCCTGGTATGACTGACGCTCATGGTAGAAGGCAC 4560
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Db 4561 ATGCCATGTTGACCTTTGACCTTACTTTACCATGGGTGTTCTGTGTGGGGTTTCAGC 4620
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Db 4621 AATAGTTAAAGGCCAGCGTAGGGGCGGCACAGGCCGTGGGAGAGCTGGGCATATACTACTA 4680
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Db 4681 TGTAGACGGAGTTGTACCCCTTCCGGTATGGTTCTGAAATGCAACATTTGTTGAAAGCCTT 4740
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DB 3421 GTATACTGCTCACCATGGCAGCAAGGGGCGCGGTGGCTCATCCCAAGGCTCTATACA 3480
QY 3481 CCCAATAACCGTTGACGGGCTTAATGACAGGACATCTATCAACACCATGTGGAGCTGG 3540
DB 3481 CCCAATAACCGTTGACGGGCTTAATGACAGGACATCTATCAACACCATGTGGAGCTGG 3540
QY 3541 GTCCTTTACTCGGTGCTCTTGGGGGAGACCAAGGGGTATCTGATGTAACACGACTGGGGTC 3600
DB 3541 GTCCTTTACTCGGTGCTCTTGGGGGAGACCAAGGGGTATCTGATGTAACACGACTGGGGTC 3600
QY 3601 ATTGGTTGAGGTCAACAAATCCGATGACCCCTTATTTGGTGTGTGCGGGGCGCTTCCCAT 3660
DB 3601 ATTGGTTGAGGTCAACAAATCCGATGACCCCTTATTTGGTGTGTGCGGGGCGCTTCCCAT 3660
QY 3661 GGCTGTTGCCAAGGCTTCTTCAGGTGCCCGCATTCGTGCTCCTCCGGGCGCATGTTATTGG 3720
DB 3661 GGCTGTTGCCAAGGCTTCTTCAGGTGCCCGCATTCGTGCTCCTCCGGGCGCATGTTATTGG 3720
QY 3721 GATGTTTCAACCGTCTAGAAAATTCGGCGGTTTCAGTCACTAGTCAGATTTAGGGTTAGCGCGTT 3780
DB 3721 GATGTTTCAACCGTCTAGAAAATTCGGCGGTTTCAGTCACTAGTCAGATTTAGGGTTAGCGCGTT 3780
QY 3781 GGTGTGCTGGATACCATCCCGAGTACACGACATGCGCATCTTGTATCAAAACCTTAC 3840
DB 3781 GGTGTGCTGGATACCATCCCGAGTACACGACATGCGCATCTTGTATCAAAACCTTAC 3840
QY 3841 TGTGCTTAACGAGTATTCAGTGCATAATTTAATTCGCCCGCTTGCAGCGGCAAGTCAAC 3900
DB 3841 TGTGCTTAACGAGTATTCAGTGCATAATTTAATTCGCCCGCTTGCAGCGGCAAGTCAAC 3900
QY 3901 CAAATTTACACCTTTCTTACATGACGAGAGATGATGAGTCTTGGTCTTAAATCCCAAGTGT 3960
DB 3901 CAAATTTACACCTTTCTTACATGACGAGAGATGATGAGTCTTGGTCTTAAATCCCAAGTGT 3960
QY 3961 GGCTACACAGCATCAATGCCAAAGTACATGCACGCGAGCTACGCGGCTGAATCCAAATGG 4020
DB 3961 GGCTACACAGCATCAATGCCAAAGTACATGCACGCGAGCTACGCGGCTGAATCCAAATGG 4020
QY 4021 CTATTTTAAATGGCAAAATGTACCACACAGGGGCTTCACTTACGTACAGCACATATGGCAT 4080
DB 4021 CTATTTTAAATGGCAAAATGTACCACACAGGGGCTTCACTTACGTACAGCACATATGGCAT 4080
QY 4081 GTACCTGACCGGAGCATGTTCCCGGAACCTATGATGTAATCTTGTGACGAATGCCATGC 4140
DB 4081 GTACCTGACCGGAGCATGTTCCCGGAACCTATGATGTAATCTTGTGACGAATGCCATGC 4140
QY 4141 TACCGATGCAACCAACCGTGTGGGCAATTTGGAAGGTCTTAACCGAAGCTCCATCCAAAAA 4200
DB 4141 TACCGATGCAACCAACCGTGTGGGCAATTTGGAAGGTCTTAACCGAAGCTCCATCCAAAAA 4200
QY 4201 TGTTAGGCTAGTGGTCTTGGCCAGGCTACCCCGCTGGAGTAATCCCTTACACCATATGC 4260
DB 4201 TGTTAGGCTAGTGGTCTTGGCCAGGCTACCCCGCTGGAGTAATCCCTTACACCATATGC 4260
QY 4261 CAACATAAATCTGAGATTTCAATTAACCGATGAAGGCACTATCCCTTTTCAATGGAAGGAT 4320
DB 4261 CAACATAAATCTGAGATTTCAATTAACCGATGAAGGCACTATCCCTTTTCAATGGAAGGAT 4320
QY 4321 TAAGGAGGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACATG 4380
DB 4321 TAAGGAGGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACATG 4380

QY 4381 TGATGAGCTTGCTAAACGAGTTAGCTCGAAAGGGAATAACAGCTGCTCTCTTACTATAGGGG 4440
DB 4381 TGAATGAGCTTGCTAAACGAGTTAGCTCGAAAGGGAATAACAGCTGCTCTCTTACTATAGGGG 4440
QY 4441 ATGTGACATCTCAAAAAATCCCTGAGGGCGACTGTGTAGTAGTTGCCACTGATGCTTGTG 4500
DB 4441 ATGTGACATCTCAAAAAATCCCTGAGGGCGACTGTGTAGTAGTTGCCACTGATGCTTGTG 4500
QY 4501 TACAGGGGTACACTGGTACACTTTGATTCCGTGTATGACTGACAGCCCTCATGTTAGAGGCAC 4560
DB 4501 TACAGGGGTACACTGGTACACTTTGATTCCGTGTATGACTGACAGCCCTCATGTTAGAGGCAC 4560
QY 4561 ATGCCATGTTGACCTTACACCTTACTTTCAACATGGGTGTTCTGTGTGCGGGGTTTACG 4620
DB 4561 ATGCCATGTTGACCTTACACCTTACTTTCAACATGGGTGTTCTGTGTGCGGGGTTTACG 4620
QY 4621 AATAGTTAAAGGCCAGCGTATAGGGGCCGACAGCGCGTGGGAGAGCTGGCATATATCTACTA 4680
DB 4621 AATAGTTAAAGGCCAGCGTATAGGGGCCGACAGCGCGTGGGAGAGCTGGCATATATCTACTA 4680
QY 4681 TGTAGACGGGAGTTGTACCCCTTCGGGTATGGTTTCTCTGAAATGCAACATTTTGAAGCCCT 4740
DB 4681 TGTAGACGGGAGTTGTACCCCTTCGGGTATGGTTTCTCTGAAATGCAACATTTTGAAGCCCT 4740
QY 4741 CGACCGACGCAAGGCGATGTTGTTGTCATCAACAGAGCTCAAACTATTTCTGGACAC 4800
DB 4741 CGACCGACGCAAGGCGATGTTGTTGTCATCAACAGAGCTCAAACTATTTCTGGACAC 4800
QY 4801 CTATGCGCACCCAACTCTGGGTTACCTGCGATAGAGAGCAAAATTTGGACGAGTGGGTGATCT 4860
DB 4801 CTATGCGCACCCAACTCTGGGTTACCTGCGATAGAGAGCAAAATTTGGACGAGTGGGTGATCT 4860
QY 4861 CTTTTCCTATGTTGTCACCCCGAACCTTCAATTTGTCAATCTGCAAAAAGAACTGCTGACAA 4920
DB 4861 CTTTTCCTATGTTGTCACCCCGAACCTTCAATTTGTCAATCTGCAAAAAGAACTGCTGACAA 4920
QY 4921 TTAATGTTTGTGACTGACGCCCACTACAACTGTGTCTCATGATATGGCTATGTGCTGCC 4980
DB 4921 TTAATGTTTGTGACTGACGCCCACTACAACTGTGTCTCATGATATGGCTATGTGCTGCC 4980
QY 4981 CAATGACGCAACAACGTTGGAGGAGCCCGCTTGGGAAAAAACTTGTGGGGTTCTGTG 5040
DB 4981 CAATGACGCAACAACGTTGGAGGAGCCCGCTTGGGAAAAAACTTGTGGGGTTCTGTG 5040
QY 5041 GCGCTTGGACGGCGCTGACCGCTGCTGGCCAGAGCCAGCGAGGTGACAGATACCA 5100
DB 5041 GCGCTTGGACGGCGCTGACCGCTGCTGGCCAGAGCCAGCGAGGTGACAGATACCA 5100
QY 5101 AATGTGCTTCACTGAAGTCAATCTTCTGGGACAGCCGCACTCGCTGTTGGCGTTGGAGT 5160
DB 5101 AATGTGCTTCACTGAAGTCAATCTTCTGGGACAGCCGCACTCGCTGTTGGCGTTGGAGT 5160
QY 5161 GGCTATGGCTTATCTAGCCATGACATTTTGGCGCCACTTGTGTGCGGGCTGTGCTGTC 5220
DB 5161 GGCTATGGCTTATCTAGCCATGACATTTTGGCGCCACTTGTGTGCGGGCTGTGCTGTC 5220
QY 5221 TATTTACATCAGTCCCTACCGGTGCTATGTCGCCCGCAGTGGTTCACGAAGAAATCGT 5280
DB 5221 TATTTACATCAGTCCCTACCGGTGCTATGTCGCCCGCAGTGGTTCACGAAGAAATCGT 5280
QY 5281 GGAGGAGTGTGCATCATTTCACTTCCCTTGGAGGCCATGGTCTGCAATTTGACAGCTGAA 5340
DB 5281 GGAGGAGTGTGCATCATTTCACTTCCCTTGGAGGCCATGGTCTGCAATTTGACAGCTGAA 5340
QY 5341 GAGTACAAATCAACCAACTAGTCTTCAATTTGGAAACCCGCCCTTGAACAACTTAAACAC 5400
DB 5341 GAGTACAAATCAACCAACTAGTCTTCAATTTGGAAACCCGCCCTTGAACAACTTAAACAC 5400
QY 5401 CTTTCTTGGGCTCATGACGCTCAATCTTGTCTATCATAGATATTCCTGCTGTTTGTAGT 5460
DB 5401 CTTTCTTGGGCTCATGACGCTCAATCTTGTCTATCATAGATATTCCTGCTGTTTGTAGT 5460
QY 5461 CACTTTTACCTGACAAATCCCTTTTGATCATGCTGTTGCTTTTCTTTCATTTGCGGGTATTACTAC 5520


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QY 7681 AGTTCCAAAGGAGGAGGCTTTCGTGAAGACCCCCAGAAACCAACAAAGAAACCCCAAG 7740
Db 7681 AGTTCCAAAGGAGGAGGCTTTCGTGAAGACCCCCAGAAACCAACAAAGAAACCCCAAG 7740
QY 7741 GCTTATCTCGTACCCCAACCTTGAATGAGATGTGTGAGAAGATGTACTACGGTCAGGT 7800
Db 7741 GCTTATCTCGTACCCCAACCTTGAATGAGATGTGTGAGAAGATGTACTACGGTCAGGT 7800
QY 7801 TGCTCCTGACGTAGTTAAAGCTGTATGGGAGATCGGTACCGGTTTGTAGATCCAGCTAC 7860
Db 7801 TGCTCCTGACGTAGTTAAAGCTGTATGGGAGATCGGTACCGGTTTGTAGATCCAGCTAC 7860
QY 7861 CCGTGTCAAGGCTCTGTTGTGATGTGTGTCACCCGATGCGTGGAGCCACATGGATATAC 7920
Db 7861 CCGTGTCAAGGCTCTGTTGTGATGTGTGTCACCCGATGCGTGGAGCCACATGGATATAC 7920
QY 7921 AGTGTGTTTGAAGTACCATCACACCCGAGATATCATGTGGAGACAGACATCTACTC 7980
Db 7921 AGTGTGTTTGAAGTACCATCACACCCGAGATATCATGTGGAGACAGACATCTACTC 7980
QY 7981 AGCAGTAACTCAGTGAACCAACCGAGCTGGCATTCACACCATTCGAGGCACTTATA 8040
Db 7981 AGCAGTAACTCAGTGAACCAACCGAGCTGGCATTCACACCATTCGAGGCACTTATA 8040
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Db 8101 TTCGGGCTCTATACTACTCAAGTTTCAACAGTTTGAACCTGCTGGCTGAGAGTAAATGC 8160
QY 8161 TGCAGCCGAAACGGCTGGATGAAGAAACCTCGCTTCTTATTTGCGGCGATGATTCGAC 8220
Db 8161 TGCAGCCGAAACGGCTGGATGAAGAAACCTCGCTTCTTATTTGCGGCGATGATTCGAC 8220
QY 8221 CGTAATTTTGAAGAGCGCGGAGCAGATGCACAAACAAAGCAATGCGTGTCTTGTCTAG 8280
Db 8221 CGTAATTTTGAAGAGCGCGGAGCAGATGCACAAACAAAGCAATGCGTGTCTTGTCTAG 8280
QY 8281 CTGGATGAAGTGTAGTGGTGACCAACAGATTTGTGCTCAACCCAAATACAGTTTGA 8340
Db 8281 CTGGATGAAGTGTAGTGGTGACCAACAGATTTGTGCTCAACCCAAATACAGTTTGA 8340
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Db 8341 AGAATTAACATCATCTCATCAATTTACCTCTGGAATTACCAAAAGTGGCAAGCCTTA 8400
QY 8401 CTACTTTCTTACAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCGAGGGTCTGGG 8460
Db 8401 CTACTTTCTTACAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCGAGGGTCTGGG 8460
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Db 8461 ATACAACCCAGTGTGCGTGGATTTGGTATCTAATACATCACTACCCATGTTTGTGGT 8520
QY 8521 TAGCCGTGTGTGGCTGTCCATTTATGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA 8580
Db 8521 TAGCCGTGTGTGGCTGTCCATTTATGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA 8580
QY 8581 GACTGTGACCTTTGACTGTGTGGAAAAATATACGGTGCTGTAGAGATCTGCCAG 8640
Db 8581 GACTGTGACCTTTGACTGTGTGGAAAAATATACGGTGCTGTAGAGATCTGCCAG 8640
QY 8641 CATCATCTGTGTGCAAGTATTTAGGCTTTCTCGTGTGTGCGCTACACCAACGCTGA 8700
Db 8641 CATCATCTGTGTGCAAGTATTTAGGCTTTCTCGTGTGTGCGCTACACCAACGCTGA 8700
QY 8701 GATCTCTAGATTTTCCCAATCACTAACAGACATGACCATGCCCTCGGAGCTGGG 8760
Db 8701 GATCTCTAGATTTTCCCAATCACTAACAGACATGACCATGCCCTCGGAGCTGGG 8760
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QY 8761 AAAGAAAGCCAGGGCGGTCTCGCCAGCGCCAGAGGCGTGGCGAGCACACGCAAAATT 8820
Db 8761 AAAGAAAGCCAGGGCGGTCTCGCCAGCGCCAGAGGCGTGGCGAGCACACGCAAAATT 8820
QY 8821 GGCTCGCTTCTTCTCTGGCATGTCTACATCTAGACCTCTACAGATTTGGATAGACGAG 8880
Db 8821 GGCTCGCTTCTTCTCTGGCATGTCTACATCTAGACCTCTACAGATTTGGATAGACGAG 8880
QY 8881 CGTGGCTCGGTACACCACTTTCAATTTATTTGATGTTTACTCCCGAGGGGATGTGTT 8940
Db 8881 CGTGGCTCGGTACACCACTTTCAATTTATTTGATGTTTACTCCCGAGGGGATGTGTT 8940
QY 8941 TATTACACCAAGAGATTTGAGAGTTCTCTTGTGAAGTATTTGGCTGTCAATTTT 9000
Db 8941 TATTACACCAAGAGATTTGAGAGTTCTCTTGTGAAGTATTTGGCTGTCAATTTT 9000
QY 9001 TGCCCTAGGGCTCATTTGCTGTGGATTTAGCCATCAGCTGAACCCCAAAATTCAAAATTA 9060
Db 9001 TGCCCTAGGGCTCATTTGCTGTGGATTTAGCCATCAGCTGAACCCCAAAATTCAAAATTA 9060
QY 9061 CTAACAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGGCGAGCGCAACAGGGGAGACCCCGGC 9120
Db 9061 CTAACAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGGCGAGCGCAACAGGGGAGACCCCGGC 9120
QY 9121 TTAACGACCCCGCGATGTGAGTTTGGCGACCATGTGGATCAGAACCGTTTCGGGTGAA 9180
Db 9121 TTAACGACCCCGCGATGTGAGTTTGGCGACCATGTGGATCAGAACCGTTTCGGGTGAA 9180
QY 9181 GCCATGTCTGAAGGGATGACCTCTTCTGGCTCATCTCAAAAAACCGTCTCGGTGG 9240
Db 9181 GCCATGTCTGAAGGGATGACCTCTTCTGGCTCATCTCAAAAAACCGTCTCGGTGG 9240
QY 9241 GTGAGGAGTCTGCTGTGTGGAGGAGTCAAGTCAAGTATTAATCCCGTCTGTGTGACGC 9300
Db 9241 GTGAGGAGTCTGCTGTGTGGAGGAGTCAAGTCAAGTATTAATCCCGTCTGTGTGACGC 9300
QY 9301 CTCACGAGTATTTGTCCGCTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGTTTTTG 9360
Db 9301 CTCACGAGTATTTGTCCGCTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGTTTTTG 9360
QY 9361 TTCAAGCGGAGGGCAACCCCGCTTGGAAATTAATAACT 9399
Db 9361 TTCAAGCGGAGGGCAACCCCGCTTGGAAATTAATAACT 9399

RESULT 3
US-08-424-550B-390
; Sequence 390, Application US/08424550B
; Publication No. US2002011947A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESS: ABBOTT LABORATORIES D377/AP60
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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QY	1801	CGAAGCATGCGGTAAACAACATGCTAAACACCGATGGCAACAACGCGTACGCGCTGAA	1860		
Db	1801	CGAAGCATGCGGTAAACAACATGCTAAACACCGATGGCAACAACGCGTACGCGCTGAA	1860		
QY	1861	ATTGGCTATATACAAATACCTGGGTCTAAAGAAATGTTTAAACCTCATTAATGGATGTC	1920		
Db	1861	ATTGGCTATATACAAATACCTGGGTCTAAAGAAATGTTTAAACCTCATTAATGGATGTC	1920		
QY	1921	AGGCCATTTGATTTGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAA	1980		
Db	1921	AGGCCATTTGATTTGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAA	1980		
QY	1981	TTCCACTCTCTCAACAACCGAGAGTGGCTAGGTTGCCCGTACCCACCTGTGGTAGC	2040		
Db	1981	TTCCACTCTCTCAACAACCGAGAGTGGCTAGGTTGCCCGTACCCACCTGTGGTAGC	2040		
QY	2041	TGGTTCTTTGTTACAGGTTCCGCAAGGTTTTACAGTGAATGTAAGAACCTTAGCCACAGG	2100		
Db	2041	TGGTTCTTTGTTACAGGTTCCGCAAGGTTTTACAGTGAATGTAAGAACCTTAGCCACAGG	2100		
QY	2101	ATTGATCAACCAAGACAAAGCCTCGAAAAATTTATCAGGTCCTTATATTCGCGCAACGGGTGC	2160		
Db	2101	ATTGATCAACCAAGACAAAGCCTCGAAAAATTTATCAGGTCCTTATATTCGCGCAACGGGTGC	2160		
QY	2161	TTTGTCTCTTACGGGAGTTACCAACAGGCCGTGGTGCTAAATCTGTGGGTTGTGTGG	2220		
Db	2161	TTTGTCTCTTACGGGAGTTACCAACAGGCCGTGGTGCTAAATCTGTGGGTTGTGTGG	2220		
QY	2221	CAGCAAGTATCTTATTTAGCCTACCTCTGTGTACTTGTTCCTTTGTTGGCGCGCTTC	2280		
Db	2221	CAGCAAGTATCTTATTTAGCCTACCTCTGTGTACTTGTTCCTTTGTTGGCGCGCTTC	2280		
QY	2281	TGGTTACCCCTTTGCGTCTGCTGCCATCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340		
Db	2281	TGGTTACCCCTTTGCGTCTGCTGCCATCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340		
QY	2341	TTTGTCTAAAGCTCAAGTAGCTCCCTTTGCTTTGATTTTCTTCACTGTGTCTATCTCG	2400		
Db	2341	TTTGTCTAAAGCTCAAGTAGCTCCCTTTGCTTTGATTTTCTTCACTGTGTCTATCTCG	2400		
QY	2401	CTGCAAGCTACGTTATGCTGCCCTTTTAGGTTTGTGGCCATAGGCTGGCGGCTTGCCCT	2460		
Db	2401	CTGCAAGCTACGTTATGCTGCCCTTTTAGGTTTGTGGCCATAGGCTGGCGGCTTGCCCT	2460		
QY	2461	AACTTTCTTTGTGAGCAGCTGCTGCCAACAGATTATGACTGGTGGTGCAGTCTGT	2520		
Db	2461	AACTTTCTTTGTGAGCAGCTGCTGCCAACAGATTATGACTGGTGGTGCAGTCTGT	2520		
QY	2521	AGTGCAGGGTTAGTTTGTGGCGCGCGGTAAACCGTGGTCAACCGATAGCTCTGCTTGT	2580		
Db	2521	AGTGCAGGGTTAGTTTGTGGCGCGCGGTAAACCGTGGTCAACCGATAGCTCTGCTTGT	2580		
QY	2581	AGGTCTTTGGCCTCTGTTAGCGCTTTTAAACCTCTTGCAATTGGTTAGCCTGCTTACG	2640		
Db	2581	AGGTCTTTGGCCTCTGTTAGCGCTTTTAAACCTCTTGCAATTGGTTAGCCTGCTTACG	2640		
QY	2641	TTTTGATACCGAGATAATTTGGAGGCTGACATACCACTGCTGCTGCTTGTGTCAT	2700		
Db	2641	TTTTGATACCGAGATAATTTGGAGGCTGACATACCACTGCTGCTGCTTGTGTCAT	2700		
QY	2701	GTCTCGTTTGGCTTTCTTTGCTCACTTGTCTACCTCGCTGTGCTTTAGTTAACTCCATCT	2760		
Db	2701	GTCTCGTTTGGCTTTCTTTGCTCACTTGTCTACCTCGCTGTGCTTTAGTTAACTCCATCT	2760		
QY	2761	TTGGCAACGTTGGGAGAAATGTTTTGGAAAGTTTACATTAAGACCGGAGAGTTTTTCCT	2820		
Db	2761	TTGGCAACGTTGGGAGAAATGTTTTGGAAAGTTTACATTAAGACCGGAGAGTTTTTCCT	2820		
QY	2821	TGTGCTGTTTCTTTCCCGGTGGACATATACCGCGTGGTGTCTTTCTGTGTGTGTCA	2880		
Db	2821	TGTGCTGTTTCTTTCCCGGTGGACATATATACCGCGTGGTGTCTTTCTGTGTGTGTCA	2880		
QY	2881	CGTAGCTCTTCTATGTTTTAAATCCAGTGCAGCATCGTTCTTTTGGGACTGACTCTAGGGT	2940		
Db	2881	CGTAGCTCTTCTATGTTTTAAATCCAGTGCAGCATCGTTCTTTTGGGACTGACTCTAGGGT	2940		
QY	2941	TAGGGCCCATAGAAATGTTGGTGGTCTCGGAAAGTGTCTCATCTTGGTATGT	3000		
Db	2941	TAGGGCCCATAGAAATGTTGGTGGTCTCGGAAAGTGTCTCATCTTGGTATGT	3000		
QY	3001	TCTTAAAGTTTTCTCTTAGTGTGTTGGTGAATGGTGTGTTTTCTATAAGCACTTGA	3060		
Db	3001	TCTTAAAGTTTTCTCTTAGTGTGTTGGTGAATGGTGTGTTTTCTATAAGCACTTGA	3060		
QY	3061	TGGTGAATGTTTGGCTTAATGATTTTGGCTCGAAACTACCATTCGAAGACCATTTTCCC	3120		
Db	3061	TGGTGAATGTTTGGCTTAATGATTTTGGCTCGAAACTACCATTCGAAGACCATTTTCCC	3120		
QY	3121	TTTTGAAGCAAGCAAGGCTTATAGGAATGAAGAAAGACGCTTGGCGTGTGGGACAC	3180		
Db	3121	TTTTGAAGCAAGCAAGGCTTATAGGAATGAAGAAAGACGCTTGGCGTGTGGGACAC	3180		
QY	3181	GTTTGAATGTTTGGCGGCTTGTGGCGGCTCTCGCGGACCTTGTTCGACAGGTTGGCTAT	3240		
Db	3181	GTTTGAATGTTTGGCGGCTTGTGGCGGCTCTCGCGGACCTTGTTCGACAGGTTGGCTAT	3240		
QY	3241	GCGCCAGATGGGTGGCCATTAACCGACCTTTTACGCTGCAGTGTCTCTCTGAACGTGG	3300		
Db	3241	GCGCCAGATGGGTGGCCATTAACCGACCTTTTACGCTGCAGTGTCTCTCTGAACGTGG	3300		
QY	3301	CACGCTGCACGGATGGCAGTGGTATGACCTGGTATAGACCCCGAACCTCGACCTGGAAC	3360		
Db	3301	CACGCTGCACGGATGGCAGTGGTATGACCTGGTATAGACCCCGAACCTCGACCTGGAAC	3360		
QY	3361	TATCTTCAGATTAGGATCTCTGGGCCACTAGTACATAGGGATTTGTTGTGACAACTGT	3420		
Db	3361	TATCTTCAGATTAGGATCTCTGGGCCACTAGTACATAGGGATTTGTTGTGACAACTGT	3420		
QY	3421	GTATACTGCTCACATGGCAGCAAGGGCGCGGTGGCTCATCCCAACAGGCTCTATACA	3480		
Db	3421	GTATACTGCTCACATGGCAGCAAGGGCGCGGTGGCTCATCCCAACAGGCTCTATACA	3480		
QY	3481	CCCAATTAACCGTTGACCGGCTAATGACCAAGACATCTATCAACACCATGTGGAGCTGG	3540		
Db	3481	CCCAATTAACCGTTGACCGGCTAATGACCAAGACATCTATCAACACCATGTGGAGCTGG	3540		
QY	3541	GTCCCTTACTCGGTGCTCTTGGCGGGAGACCAAGGGTATCTGGTAAACGACTGGGCTC	3600		
Db	3541	GTCCCTTACTCGGTGCTCTTGGCGGGAGACCAAGGGTATCTGGTAAACGACTGGGCTC	3600		
QY	3601	ATTGGTTGAGTCAACAAATCCGATGACCTTATTTGGTGTGTGCGGGGCGCTTCCCAT	3660		
Db	3601	ATTGGTTGAGTCAACAAATCCGATGACCTTATTTGGTGTGTGCGGGGCGCTTCCCAT	3660		
QY	3661	GGCTGTTGCCAAGGTTCTTCAGGTGCCCGATTCGTGCTCTCCCGGCGATGTTATTGG	3720		
Db	3661	GGCTGTTGCCAAGGTTCTTCAGGTGCCCGATTCGTGCTCTCCCGGCGATGTTATTGG	3720		
QY	3721	GATGTTCAACCGCTCTAGAAATTTCTGGCGGTTTCACTAGTCAAGTATAGGGTTAGCCGTT	3780		
Db	3721	GATGTTCAACCGCTCTAGAAATTTCTGGCGGTTTCACTAGTCAAGTATAGGGTTAGCCGTT	3780		
QY	3781	GGTGTGCTGGATACCAATCCCAAGTACACAGACATGCCACTCTTTGATACAAAACCTTAC	3840		
Db	3781	GGTGTGCTGGATACCAATCCCAAGTACACAGACATGCCACTCTTTGATACAAAACCTTAC	3840		
QY	3841	TGTCCTTAAACAGTATTCAGTGCAAAATTTTAAATTTGCCCCCACTGGCAGCGGCAAGTCAAC	3900		
Db	3841	TGTCCTTAAACAGTATTCAGTGCAAAATTTTAAATTTGCCCCCACTGGCAGCGGCAAGTCAAC	3900		
QY	3901	CAAAATTACCACTTTCTTACATGCAGGAGAAAGTATGAGGTCTTTGGTCTTAAATCCCAGTGT	3960		
Db	3901	CAAAATTACCACTTTCTTACATGCAGGAGAAAGTATGAGGTCTTTGGTCTTAAATCCCAGTGT	3960		
QY	3961	GGCTACAAACAGCATCAATGCCAAAGTACATGCACGGCAGTACGGCGGTGAATCCAAATTG	4020		
Db	3961	GGCTACAAACAGCATCAATGCCAAAGTACATGCACGGCAGTACGGCGGTGAATCCAAATTG	4020		

3	361	GGCTACAAACAGCATCAATGCGCAAAAGTACATGCAACGCGACGTCGCGCGTGAATCCAAATTG	4020
Qy	4021	CTATTTTAAATGGCAAAATGTACCAACACAGAGGGCTTTCACTTACGTACAGCACATATGGCAT	4080
	4021	CTATTTTAAATGGCAAAATGTACCAACACAGAGGGCTTTCACTTACGTACAGCACATATGGCAT	4080
	4081	GTACTGTACCGGAGCATGTTCCCGGAACATAATGATGTAATCATTTTGTGACGAATGCCATGC	4140
Db	4081	GTACTGTACCGGAGCATGTTCCCGGAACATAATGATGTAATCATTTTGTGACGAATGCCATGC	4140
	4141	TACCGATGCAACCAACCGGTGTTGGGCATTGGAAAGGTCTTAACCGAAGCTCCATCCCAAAAA	4200
	4141	TACCGATGCAACCAACCGGTGTTGGGCATTGGAAAGGTCTTAACCGAAGCTCCATCCCAAAAA	4200
Qy	4201	TGTTAGGCTAGTGGTCTCTTGCCACGGCTACCCCCCTCGAGTAATCCTTACACCAATGC	4260
	4201	TGTTAGGCTAGTGGTCTCTTGCCACGGCTACCCCCCTCGAGTAATCCTTACACCAATGC	4260
	4261	CAACATTAACGTGAGATTCAATTAAACCGATGAAGGCACATATCCCTTTCATGGAAAAAAGAT	4320
Db	4261	CAACATTAACGTGAGATTCAATTAAACCGATGAAGGCACATATCCCTTTCATGGAAAAAAGAT	4320
	4321	TAAGGAGGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
	4321	TAAGGAGGAAATCTGAAGAAAGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
Qy	4381	TGATGAGCTTGCTAAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGG	4440
	4381	TGATGAGCTTGCTAAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGG	4440
	4441	ATGTGACATCTCAAAAAATCCCTGAGGCGCATGTGTAGTAGTTGGCCACTGATGCTTGTG	4500
Db	4441	ATGTGACATCTCAAAAAATCCCTGAGGCGCATGTGTAGTAGTTGGCCACTGATGCTTGTG	4500
	4501	TACAGGGTACACTGGTGACATTGATTCGGTGATGACTGCAGCCTCATGTAGAGGCAC	4560
	4501	TACAGGGTACACTGGTGACATTGATTCGGTGATGACTGCAGCCTCATGTAGAGGCAC	4560
Qy	4561	ATGCATGTTTGACCTTCGACCTACTTTTACCATGGGTGTTCTGTGTGTCGGGGTTTCAGC	4620
	4561	ATGCATGTTTGACCTTCGACCTACTTTTACCATGGGTGTTCTGTGTGTCGGGGTTTCAGC	4620
	4621	AATAGTTAAAGGCCAGCGTAGGGGCCGACAGGCCGTTGGGAGAGCTGGCATATACTACTA	4680
Db	4621	AATAGTTAAAGGCCAGCGTAGGGGCCGACAGGCCGTTGGGAGAGCTGGCATATACTACTA	4680
	4681	TGTAGACGGAGTTGTACCCCTTCGGGTATGGTTCCTGGAATGCAATCTGTTGAGGCTT	4740
	4681	TGTAGACGGAGTTGTACCCCTTCGGGTATGGTTCCTGGAATGCAATCTGTTGAGGCTT	4740
Qy	4741	CGACGACGCCAAGGCATGTTGTTGTCATCAACAGAAGCTCAAACTATCTTGACAC	4800
	4741	CGACGACGCCAAGGCATGTTGTTGTCATCAACAGAAGCTCAAACTATCTTGACAC	4800
	4801	CTATTCGACCCAAACCTGGGTACTCCTGCGATAGGAGCAAAATTTGACGAGTGGGCTGATCT	4860
Db	4801	CTATTCGACCCAAACCTGGGTACTCCTGCGATAGGAGCAAAATTTGACGAGTGGGCTGATCT	4860
	4861	CTTTTCTATGGTCAACCCCGAAACCTTCAITTTGTCAATCTGCAAAAAAGAACTGCTGACAA	4920
	4861	CTTTTCTATGGTCAACCCCGAAACCTTCAITTTGTCAATCTGCAAAAAAGAACTGCTGACAA	4920
Qy	4921	TTATGTTTTTGTGATCTGACGCCAACTACAACTGTGTGCATCAGTATGGCTATGCTGCTCC	4980
	4921	TTATGTTTTTGTGATCTGACGCCAACTACAACTGTGTGCATCAGTATGGCTATGCTGCTCC	4980
	4981	CAATGACGCACCAACCGGTGGCAGGGAGCCCGCTTGGGAAAAAAACCTTGTGGGGTTCGTG	5040
Db	4981	CAATGACGCACCAACCGGTGGCAGGGAGCCCGCTTGGGAAAAAAACCTTGTGGGGTTCGTG	5040
	5041	CGCCTTGGACGGCGCTGACGCTGTCTGTGCCACCAAGAGCCAGCGAGGTGACCAAGATACCA	5100
	5041	CGCCTTGGACGGCGCTGACGCTGTCTGTGCCACCAAGAGCCAGCGAGGTGACCAAGATACCA	5100

Qy	5101	AATGTGCTTCAC	TGAAGTCAATA	ACTTCTCGGACAGCCGCAC	TGCGCTTGTGGCGCTTGGAGT	5160
Db	5101	AATGTGCTTCAC	TGAAGTCAATA	ACTTCTCGGACAGCCGCAC	TGCGCTTGTGGCGCTTGGAGT	5160
Qy	5161	GGCTATGGCTTAT	CTAGCCATTGACACT	TTTGGCGCCACTTGTGTGCGGCGT	TGCTGGTC	5220
Db	5161	GGCTATGGCTTAT	CTAGCCATTGACACT	TTTGGCGCCACTTGTGTGCGGCGT	TGCTGGTC	5220
Qy	5221	TATTACATCAGT	CCCTACCGGTGCTACT	GTGCGCCCGCAGTGGTTGACGAAAGAAAT	TCGT	5280
Db	5221	TATTACATCAGT	CCCTACCGGTGCTACT	GTGCGCCCGCAGTGGTTGACGAAAGAAAT	TCGT	5280
Qy	5281	GGAGGAGTGTG	CAATCAATCCCTTGGAGGCCAT	TGGTTGCTGCAAAATGCAAGCTGAA		5340
Db	5281	GGAGGAGTGTG	CAATCAATCCCTTGGAGGCCAT	TGGTTGCTGCAAAATGCAAGCTGAA		5340
Qy	5341	GAGTACAAATC	ACCAACTAGTCTCTTTCACATTTGGAAACGGCCCTT	TGAAAACTTAACAC		5400
Db	5341	GAGTACAAATC	ACCAACTAGTCTCTTTCACATTTGGAAACGGCCCTT	TGAAAACTTAACAC		5400
Qy	5401	CTTTCTTGGGCCT	CATGACAGTCAAAATCCTTGTGCTATCATAGAGTAT	TGCTGTGGTTTAGT		5460
Db	5401	CTTTCTTGGGCCT	CATGACAGTCAAAATCCTTGTGCTATCATAGAGTAT	TGCTGTGGCTTAGT		5460
Qy	5461	CACTTTACCTG	ACAATCCCTTTGCAATCATGCGTGT	TGCTTTTATTTGCGGGTATTA	CTAC	5520
Db	5461	CACTTTACCTG	ACAATCCCTTTGCAATCATGCGTGT	TGCTTTTATTTGCGGGTATTA	CTAC	5520
Qy	5521	CCCACTACCTT	CACAGATCAAAATGTTCTGTCAATTTTGGAGGGCGCAAT	TGCGTCCAA		5580
Db	5521	CCCACTACCTT	CACAGATCAAAATGTTCTGTCAATTTTGGAGGGCGCAAT	TGCGTCCAA		5580
Qy	5581	GCTTTACAGCG	CTAGAGGCGCACTGCGCTTCATATGCGCGGCGCTCGGGACACGCTCT		5640	
Db	5581	GCTTTACAGCG	CTAGAGGCGCACTGCGCTTCATATGCGCGGCGCTCGGGACACGCTCT		5640	
Qy	5641	TGGTACATGGA	CACTCGGTGGTTTGTCTTTGACATGCTAGCGCGCTATGCTGCCGCCTC		5700	
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Qy	5701	ATCCACTGCTT	GCAATTTAAATGCTTGATGGGTGAGTGGCCCACTATGAGTACAGCT		5760	
Db	5701	ATCCACTGCTT	GCAATTTAAATGCTTGATGGGTGAGTGGCCCACTATGAGTACAGCT		5760	
Qy	5761	TGCTGTTTGTAG	CTACTCCGCGTTCAATCCGCGCGCAGAGTGTGCGGGCTCTTGTTCAGC		5820	
Db	5761	TGCTGTTTGTAG	CTACTCCGCGTTCAATCCGCGCGCAGAGTGTGCGGGCTCTTGTTCAGC		5820	
Qy	5821	TTGTGCAATG	TTTGTGCAACACGACGAGGCCAGATCACTGGCCCAACAGACTTCTTAC		5880	
Db	5821	TTGTGCAATG	TTTGTGCAACACGACGAGGCCAGATCACTGGCCCAACAGACTTCTTAC		5880	
Qy	5881	TATGCTTTGTG	AGCAACACTGTATGTAAATGAGTACTTTATTTGCCACTCGTGACATCCG		5940	
Db	5881	TATGCTTTGTG	AGCAACAACACTGTATGTAAATGAGTACTTTATTTGCCACTCGTGACATCCG		5940	
Qy	5941	CAGGAAGATA	CTGGGCATTTCTGAGGCACTACCCCTCGAGTGTATATCAGCTTGCAT		6000	
Db	5941	CAGGAAGATA	CTGGGCATTTCTGAGGCACTACCCCTCGAGTGTATATCAGCTTGCAT		6000	
Qy	6001	CCGTTGCTCCA	CACCCCGACGAGGATGATTGCGGCCTCATTTGCTGGGCTAGAGAT		6060	
Db	6001	CCGTTGCTCCA	CACCCCGACGAGGATGATTGCGGCCTCATTTGCTGGGCTAGAGAT		6060	
Qy	6061	TTGGCAGTAT	GTGTGCAATTTCTTTGTGATTTGCTTTAATGTCTTAAAGCTGGAGTTCA		6120	
Db	6061	TTGGCAGTAT	GTGTGCAATTTCTTTGTGATTTGCTTTAATGTCTTAAAGCTGGAGTTCA		6120	
Qy	6121	GAGCATGGTT	TAACTTCCTCGGTTGTCTTCTTACAGCTGCCAGAGGGGTACAGGGCCC		6180	
Db	6121	GAGCATGGTT	TAACTTCCTCGGTTGTCTTCTTACAGCTGCCAGAGGGGTACAGGGCCC		6180	


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Qy 8401 CTACTTTCTTAAAGAGATCTCTGATCCCTTGGCAGGTGCTCTGCGAGGGTCTGGG 8460
Db 8401 CTACTTTCTTAAAGAGATCTCTGATCCCTTGGCAGGTGCTCTGCGAGGGTCTGGG 8460
Qy 8461 ATACAAACCCAGTGTGGTGGATTTGGGTATCTAATACATCACTACCCATGTTTGTGGT 8520
Db 8461 ATACAAACCCAGTGTGGTGGATTTGGGTATCTAATACATCACTACCCATGTTTGTGGT 8520
Qy 8521 TAGCGGTGTGTGGTGTCCATTTTCATGAGCAGATGCTCTTTGAGGACAACTTCCCGA 8580
Db 8521 TAGCGGTGTGTGGTGTCCATTTTCATGAGCAGATGCTCTTTGAGGACAACTTCCCGA 8580
Qy 8581 GACTGTGACCTTTGACTGTGATGGAAAAATTAACGGTGTCTGTAGAAGATCTGCCAG 8640
Db 8581 GACTGTGACCTTTGACTGTGATGGAAAAATTAACGGTGTCTGTAGAAGATCTGCCAG 8640
Qy 8641 CATCATTCGTGTGACGGTATTGAGGCTTTCTCGGTGTGGCTACACCAAGCTGA 8700
Db 8641 CATCATTCGTGTGACGGTATTGAGGCTTTCTCGGTGTGGCTACACCAAGCTGA 8700
Qy 8701 GATCTCAGATTTCCCAATCACTAAACAGATGACCATGCCCTGCCAGCTGGCG 8760
Db 8701 GATCTCAGATTTCCCAATCACTAAACAGATGACCATGCCCTGCCAGCTGGCG 8760
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Db 8761 AAAGAAAGCCAGGGCGGTCTCGCAGGCCAAGAGCGTGGCGAGCACACGAAAATT 8820
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Db 8821 GGCTCGCTTCTCTCGCATGTCTACATCTAGACCTTACACAGATTGGATAGACGAG 8880
Qy 8881 CGTGCCTGGTACACCACTTTCAATTATTGTGATGTTTACTCCCGAGGGGATGTGT 8940
Db 8881 CGTGCCTGGTACACCACTTTCAATTATTGTGATGTTTACTCCCGAGGGGATGTGT 8940
Qy 8941 TATTACACACAGAGAAATGTCAGAGTTCTCTGTGAAGTATTGGCTGTCAATTGTTTT 9000
Db 8941 TATTACACACAGAGAAATGTCAGAGTTCTCTGTGAAGTATTGGCTGTCAATTGTTTT 9000
Qy 9001 TGCCCTAGGGTCAATGCTGTGTGATAGCATGATGATGAAACCCCAAAATTA 9060
Db 9001 TGCCCTAGGGTCAATGCTGTGTGATAGCATGATGATGAAACCCCAAAATTA 9060
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Db 9061 TTAACAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGGCGAGCGGCAACAGGGGAGACCC 9120
Qy 9117 GGGCTTAACGACCCCGC 9133
Db 9121 GGGCTTAACGACCCCGC 9137
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RESULT 4

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US-08-424-550B-393
; Sequence 393, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 393:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9143 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..445
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 446..9037
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 9038..9143
; US-08-424-550B-393
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Query Match 96.4%; Score 9059.8; DB 8; Length 9143;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 9096; Conservative 0; Mismatches 37; Indels 4; Gaps 1;

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Db 1 ACCAACAACACTCCAGTTTGTACACTCCGCTAGGAATGCTCTGGAGCACCCCCCTAG 60

Qy 61 CAGGCGTGGGGGATTTCCCTCTGTCAGAAGGGTGGAGCCAAACCACTTAGTAT 120
Db 61 CAGGCGTGGGGGATTTCCCTCTGTCAGAAGGGTGGAGCCAAACCACTTAGTAT 120

Qy 121 GTAGCGCGGGACTCATGACGCTCGCGTGTATGACAAAGCGCCAGCTTGATGGTGC 180
Db 121 GTAGCGCGGGACTCATGACGCTCGCGTGTATGACAAAGCGCCAGCTTGATGGTGC 180

Qy 181 CCTGATGGCGGTTTCATGCGTTTGGTGTGGCGCTTTTAGGCAGCCTTCCACGCCCA 240
Db 181 CCTGATGGCGGTTTCATGCGTTTGGTGTGGCGCTTTTAGGCAGCCTTCCACGCCCA 240

Qy 241 CCTCCAGATAGAGCGCGGCTGTAGGAAAGACCGGGGACCGGTCACTACCAAGGACG 300
Db 241 CCTCCAGATAGAGCGCGGCTGTAGGAAAGACCGGGGACCGGTCACTACCAAGGACG 300

Qy 301 CAGACCTCTTTTGGATATCAGCGCTCCGGAAGTAGTTGGCAAGCCACCTATATGT 360
Db 301 CAGACCTCTTTTGGATATCAGCGCTCCGGAAGTAGTTGGCAAGCCACCTATATGT 360

Qy 361 TGGGATGTTGGGGTGTAGCCATCCATACCGTACTGCTGATAGGGTCTCTCGAGGGGAT 420
Db 361 TGGGATGTTGGGGTGTAGCCATCCATACCGTACTGCTGATAGGGTCTCTCGAGGGGAT 420
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DB 421 CTGGAGTCTCGTAGACCGTAGCACATGCTGTTATTTCTACTCAAAAGAGCTCTGTACC 480
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DB 481 TCGGCCAAGACCGCGAAGAACAGAGACGACGAGGTTCAATCTGTGTCATTAAAC 540
QY 541 ATCTGTGAAAGGGGACAAAGAGCAAGCGCAAGTCCAGCGCGATGCTCGGCCCTGTA 600
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QY 601 TTACAAAATTGCTGTATTCATGATGGCTTGAGACATTTGGCTCAGGCTGCTTTGCCACG 660
DB 601 TTACAAAATTGCTGTATTCATGATGGCTTGAGACATTTGGCTCAGGCTGCTTTGCCACG 660
QY 661 TCATGGTTGGGAGCGCCGAAGACCCCTCGGCATTAAGTCTCGCAATCTTTGGAATCTTCTGGA 720
DB 661 TCATGGTTGGGAGCGCCGAAGACCCCTCGGCATTAAGTCTCGCAATCTTTGGAATCTTCTGGA 720
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DB 721 TTACCCCTTTGGGTCGATTTGGTGATGTTACAACTCACACCTCTAGTAGGCCCGCTGGT 780
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QY 841 CTGGGCTACTGTTGGTTCGGTGCACCTTTTGTGTGATGTCGTCTATCTTTGGCCTG 900
DB 841 CTGGGCTACTGTTGGTTCGGTGCACCTTTTGTGTGATGTCGTCTATCTTTGGCCTG 900
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QY 1141 GACCTGTGACGCGCTTGACATTTGGTGAAGTTGTTGTTGCTGCTGATTTAGTCGGTGA 1200
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DB 1201 GCTTGTGAGGCTAGGCTTTATTCATAGACCTCAATGAACCTGGTACTGTTGTTACTGGA 1260
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DB 1321 CGAGGCTGTGATCTTTCTTGACCAAACTGGCTTTCACAAAGTACCATACGCTATTTCGAC 1380
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DB 1501 CAGGGTGCCCACTGATGCTCAATAGCTGAGTTTGTCTCGCCTTTGATGATACCATGTCC 1560
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DB 1561 TTGCCACTCTTATTTGAGTGAGATGCTCAGAAGTCATTTGTTACAGTCCAAAGTGAC 1620
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DB 1621 CAGGCTATCACTCTAGAGTATAAACAATCCATATCTTGGTACCCCTATACAATCCCTGG 1680
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DB 1681 TGCAGGGGATGTTATGTTTAAATCAAAAAATAACAATGAGGTTGCTGCCGTATTCGAA 1740
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DB 1741 TGTGCCATCGTACTGTCACATATGGGCACTGATGCGAGTGGAAACGACACTCGCACTTA 1800
QY 1801 CGAAGCATGCGGTGTAACACCATGCTTAAACAACCGCATGGCAACAGGCTCAGCCCTGAA 1860
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QY 1861 ATTGGCTATATTAACAATACCTGGTCTAAAGAAATGTTTAAACCTCAATATGATGTC 1920
DB 1861 ATTGGCTATATTAACAATACCTGGTCTAAAGAAATGTTTAAACCTCAATATGATGTC 1920
QY 1921 AGGCCATTTGTTATTTGAGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTA 1980
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DB 1981 TTCACTCTCTTACACCGAGAGTGGGCTAGGTTGCCCGGTACCCACCTGTGGTACG 2040
QY 2041 TGGTCTTGGTTA CAGGTTCCGCAAGGGTTTTACAGTATGTAAGAACCTTAGCCACAGG 2100
DB 2041 TGGTCTTGGTTA CAGGTTCCGCAAGGGTTTTACAGTATGTAAGAACCTTAGCCACAGG 2100
QY 2101 ATTGATCAACCAAGACAAAGCTCGGAAATATCAGTCTTATATTCGCGCACGGTGC 2160
DB 2101 ATTGATCAACCAAGACAAAGCTCGGAAATATCAGTCTTATATTCGCGCACGGTGC 2160
QY 2161 TTTGTCTCTTACGGGAGTTACACCAAGCGGTGGTCTAATTTCTGTTGGGTTGTGG 2220
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DB 2521 AGTGGCAGGTTAGTTTGTGGGCGGCGGTAAACGCTGCTCAACGCTAGCTCTCTTGT 2580
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Db	2581	AGTCTCTTGGCCCTCTGGTAGCGCTTTTAAACCCCTCTTGCAATTTGGCTACGCCCTGCTTCAGC	2641
Qy	2641	TTTTGATACCGAGATAAATTGGAGGGCTGACAAATACCACTGTAGCTAGCAATTAGTGTTCAT	2700
Db	2641	TTTTTGACACCGAGATAAATTGGAGGGCTGACAAATACCACTGTAGCTAGCAATTAGTGTTCAT	2700
Qy	2701	GTCTCGTTTTGGCTTCTTTGCTCACTTGTTTACTCTGGCTGGCTGCTTTAGTTAACTCCTATCT	2760
Db	2701	GTCTCGTTTTGGCTTCTTTGCTCACTTGTTTACTCTGGCTGGCTTGTAGTTAACTCCTATCT	2760
Qy	2761	TTGGCAACGTTTGGGAGAAATCGTTTTTGGAAAGTTTACATAAGACCGGAGAGGTTTTTCCT	2820
Db	2761	TTGGCAACGTTTGGGAGAAATCGTTTTTGGAAAGTTTACATAAGACCGGAGAGGTTTTTCCT	2820
Qy	2821	TGTGCTGTTTTGTTTTCCCGCGTGGACATATAGACCGCTGGTGACTTTCTGTGTGTGCTCA	2880
Db	2821	TGTGCTGTTTTGTTTTCCCGCGTGGACATATAGACCGCTGGTGACTTTCTGTGTGTGCTCA	2880
Qy	2881	CGTAGCTCTTCTATGTTTAAACATCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGT	2940
Db	2881	CGTAGCTCTTCTATGTTTAAACATCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGT	2940
Qy	2941	TAGGGCCCATAGAAATGTTGGTGGCTCTCGGAAGTGTCATGCTTGGTATTTCTCAATATGT	3000
Db	2941	TAGGGCCCATAGAAATGTTGGTGGCTCTCGGAAGTGTCATGCTTGGTATTTCTCAATATGT	3000
Qy	3001	TCTTAAAGTTTTCTCTTAGTGTTTGGTGAGAAATGGTGTGTTTTCTTATAGACACTTGC	3060
Db	3001	TCTTAAAGTTTTCTCTTAGTGTTTGGTGAGAAATGGTGTGTTTTCTTATAGACACTTGC	3060
Qy	3061	TGGTGATGCTTGCTTAATGATTTTGCTCGAAACTACCATTTGCAAGAGCCATTTTTCCC	3120
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Qy	3121	TTTTTGAAAGCAAGCGAGGCTATAGGAATGAAGGAAGACGCTTGGGTGTGGGGACAC	3180
Db	3121	TTTTTGAAAGCAAGCGAGGCTATAGGAATGAAGGAAGACGCTTGGGTGTGGGGACAC	3180
Qy	3181	GGTTGATGGTTTGCCGTTGTTCGGCGACTTCGGCGACCTTGTTTTTCGACGGGTTGGCTAT	3240
Db	3181	GGTTGATGGTTTGCCGTTGTTCGGCGACTTCGGCGACCTTGTTTTTCGACGGGTTAGCTAT	3240
Qy	3241	GCCGCCAGATGGGTGGGCCAATTACCGCACCTTTTACGCTCGAGTGTCTCTCTGAACGTGG	3300
Db	3241	GCCGCCAGATGGGTGGGCCAATTACCGCACCTTTTACGCTCGAGTGTCTCTCTGAACGTGG	3300
Qy	3301	CACGCTGTACCGATGGCAGTGCTATGACTGTGTATAGACCCCGAACTTGGACTGGAAC	3360
Db	3301	CACGCTGTACCGATGGCAGTGGTCACTGACTGGTATAGACCCCGAACTTGGACTGGAAC	3360
Qy	3361	TATCTTCAGATTAGATCTCTGGCCACTAGCTACATGGGATTTCTTTGTGACAACGTTT	3420
Db	3361	TATCTTCAGATTAGATCTCTGGCCACTAGCTACATGGGATTTCTTTGTGACAACGTTT	3420
Qy	3421	GTATATGCTCTCACCATGGCAGCAAGGGCGCGGTGGCTCATCCCCACAGGCTCTATACA	3480
Db	3421	GTATATGCTCTCACCATGGCAGCAAGGGCGCGGTGGCTCATCCCCACAGGCTCTATACA	3480
Qy	3481	CCCAATAACCGTTGACGCGGTAAATGACACAGGACATCTATCAACACCATGTGAGCTGG	3540
Db	3481	CCCAATAACCGTTGACGCGGTAAATGACACAGGACATCTATCAACACCATGTGAGCTGG	3540
Qy	3541	GTCCCTTACTCGGTGCTCTTCGGGGGAGACCAAGGGGTATCTGGTAAACGACTGGGGTC	3600
Db	3541	GTCCCTTACTCGGTGCTCTTCGGGGGAGACCAAGGGGTATCTGGTAAACGACTGGGGTC	3600
Qy	3601	ATTGGTTGAGTCAACAAATCCGATGACCCCTTATTGGTGTGTGTGCGGGGCCCTTCCCAT	3660
Db	3601	ATTGGTTGAGTCAACAAATCCGATGACCCCTTATTGGTGTGTGTGCGGGGCCCTTCCCAT	3660
Qy	3661	GGCTGTTGCCAAGGTTCTTCAGGTGCCCGGATTTCTGTGCTCTCCGGGCAATGTTATGG	3720
Db	3661	GGCTGTTGCCAAGGTTCTTCAGGTGCCCGGATTTCTGTGCTCTCCGGGCAATGTTATGG	3720

QY	3721	GATGTTCA	CGCGTCT	CTAGAA	AAATTTCTGCGG	GTTCAGT	GCAGAT	TATAGG	GTTCAGG	CCGCTT	3780	
DB	3721	GATGTTCA	CGCGTCT	CTAGAA	AAATTTCTGCGG	GTTCAGT	GCAGCAGAT	TATAGG	GTTCAGG	CCGCTT	3780	
QY	3781	GGTGTGCT	TGGATAC	CAATCCC	CAGTACAG	GACACATGCC	CACCTCTTG	GATACAAA	CCCTAC	3840		
DB	3781	GGTGTGCT	TGGATAC	CAATCCC	CAGTACAG	GACACATGCC	CACCTCTTG	GATACAAA	CCCTAC	3840		
QY	3841	TGTGCCTAA	ACGAGTAT	TTCAGT	GCAAAATTTTAA	TTTGCC	CCCCAC	TGGCAG	CGCGCA	AGTCAAC	3900	
DB	3841	TGTGCCTAA	ACGAGTAT	TTCAGT	GCAAAATTTTAA	TTTGCC	CCCCAC	TGGCAG	CGCGCA	AGTCAAC	3900	
QY	3901	CAAAATTAC	CACTTTCT	TTCATG	CAGGAGAA	GTATGAGG	TCTTGCT	CTTAAT	CCCCAG	TGT	3960	
DB	3901	CAAAATTAC	CACTTTCT	TTCATG	CAGGAGAA	GTATGAGG	TCTTGCT	CTTAAT	CCCCAG	TGT	3960	
QY	3961	GGCTACAA	CAGCATCA	NTGCNA	AGTACATG	CAACGCG	ACGTAGCG	CGGTGA	ATCCAA	ATTG	4020	
DB	3961	GGCTACAA	CAGCATCA	NTGCNA	AGTACATG	CAACGCG	ACGTAGCG	CGGTGA	ATCCAA	ATTG	4020	
QY	4021	CTATTTTAA	TGGCAAA	TGTACCA	CAACAG	GGGCTTCA	CTTACG	TACGAC	ACATATG	GCGAT	4080	
DB	4021	CTATTTTAA	TGGCAAA	TGTACCA	CAACAG	GGGCTTCA	CTTACG	TACGAC	ACATATG	GCGAT	4080	
QY	4081	GTACCTGA	CCGGAG	CATGTTCC	CGGAACTATG	ATGATCAT	TATTGTG	GACGAA	TGCCAT	ATG	4140	
DB	4081	GTACCTGA	CCGGAG	CATGTTCC	CGGAACTATG	ATGATCAT	TATTGTG	GACGAA	TGCCAT	ATG	4140	
QY	4141	TACCGATG	CAACAC	CGTGTG	TGGCAT	TGAAAG	GTCTTA	ACCGA	AGCTTC	ATCCAAAA	4200	
DB	4141	TACCGATG	CAACAC	CGTGTG	TGGCAT	TGAAAG	GTCTTA	ACCGA	AGCTTC	ATCCAAAA	4200	
QY	4201	TGTTAGG	CTAGTG	CTCTTCC	CA	CGGCTAC	CCCCCTG	GAGTAA	TCC	TACACCA	ATG	4260
DB	4201	TGTTAGG	CTAGTG	CTCTTCC	CA	CGGCTAC	CCCCCTG	GAGTAA	TCC	TACACCA	ATG	4260
QY	4261	CAACATA	ACTGAG	ATTCAA	TTAA	CCGTAAG	GCAC	TATCCCC	TTTTCATG	GAAAAA	AGAT	4320
DB	4261	CAACATA	ACTGAG	ATTCAA	TTAA	CCGTAAG	GCAC	TATCCCC	TTTTCATG	GAAAAA	AGAT	4320
QY	4321	TAGGAGG	AAAA	TTCTGA	AGAAA	GGGAGAC	CTTTAT	CTTTT	GAGGCTAC	CAAAAA	CACTG	4380
DB	4321	TAGGAGG	AAAA	TTCTGA	AGAAA	GGGAGAC	CTTTAT	CTTTT	GAGGCTAC	CAAAAA	CACTG	4380
QY	4381	TGATGAC	CTGCTA	ACGATAG	CTCGA	AGGGA	TAACAG	CTGTCT	CTTACTAT	ATAGGG	4440	
DB	4381	TGATGAC	CTGCTA	ACGATAG	CTCGA	AGGGA	TAACAG	CTGTCT	CTTACTAT	ATAGGG	4440	
QY	4441	ATGTGAC	ATCTCA	AAAA	TCCTGAGG	CGACTGTG	TAGTAG	TAGTTGCC	ACTGATG	CTTGTG	4500	
DB	4441	ATGTGAC	ATCTCA	AAAA	TCCTGAGG	CGACTGTG	TAGTAG	TAGTTGCC	ACTGATG	CTTGTG	4500	
QY	4501	TACAGG	GTACATG	TGTGAC	TTTGAT	TCGTTATG	ACTGCAG	CGCTCATG	TGTAGA	AGGCAC	4560	
DB	4501	TACAGG	GTACATG	TGTGAC	TTTGAT	TCGTTATG	ACTGCAG	CGCTCATG	TGTAGA	AGGCAC	4560	
QY	4561	ATGCCAT	TGTTGAC	CTTGAC	CTTACT	TTCACCA	TGGGTG	TTTCGTG	TGTGCGG	GGTTTCAG	4620	
DB	4561	ATGCCAT	TGTTGAC	CTTGAC	CTTACT	TTCACCA	TGGGTG	TTTCGTG	TGTGCGG	GGTTTCAG	4620	
QY	4621	AATAGT	TTAAAG	CCGAG	CGTATAGG	GGCGCGCACAG	GGCGGTGGG	GAGAGCT	TGGCATAT	TACTACTA	4680	
DB	4621	AATAGT	TTAAAG	CCGAG	CGTATAGG	GGCGCGCGCACAG	GGCGGTGGG	GAGAGCT	TGGCATAT	TACTACTA	4680	
QY	4681	TGTAGAC	GGGAGTTG	TATCCCC	CTTCGG	GTATG	GTTCCTG	AAATGCA	ACATTTG	TGAAGC	CTT	4740
DB	4681	TGTAGAC	GGGAGTTG	TATCCCC	CTTCGG	GTATG	GTTCCTG	AAATGCA	ACATTTG	TGAAGC	CTT	4740
QY	4741	CGACGAC	CCAG	CCATG	TATG	TTGTCAT	CAACAG	AGGCTCA	AAACTAT	TTCTG	AGCAC	4800
DB	4741	CGACGAC	CCAG	CCATG	TATG	TTGTCAT	CAACAG	AGGCTCA	AAACTAT	TTCTG	AGCAC	4800

QY 4801 CTAATGCCAACCACTGGGTACCTGCGATAGGACAAATTTGGACGAGTGGGCTGATCT 4860
DB CTAATGCCAACCACTGGGTACCTGCGATAGGACAAATTTGGACGAGTGGGCTGATCT 4860
QY 4861 CTTTTCATATGTCACCCCGAACTTTCATTTGTCATTAATGTCATAATCTGCAAAAGAACTGCTGCAAA 4920
DB CTTTTCATATGTCACCCCGAACTTTCATTTGTCATTAATGTCATAATCTGCAAAAGAACTGCTGCAAA 4920
QY 4921 TTATGTTTTGTTGACTGAGCCCACTCAACTGTCATCATAGTATGCTATGCTGCTCC 4980
DB TTATGTTTTGTTGACTGAGCCCACTCAACTGTCATCATAGTATGCTATGCTGCTCC 4980
QY 4981 CAATGACCAACCACTGGGAGCCCGCTTGGGAAACCTTGTGGGGTTCTGTG 5040
DB CAAATGACCAACCACTGGGAGCCCGCTTGGGAAACCTTGTGGGGTTCTGTG 5040
QY 5041 GCGCTTGGACGCGCTGACCGCTGCTGGCCAGAGCCAGCGAGGTGACCAATACCA 5100
DB GCGCTTGGACGCGCTGACCGCTGCTGGCCAGAGCCAGCGAGGTGACCAATACCA 5100
QY 5101 AATGTGCTTCACTGAAGTCAATACCTTCTGGGACAGCCGACTCGCTGTTGGGTTGGAGT 5160
DB AATGTGCTTCACTGAAGTCAATACCTTCTGGGACAGCCGACTCGCTGTTGGGTTGGAGT 5160
QY 5161 GCGTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACTTGTGTGGCGGCTGCTGCTC 5220
DB GCGTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACTTGTGTGGCGGCTGCTGCTC 5220
QY 5221 TATTACATCAGTCCCTACCGGTGCTACTGTGCGCCAGTGTGACGAAGAAGAAATCGT 5280
DB TATTACATCAGTCCCTACCGGTGCTACTGTGCGCCAGTGTGACGAAGAAGAAATCGT 5280
QY 5281 GGAGAGGTGCATCATTTCCCTTGGAGGCCATGTTGCTGCAATTTGACAACTGAA 5340
DB GGAGAGGTGCATCATTTCCCTTGGAGGCCATGTTGCTGCAATTTGACAACTGAA 5340
QY 5341 GAGTACAAATCACCAAACTAGTCCCTTTCACATTTGGAAACCGCCCTTGAACAACTTAAAC 5400
DB GAGTACAAATCACCAAACTAGTCCCTTTCACATTTGGAAACCGCCCTTGAACAACTTAAAC 5400
QY 5401 CTTTCTGGGCTCATGACGTACAAATCTTGTCTATCATAGAGTATGCTGTGGTTTGTAGT 5460
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QY 5461 CACTTTTACCTGACAACTCCTTTGTCATCATGCGTGTTCATTTGCGGGTATTACTAC 5520
DB CACTTTTACCTGACAACTCCTTTGTCATCATGCGTGTTCATTTGCGGGTATTACTAC 5520
QY 5521 CCCACTACTCAAAAGTCAAAATGTTCTGTCTATTTTGGAGGCGCAATTTGCGTCCAA 5580
DB CCCACTACTCAAAAGTCAAAATGTTCTGTCTATTTTGGAGGCGCAATTTGCGTCCAA 5580
QY 5581 GCTTACAGCGGTAGAGGCGCATGCGGTTTATGATGCGCGGGCTGCGGGAACTGCTCT 5640
DB GCTTACAGCGGTAGAGGCGCATGCGGTTTATGATGCGCGGGCTGCGGGAACTGCTCT 5640
QY 5641 TGGTACATGGAATCGGTGGGTTTGTCTTTGACATGCTAGCGGCTATGCTGCGCGCTC 5700
DB TGGTACATGGAATCGGTGGGTTTGTCTTTGACATGCTAGCGGCTATGCTGCGCGCTC 5700
QY 5701 ATCCACTGCTTGTGACATTTAAATGCTTGTGATGGGTGAGTGGCCCACTATGATCAGCT 5760
DB ATCCACTGCTTGTGACATTTAAATGCTTGTGATGGGTGAGTGGCCCACTATGATCAGCT 5760
QY 5761 TGTGCTTTTGTGCTTGTGATGCGGTTCAATTCGCGCGGAGGAGTGTGGGCTTGTGTCAGC 5820
DB TGTGCTTTTGTGCTTGTGATGCGGTTCAATTCGCGCGGAGGAGTGTGGGCTTGTGTCAGC 5820
QY 5821 TTGTGCAATGTTTGTGTTGACAAACAGCGGCGAGATCACTGCGCCCAACAGACTTCTTAC 5880
DB TTGTGCAATGTTTGTGTTGACAAACAGCGGCGAGATCACTGCGCCCAACAGACTTCTTAC 5880
QY 5881 TATGCTTGTGAGGAGCAACACTGTATGTAAATGAGTACTTTTATTTGCCACTCTGTCGATCCG 5940

DB 5881 TATGCTTGTGAGGAGCAACACTGTATGTAAATGAGTACTTTTATTTGCCACTCTGTCACATCCG 5940
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DB CAGGAAGATACCTGGGCATTCTGGAGGCATCTACCCCTGGAGTGTCTATCAGCTTGCAT 6000
QY 6001 CCGTTGGCTCCACACCCCGACGAGGATGATTGGGGCTCATTTGCTTGGGGTCTAGAGAT 6060
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DB GAGCATGGTTAAACATTCTGCTTCTTCTACAGCTGCCAGAGGGGTACAGGGGCC 6180
QY 6181 CTGGATTGGATCAGGTATGCTTCAAGCACGCTGTCCATGCGGTGCTGAACCTCATCTTTTC 6240
DB CTGGATTGGATCAGGTATGCTTCAAGCACGCTGTCCATGCGGTGCTGAACCTCATCTTTTC 6240
QY 6241 TGTGAGAAATCGTTTGCAGAACTTTTACAAAGGCCAGAACTTGTTCAAATTTACTGAG 6300
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QY 6301 AGGGGCTGTTCCAGTCAACGCTAGCTGTGTGGGTGCGGTAGACCGGACCCCACTGATG 6360
DB AGGGGCTGTTCCAGTCAACGCTAGCTGTGTGGGTGCGGTAGACCGGACCCCACTGATG 6360
QY 6361 GACTAGTCTGCTGCTCAATTTAGGGACTACTGTAAATATAGAAAAATGGGAGA 6420
DB GACTAGTCTGCTGCTCAATTTAGGGACTACTGTAAATATAGAAAAATGGGAGA 6420
QY 6421 TCACATTTTGTATACGAGTATCCTCTTCAAATGTCTGTTTCAACCCAGGTGCCCCCAAC 6480
DB TCACATTTTGTATACGAGTATCCTCTTCAAATGTCTGTTTCAACCCAGGTGCCCCCAAC 6480
QY 6481 CTTGAGAGTGCAGTGGCGGTGGAAGGCTACAGTTTCAAGTGTATCTAGGTGAGCCCA 6540
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QY 6541 AACTCTTTGGACGACATCTGCTTGTGTAGCGGTCTGACCGGTAAAGGTAAACCTGTTAA 6600
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QY 6601 GCTTCCCTTCCGCGTTGACGCTACACACCTGCTGCGCATGCAACCTTAAATTTGCGTGA 6660
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QY 6721 GTCCGCTCTGTTTCAAACAGGAGTTGCGGCTACAAACAAATGCTTTGAGGCAATTTTC 6780
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QY 6841 GCGCCAGTTCCGGGCGAGAACTGGTTGCTTACCTTGCCTTCCCTCCGAGATCCGTCCTC 6900
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DB AGGAGTGTCTGTCTGAAAAGCTGCAACGAAAGTACCGGTTAGAAAGTCTTCAAACT 6960
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Db 6961 CCTTCTTACCACTGTTCTACAGTTGGCCATGCCGATGCCCTGTTGGAGCAGGTGA 7020
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Qy 7201 TTCCACTCAGTCAGCGCCCGCAACCGCCTTACAAAAGAGTTGGGAAAGAGTGAGTT 7260
Db 7201 TTCCACTCAGTCAGCGCCCGCAACCGCCTTACAAAAGAGTTGGGAAAGAGTGAGTT 7260
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Db 7621 GGAATTGACAGAGTGTGTCGAGGAGGTGAGATACCGAGTCATTATCGGCAAACTGTGAT 7680
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Db 8881 CGTGGCTCGGTACACCACTTTTCAATTTATGTGATGTTTACTCCCGGAGGGGATGTGTT 8940
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Db 8941 TATTACACCAAGAGATTGCAAGAGTTCCCTTGTCAAGTATTTGCTGTCTATTGTTTT 9000
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Qy 9117 GGGCTTAACGACCCCGC 9133
Db 9121 GGGCTTAACGACCCCGC 9137

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RESULT 5
US-08-424-550B-11
; Sequence 11, Application US/08424550B
; Publication No. US2002011947A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-NATIAS
; APPLICANT: GEORGE J. DAMSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSAHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESS: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8912 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-424-550B-11

Query Match      92.5%; Score 8692.6; DB 8; Length 8912;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 8781; Conservative 56; Mismatches 52; Indels 10; Gaps 8;

QY      196 TGGGTTCGGTGGTGGCGCTTTAGGCGAGCTCCACGCCACACCTCCAGATAGAGC 255
DB      11 TGGGTTCGGTGGTGGCGCTTTAGGCGAGCTCCACGCCACACCTCCAGATAGAGC 70
QY      256 GCGCGCATGTAGGGAAGACCGGGACCGGTCACTACCAAGGACGAGACCTCTTTTGA 315
DB      71 GCGCGCATGTAGGGAAGACCGGGACCGGTCACTACCAAGGACGAGACCTCTTTTGA 130
QY      316 GTATCAGCCTCCGGAAGTAGTTGGCAAGCCACCTATATGTGTGGATGGTTGGGT 375
DB      131 GTATCAGCCTCCGGAAGTAGTTGGCAAGCCACCTATATGTGTGGATGGTTGGGT 190
QY      376 TAGCCATCATACCGTACTCGCTGATAGGTCCTTGGCAGGGGATCTGGAGTCTCGTAG 435
DB      191 TAGCCATCATACCGTACTCGCTGATAGGTCCTTGGCAGGGGATCTGGAGTCTCGTAG 250
QY      436 ACCGTAGCACATGCTGTATTTCTACTCAAAACAAGTCTGTACCTGCGCCCAAGACGCG 495
DB      1331 ATGCTCAATAGCTGAGTTTTGCTCGCCTTTGATGATACCATGTCTTCCACTCTTATTT 1390
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QY      496 CAAGAACAAGCAGACGAGGCTTCATATCCTGTCTCCATTAACATCATCTGTTGAAGGGG 555
DB      311 CAAGAACAAGCAGACGAGGCTTCATATCCTGTCTCCATTAACATCATCTGTTGAAGGGG 370
QY      556 ACAACGAGCAAGCGCAAGTCCAGCGGATGCTCGGCTCGTAATTAACAAAATTTGCTGG 615
DB      371 ACAACGAGCAAGCGCAAGTCCAGCGGATGCTCGGCTCGTAATTAACAAAATTTGCTGG 430
QY      616 TATCATGATGGCTTGAGACATTTGGCTCAGGCTGCTTTGCCAGCTCATGTTGGGAGC 675
DB      431 TATCATGATGGCTTGAGACATTTGGCTCAGGCTGCTTTGCCAGCTCATGTTGGGAGC 490
QY      676 CCAAGACCTCGCCATAGTCTCGCAATCTTGGAAATCTCTTGATATACCTTTGGGGTG 735
DB      491 CCAAGACCTCGCCATAGTCTCGCAATCTTGGAAATCTCTTGATATACCTTTGGGGTG 550
QY      736 GATTGGTGAATTTACAACTCACACACCTCTAGTAGGCGCTGGTGGCAGGAGCGTCTG 795
DB      551 GATTGGTGAATTTACAACTCACACACCTCTAGTAGGCGCTGGTGGCAGGAGCGTCTG 610
QY      796 TCGACCAAGTCTGCCAGATAGTACGCTTGTGAGAGATGGAGTCAACTGGGCTACTGTTG 855
DB      611 TCGACCAAGTCTGCCAGATAGTACGCTTGTGAGAGATGGAGTCAACTGGGCTACTGTTG 670
QY      856 GTTCGGTGTCCACCTTTTGGGTATGTCTGCTATCTTTGGCCTGCTCCCTGAGTGGGGC 915
DB      671 GTTCGGTGTCCACCTTTTGGGTATGTCTGCTATCTTTGGCCTGCTCCCTGAGTGGGGC 730
QY      916 CGGGGTCACTGACCCAGACACAAATACCAATCTGACCAATTTGCTGCCACGCTAATCA 975
DB      731 CGGGGTCACTGACCCAGACACAAATACCAATCTGACCAATTTGCTGCCACGCTAATCA 790
QY      976 GGTATCTATTTGTTCTCTTCCACTTGTGCTACAGAGCTGGTGTGTGATCTGTGCGGA 1035
DB      791 GGTATCTATTTGTTCTCTTCCACTTGTGCTACAGAGCTGGTGTGTGATCTGTGCGGA 850
QY      1036 CGAGTGTGGGTTCGCCCAATCGTACATCTCACACCTTCCAATTTGAGCTGGCAGCGA 1095
DB      851 CGAGTGTGGGTTCGCCCAATCGTACATCTCACACCTTCCAATTTGAGCTGGCAGCGA 910
QY      1096 CTCCTTCTTGCTGACCAACATTTGTTTATGGGCGCTCTTGTGACCTGTGACGCGCT 1155
DB      911 CTCCTTCTTGCTGACCAACATTTGTTTATGGGCGCTCTTGTGACCTGTGACGCGCT 970
QY      1156 TGACATTTGGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1215
DB      971 TGACATTTGGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1030
QY      1216 GCTTATTCACATAGACCTCAATGAACTGGTACTTGTGTACCTGGAAGTGGCCACTGGAAT 1275
DB      1031 GCTTATTCACATAGACCTCAATGAACTGGTACTTGTGTGTGTGTGTGTGTGTGTGTGT 1090
QY      1276 AGATCTCTGGTTCCTAGGGTTTATCGGGTGGATGGCGGCAAGGTCGAGGCTGTCTCT 1335
DB      1091 AGATCTCTGGTTCCTAGGGTTTATCGGGTGGATGGCGGCAAGGTCGAGGCTGTCTCT 1150
QY      1336 CTGACCAAACTGGCTTCACAAGTACCATAGCTATTGCGCATGTATGTTAGCAGTGTACA 1395
DB      1151 CTGACCAAACTGGCTTCACAAGTACCATAGCTATTGCGCATGTATGTTAGCAGTGTACA 1210
QY      1396 CTACTGCGGTTCGCGCTCTGATCTACTATGCTCTCGGGGCAAGTGGTATCAGTTGCT 1455
DB      1211 CTACTGCGGTTCGCGCTCTGATCTACTATGCTCTCGGGGCAAGTGGTATCAGTTGCT 1270
QY      1456 CTTAGCGCTTATGCTTTTACATAGAGCGACCTCTGGAAACCCCATCAGGGTGCCCACTGG 1515
DB      1271 CTTAGCGCTTATGCTTTTACATAGAGCGACCTCTGGAAACCCCATCAGGGTGCCCACTGG 1330
QY      1516 ATGCTCAATAGCTGAGTTTTGCTCGCCTTTGATGATACCATGTCTTCCACTCTTATTT 1575
DB      1331 ATGCTCAATAGCTGAGTTTTGCTCGCCTTTGATGATACCATGTCTTCCACTCTTATTT 1390
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Qy	1576	GAGTGAGAGTGTGTCAGAGTCAATTTGTTTACAGTCCAAAGTGGACAGGCGCTACACTCT	1635	Qy	2655	TAATTTGAGGGCTGACAAATACCACTGTAGTAGCATTAGTTGTTCATGTCTCGTTTTGGCT	2714
Db	1391	GAGTGAGAGTGTGTCAGAGTCAATTTGTTTACAGTCCAAAGTGGACAGGCGCTACACTCT	1450	Db	2467	TAATTTGAGGGCTGACAAATACCACTGTAGTAGCATTAGTTGTTCATGTCTCGTTTTGGCT	2526
Qy	1636	AGAGTATAACAACTCCATATCTTGGTACCCCTATACAAATCCTCGTGGAGGGATGTAT	1695	Qy	2715	TCCTTGTCTCACTTGTATACCTCGCTGCTGCTTAACTCTCTATCTTTGGCAACGTTGGG	2774
Db	1451	AGAGTATAAABAACCTCCATATCTTGGTACCCCTATACAAATCCTCGTGGAGGGATGTAT	1510	Db	2527	TCCTTGTCTCACTTGTATACCTCGCTGCTGCTTAACTCTCTATCTTTGGCAACGTTGGG	2586
Qy	1696	GTTTAAATTTCAAAATTAACACATGGGGTGTGCGGTATTTCGCAATGTGCCATCGTACTG	1755	Qy	2775	AGAATTCGTTTGGAACTTACACTAAGACCGGAGAGGTTTTTCTTGTGTGCTGCTTTGTT	2834
Db	1511	GTTTAAATTTCAAAATTAACACATGGGGTGTGCGGTATTTCGCAATGTGCCATCGTACTG	1569	Db	2587	AGAATTCGTTTGGAACTTACACTAAGACCGGAGAGGTTTTTCTTGTGTGCTGCTTTGTT	2646
Qy	1756	CACATATGGGCACTGATGACAGTGTGGAAAGCACACTCGCAACACTTTACGAAGCATCGGTGT	1815	Qy	2835	TCCTCGTGTGACATATGACGCGTGTGACTTTTCTGTGTGTGTCACGTAGCTCTTCTAT	2894
Db	1570	CACATATGGGCACTGATGACAGTGTGGAAAGCACACTCGCAACACTTTACGAAGCATCGGTGT	1629	Db	2647	TCCTCGTGTGACATATGACGCGTGTGACTTTTCTGTGTGTGTCACGTAGCTCTTCTAT	2706
Qy	1816	AACACCATGGCTAACACCGCATGGCACAGCGCTCAGCCCTGAATTTGGCTATATTACA	1875	Qy	2895	GTTTAACTCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGTTAGGGCCCATAGAA	2954
Db	1630	AACACCATGGCTAACACCGCATGGCACAGCGCTCAGCCCTGAATTTGGCTATATTACA	1689	Db	2707	GTTTAACTCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGTTAGGGCCCATAGAA	2766
Qy	1876	ATACCTGGGTCTAAAGAAATGTTTAAACCTCATAAATTTGGATGTCAGGCCAATTTGTAATTT	1935	Qy	2955	TGTTGGTGCCTCTCGGAAAGTGTCACTCTTGGTATTCTCATTTATGTTCTTAAAGTTTTTCC	3014
Db	1690	ATACCTGGGTCTAAAGAAATGTTTAAACCTCATAAATTTGGATGTCAGGCCAATTTGTAATTT	1749	Db	2767	TGTTGGTGCCTCTCGGAAAGTGTCACTCTTGGTATTCTCATTTATGTTCTTAAAGTTTTTCC	2826
Qy	1936	TGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAATTCCTCTCTACC	1995	Qy	3015	TCCTAGTGTGTTGGTGAATGTTGTTTCTTATAAGACACTTGCATGGTGATGCTTTGC	3074
Db	1750	TGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCCTGTGAATTCCTCTCTACC	1809	Db	2827	TCCTAGTGTGTTGGTGAATGTTGTTTCTTATAAGACACTTGCATGGTGATGCTTTGC	2886
Qy	1996	ACCGAGAGTGGGTAGTTGGCCGTTACCCACCTGTGTGTTACGTGGTTCTTGGTTACA	2055	Qy	3134	CTAATGATTTTGGCTCGAAACTACCATTTGCAAGAGCCATTTTCCCTTTTGAAGGCAAGG	3134
Db	1810	ACCGAGAGTGGGTAGTTGGCCGTTACCCACCTGTGTGTTACGTGGTTCTTGGTTACA	1869	Db	2887	CTAATGATTTTGGCTCGAAACTACCATTTGCAAGAGCCATTTTCCCTTTTGAAGGCAAGG	2946
Qy	2056	GGTTCCGCAAGGTTTACAGTGATGTAAGAGCTAGCCACAGGATGTACCAAGAA	2115	Qy	3135	CAAGGGTCTATAGGAATGAAGAGAGCGTTGGCGTGTGGGGACACCGTTGATGTTTGC	3194
Db	1870	GGTTCCGCAAGGTTTACAGTGATGTAAGAGCTAGCCACAGGATGTACCAAGAA	1928	Db	2947	CAAGGGTCTATAGGAATGAAGAGAGCGTTGGSKGTGGGGACACCGTTGATGTTTGS	3006
Qy	2116	CAAAAGCCTGGAATAATATCAGTCTTATATTCGCGCACCGGTGCTTTGCTCTTACGGG	2175	Qy	3195	CCGTTGTTGCGCGTCTCGCGACCTTGTGTTTGCAGGGTTGGCTATGCCGCGAGATGGT	3254
Db	1929	CAAAAGCCTGGAATAATATCAGTCTTATATTCGCGCACCGGTGCTTTGCTCTTACGGG	1988	Db	3007	SCGTTGTBGGCGGTCTCGCGACCTTGTGTTTGCAGGGTTAGCTATGCCGCGAGATGGT	3066
Qy	2176	AGTTACCAACCAAGCGGTGCTTAATCTGTTGGGGTTGTGGCAGCAAGTATCTTAT	2048	Qy	3255	GGGCGATTAACGCAACCTTTTACGCTGCAGTGTCTCTCTGAAACGTGGCACGCTGTACGGGA	3314
Db	1989	AGTTACCAACCAAGCGGTGCTTAATCTGTTGGGGTTGTGGCAGCAAGTATCTTAT	2048	Db	3067	GGGCGATTAACGCAACCTTTTACGCTGCAGTGTCTCTCTGAAACGTGGCACGCTGTACGGGA	3126
Qy	2236	TTTAGCCTACCTCTGTTACTTGTCCCTTGTGTTTGGGCGCGCTTCTGGTTACCCCTTGGC	2295	Qy	3315	TGSCAGTGTCTATGACTGTGTATAGACCCCGAACCTCTGAACTTGGAACTATCTTCAGATTAG	3374
Db	2049	TTTAGCCTACCTCTGTTACTTGTCCCTTGTGTTTGGGCGCGCTTCTGGTTACMCTTTGGC	2108	Db	3127	TGSCAGTGTCTATGACTGTGTATAGACCCCGAACCTCTGAACTTGGAACTATCTTCAGATTAG	3186
Qy	2296	TCCTGTGTCCCATCCAGTCCGTATCTCAAGCTGGCTGGGATGTTTGTCTAAAGCTCA	2355	Qy	3375	GATCTCTGGCCACTAGCTACATGGGATTTGTTGTGACAAAGTGTGTTGATCTGCTCACC	3434
Db	2109	TCCTGTGTCCCATCCAGTCCGTATCTCAAGCTGGCTGGGATGTTTGTCTAAAGCTCA	2168	Db	3187	GATCTCTGGCCACTAGCTACATGGGATTTGTTGTGACAAAGTGTGTTGATCTGCTCACC	3246
Qy	2356	AGTAGCTCTTTTGGTTTGTGATTTTCTTCACTGTGTCTATCTCCGCTGCAGGCTACGTTA	2415	Qy	3435	ATGSCAGCAAGGGCGCGGTGGCTCATGCCACAGGCTCTATACACCCCAATACCCGTTG	3494
Db	2169	AGTAGCTCTTTTGGTTTGTGATTTTCTTCACTGTGTCTATCTCCGCTGCAGGCTACGTTA	2228	Db	3247	ATGSCAGCAAGGGCGCGGTGGCTCATGCCACAGGCTCTCATACACCCCAATACCCGTTG	3306
Qy	2416	TGCTGCCCTTTTAGGGTTTGGCCATGGCTGCGGGCTGGCCCTAATCTTTTGTGTC	2475	Qy	3495	ACGCGGCTAATGACACAGGACATCTCAACACCATGTGGAGCTGGGTCCCTTACTCGGT	3554
Db	2229	TGCTGCCCTTTTAGGGTTTGGCCATGGCTGCGGGCTGGCCCTAATCTTTTGTGTC	2288	Db	3307	ACGCGGCTAATGACACAGGACATCTCAACACCATGTGGAGCTGGGTCCCTTACTCGGT	3366
Qy	2476	AGCAGCTGCTGCCCAACAGATTAATGACTGTGGGTGGGCTGCTAGTGGCAGGGTTAGT	2535	Qy	3555	GCTCTTCCGGGGAGACCAAGGGGTATCTGGTAAACACGACTGGGGCTCATTTGGTTGAGGTCA	3614
Db	2289	AGCAGCTGCTGCCCAACAGATTAATGACTGTGGGTGGGCTGCTAGTGGCAGGGTTAGT	2348	Db	3367	GCTCTTCCGGGGAGACCAAGGGGTATCTGGTAAACACGACTGGGGCTCATTTGGTTGAGGTCA	3426
Qy	2536	TTTGTGGGCGGCGGTAAACCGTGGTCAACGATAGCTGCTGCTGTAGGTCTCTGGCCCTCT	2595	Qy	3615	ACAAATCCGATGACCTTATTTGTTGTGTGTGCGGGGCCCTTCCCATGGCTGTTGCCAAGG	3674
Db	2349	TTTGTGGGCGGCGGTGACCGTGGTCA-CGATAGCTCTGCTTGTAGGTCTTGGCCCTCT	2407	Db	3427	ACAAATCCGATGACCTTATTTGTTGTGTGTGCGGGGCCCTTCCCATGGCTGTTGCCAAGG	3486
Qy	2596	GGTAGCGCTTTT-TAACCTCTTTGATTTGGTTAGCCCTGCTTCAGCTTTTGGATACCGAGA	2654	Qy	3675	GTTCTTCAGGTGCCCGATTTCTGCTCCCTCCGGGCATGTTATTGGGATGTTTCCCGCTG	3734
Db	2408	GGTAGCGCTTTT-TAACCTCTTTGATTTSSTKAGCGCTGCTT-AGCTTTTGGACACCGAGA	2466	Db	3487	GTTCTTCAGGTGCCCGATTTCTGCTCCCTCCGGGCATGTTATTGGGATGTTTCCCGCTG	3546
				Qy	3735	CTAGAAATTTCTGGCGGTTTCACTCAGTCAGATCAGATTAGGGTTAGGGCTGTTGGTGTGCTGGAT	3794

Db 3547 CTAGAAATCTGGCGGTTCACTGGCCAGATTAGGGTTAGGCGTGTGGTGTGCTGAT 3606
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Db 3607 ACCATCCCAGTACACAGCACAATGCCACTCTTTGATACAAAACCTACTGTGCTTAACGAGT 3666
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QY 3975 CAATGCCAAAGTACATGACCGGACGTAACGGGTGAATCCCAAAATGCTATTAAATGGCA 4034
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QY 4035 AATGTACCACACACAGGGGCTTCACTTAGGTACAGCACATATGGCATGTACCTGACCGGAG 4094
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Db 4507 GTACCCCTTCGGGTAATGGTTCCTGAAATGCAACATTTGTGAAGCCTTGACGCGCAAGG 4566
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Db 8885 TTTTTTTTTTTTTTTTTT 8903

RESULT 6
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; Sequence 80, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:

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APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
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APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSAHWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
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TELEPHONE: 708-937-6365
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INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 4268 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-424-550B-80

Query Match 44.2%; Score 4159; DB 8; Length 4268;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 4215; Conservative 20; Mismatches 30; Indels 30; Gaps 2;

Qy 3456 TGGCTCATCCACAGGCTCTATACCCCAATAACCGTTGACGCGGCTAATGACCAAGGACA 3515
Db 1 TGGCTCATCCACAGGCTCCATACCCCAATAACCGTTGACGCGGCTAATGACCAAGGACA 60
Qy 3516 TCTATCAACCAACCATGTGGAGCTGGGTCCCTTACTCGGTGCTCTTGGCGGAGACCAAGG 3575
Db 61 TCTATCAACCAACCATGTGGAGCTGGGTCCCTTACTCGGTGCTCTTGGCGGAGACCAAGG 120
Qy 3576 GGTATCTGGTAAACAGACTGGGTTCATTTGAGTCAACAAATCCGATGACCCCTTATT 3635
Db 121 GGTATCTGGTAAACAGACTGGGTTCATTTGAGTCAACAAATCCGATGACCCCTTATT 180
Qy 3636 GGTGTGTGTGGGGGCCCTTCCCATGGCTGTGGCAAGGTTCTTCAGGTGCCCCGATTC 3695
Db 181 GGTGTGTGTGGGGGCCCTTCCCATGGCTGTGGCAAGGTTCTTCAGGTGCCCCGATTC 240
Qy 3696 TGTGCTCTCCGGGATGTTATTGGGATGTTTCAACCGCTGTAGAAATTTCTGCGGCTTCAG 3755
Db 241 TGTGCTCTCCGGGATGTTATTGGGATGTTTCAACCGCTGTAGAAATTTCTGCGGCTTCAG 300
Qy 3756 TCAGTCAAGATTAGGTTAGGCGGTTGGTGTGCTGGATACCATCCCGATACAGACAC 3815
Db 301 TCAGTCAAGATTAGGTTAGGCGGTTGGTGTGCTGGATACCATCCCGATACAGACAC 360

Db 2521 CCTGGAGTTCATATACAGCTTCGATCCGTTGGCTYCACACCCCGACGGAGGATGATCGG 2580
Qy 6036 GCCTCATTTGCTGGGCTTAGAGATTTGGCAGTATGTGCAATTTCTTTGTGATTTGCT 6095
Db 2581 GCCTCATTTGCTGGGCTTAGAGATTTGGCAGTATGTGCAATTTCTTTGTGATTTGCT 2640
Qy 6096 TTAATGTCCTTTAAAGCTGGAGTTACAGACATGGTTAAACATTTCTCTTCTACA 6155
Db 2641 TTAATGTCCTTTAAAGCTGGAGTTACAGACATGGTTAAACATTTCTCTTCTACA 2700
Qy 6156 GCTGCAGAGGGGTACAGGGCCCTCGATTTGGATCAGGTATGCTCAAGACGCTGTC 6215
Db 2701 GCTGCAGAGGGGTACAGGGCCCTCGATTTGGATCAGGTATGCTCAAGACGCTGTC 2760
Qy 6216 CATGGGTGCTGAATCATCTTTCTGTTGAGATGGTTTGCRAAACTTTTACAAGGAC 6275
Db 2761 CATGGGTGCTGAATCATCTTTCTGTTGAGATGGTTTGCRAAACTTTTACAAGGAC 2820
Qy 6276 CCAGAACTTTGTTCAAACTTACTGGAGAGGGCTGTTCCAGTCAACGCTAGGCTGTGGGT 6335
Db 2821 CCAGAACTTTGTTCAAACTTACTGGAGAGGGCTGTTCCAGTCAACGCTAGGCTGTGGGT 2880
Qy 6336 CGGCTAGACGGACCCAACTGATTTGGAATGACTAGTCTTGTGCTGCAATTTATGGCGTTAGGACT 6395
Db 2881 CGGCTAGACGGACCCAACTGATTTGGAATGACTAGTCTTGTGCTGCAATTTATGGCGTTAGGACT 2940
Qy 6396 ACTGTAATATAGAGAAATGGAGATCACATTTTGTACAGCAGTATCCTCTCAAAATG 6455
Db 2941 ACTGTAATATAGAGAAATGGAGATCACATTTTGTACAGCAGTATCCTCTCAAAATG 3000
Qy 6456 TCTGTTTCAACCGAGTGCCCACTTGGAGCTGCAAGTGGCGGTGAGCGCGTACAGG 6515
Db 3001 TCTGTTTCAACCGAGTGCCCACTTGGAGCTGCAAGTGGCGGTGAGCGCGTACAGG 3060
Qy 6516 TTCAGTGTATCTAGTGAGGCCCAAACTCTCTTGAACGACATCTGCTTGTACGCTC 6575
Db 3061 TTCAGTGTATCTAGTGAGGCCCAAACTCTCTTGAACGACATCTGCTTGTACGCTC 3120
Qy 6576 CTGAGGTAAGGTAATACTGTTAGCTTCCCTTCCGGTTGACGGTCAACACCTGGTG 6635
Db 3121 CTGAGGTAAGGTAATACTGTTAGCTTCCCTTCCGGTTGACGGTCAACACCTGGTG 3180
Qy 6636 TGGCATGCAACTTAATTTGGTGTATGCACTTGAGACAAATGACTGTAAATTCACAAACA 6695
Db 3181 TGGCATGCAACTTAATTTGGTGTATGCACTTGAGGCAATGACTGTAAATTCACAAACA 3240
Qy 6696 ACATCTCTAGTATGAACCGCAGTGTCCGCTCTTTTCAACAGGAGTTGCGGCGTA 6755
Db 3241 ACATCTCTAGTATGAACCGCAGTGTCCGCTCTTTTCAACAGGAGTTGCGGCGTA 3300
Qy 6756 CAACCAATTTGTTGAGGCAATTTTCAAGTGGGTTGACACCAACCTGCGAGCCCTC 6815
Db 3301 CAACCAATTTGTTGAGGCAATTTTCAAGTGGGTTGACACCAACCTGCGAGCCCTC 3360
Qy 6816 CC---ATCGAAGAGGTAGTGTGAAGAAACGCGCAGTTCGGGCAAGAACTGTTGCTTA 6872
Db 3361 CCCAGATCGAAGAGGTAGTGTGAAGAAACGCGCAGTTCGGGCAAGAACTGTTGCTTA 3420
Qy 6873 CTTGCTCTCCCTCCGAGATCCGTTCCGAGGAGTGTCAATGCTGAAAGCCTGCAACGAA 6932
Db 3421 CTTGCTCTCCCTCCGAGATCCGTTCCGAGGAGTGTCAATGCTGAAAGCCTGCAACGAA 3480
Qy 6933 GTGACCCGTTAGAGGTCCTTCAACCTCCCTTCCACCTGTTACAGTTGGCCA 6992
Db 3481 GTGACCCGTTAGAGGTCCTTCAACCTCCCTTCCACCTGTTACAGTTGGCCA 3540
Qy 6993 TGCCGATCCCTGTTGGGAGCGGTGAGTGTAAACCTTTTCACTGCAATTTGATGTGCAA 7052
Db 3541 TGCCGATCCCTGTTGGGAGCGGTGAGTGTAAACCTTTTCACTGCAATTTGATGTGCAA 3600
Qy 7053 TGACCGAAACAGCGCGGCGCTGTATGATTTTACCAGTTACCTCCCAAAAGGAGGCT 7112
Db 3601 TGACCGAAACAGCGCGGCGCTGTATGATTTTACCAGTTACCTCCCAAAAGGAGGCT 3660

Qy 7113 CTGAATGTCAGACAAAGTTGGTTCGACGGCTACAAACGCTTCCAGCTTACGTTACTGGCC 7172
Db 3661 CTGAATGTCAGACAAAGTTGGTTCGACGGCTACAAACGCTTCCAGCTTACGTTACTGGCC 3720
Qy 7173 CCCGTTACCTTAAGATACGGGAAAGATTCCTCATAGTACAGCCCGCCCAAAACGGCCTA 7232
Db 3721 CCCGTTACCTTAAGATACGGGCAAGGATTCCTCATAGTACAGCCCGCCCAAAACGGCCTA 3780
Qy 7233 CAAAAAGAGTTGGGAAAGATGAGTTTTCGTCGACGATGAGCTACACCTTGGACCGAG 7292
Db 3781 CAAAAAGAGTTGGGAAAGATGAGTTTTCGTCGACGATGAGCTACACCTTGGACCGAG 3840
Qy 7293 TGATTAGCTTCAAACTGCTTCTTAAAGTTCTGTCTGCAACTCGGCGCCATCACTAGTGGTT 7352
Db 3841 TGATTAGCTTCAAACTGCTTCTTAAAGTTCTGTCTGCAACTCGGCGCCATCACTAGTGGTT 3900
Qy 7353 TCCTCAAAACAAAGATCAATTGGTGTATGTACTGACGCGCGGATGCGGAGCTTGAAGAAC 7412
Db 3901 TCCTCAAAACAAAGATCAATTGGTGTATGTACTGACGCGCGGATGCGGAGCTTGAAGAAC 3960
Qy 7413 AAAAGTCACATTAANTAGACAACTCTGTTCCCGCCCATATACACAAAGCAAGTGAGAT 7472
Db 3961 AAAAGTCACATTAANTAGACAACTCTGTTCCCGCCCATATATACCAAGCAAGTGAGAT 4020
Qy 7473 TGGCTAAGGAAAAAGCTTCAAAAGTTGTTCGGTGTCTGTCGAGCTATGATGAAGTAGCAG 7532
Db 4021 TGGCTAAGGAAAAAGCTTCAAAAGTTGTTCGGTGTCTGTCGAGCTATGATGAAGTAGCAG 4080
Qy 7533 CTCACAGCCCTCTAAGTCTCTAAGTCCCAATCATCTGCGCTTCGGGCGACTGATGTTTC 7592
Db 4081 CTCACAGCCCTCTAAGTCTCTAAGTCCCAATCATCTGCGCTTCGGGCGACTGATGTTTC 4135
Qy 7593 GTTCTGAGCAGCCGCAAGGCTGTTCTGAGCTTTCGAGAACTGTGTCGAGCAGGTGAGA 7652
Db 4136 GTTCTGAGCAGCCGCAAGGCTGTTCTGAGCTTTCGAGAACTGTGTCGAGCAGGTGAGA 4173
Qy 7653 TACGAGTCAATTATCGGCAAACTGTGATGTTTCAAAAGGAGGAGGTCTTCGTGAAGACCC 7712
Db 4174 TACGAGTCAATTATCGGCAAACTGTGATGTTTCAAAAGGAGGAGGTCTTCGTGAAGACCC 4233
Qy 7713 CCCAGAAACCAACAAAGAAACCCCAAGGCTTATC 7747
Db 4234 CCCAGAAACCAACAAAGAAACCCCAAGGCTTATC 4268

RESULT 7
US-08-424-550B-25
; Sequence 25, Application US/08424550B
; Publication No. US2002011947A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

/	APPLICANT:	SHERI L. BUIJK
/	APPLICANT:	ISA K. MUSHAWAR
/	TITLE OF INVENTION:	NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
/	TITLE OF INVENTION:	REAGENTS AND METHODS FOR THEIR USE
/	NUMBER OF SEQUENCES:	716
/	CORRESPONDENCE ADDRESS:	
/	ADDRESSEE:	ABBOTT LABORATORIES D377/AP6D
/	STREET:	100 ABBOTT PARK ROAD
/	CITY:	ABBOTT PARK
/	STATE:	IL
/	COUNTRY:	USA
/	ZIP:	60064-3500
/	COMPUTER READABLE FORM:	
/	MEDIUM TYPE:	Floppy disk
/	COMPUTER:	IBM PC compatible
/	OPERATING SYSTEM:	PC-DOS/MS-DOS
/	SOFTWARE:	PatentIn Release #1.0, Version #1.25
/	CURRENT APPLICATION DATA:	
/	APPLICATION NUMBER:	US/08/424,550B
/	FILING DATE:	
/	CLASSIFICATION:	435435
/	ATTORNEY/AGENT INFORMATION:	
/	NAME:	POREMBSKI, PRISCILLA E.
/	REGISTRATION NUMBER:	33,207
/	REFERENCE/DOCKET NUMBER:	5527.PC.01
/	TELECOMMUNICATION INFORMATION:	
/	TELEPHONE:	708-937-6365
/	TELEFAX:	708-938-2623
/	INFORMATION FOR SEQ ID NO:	392:
/	SEQUENCE CHARACTERISTICS:	
/	LENGTH:	479 base pairs
/	TYPE:	nucleic acid
/	STRANDEDNESS:	single
/	TOPOLOGY:	linear
/	MOLECULE TYPE:	DNA (genomic)
/	US-08-424-550B-392	
Query Match 4.8%; Score 449.8; DB 8; Length 479;		
Best Local Similarity 97.5%; Pred.No. 2.8e-121;		
Matches 467; Conservative 1; Mismatches 8; Indels 3; Gaps 1;		
Qy	6419	GATCACATTTTGTACAGCAGTATCCTCTCCAAATGTCGTGGTTCACCCAGGTGCCCGCA 6478
Db	1	GATCACATTTTGTACAGCAGTATCCTCTCCAAATGTCGTGGTTCACCCAGGTGCCCGCA 60
Qy	6479	ACCTTGAGAGCTGCAGTGGCGGTGACGGGTACAGGTTTCAGTGTTCATCTAGGTGAGCCC 6538
Db	61	ACCTTGAGAGCTGCAGTGGCGGTGACGGGTACAGGTTTCAGTGTTCATCTAGGTGAGCCC 120
Qy	6539	AAAACCTCCTTGGACGACATCTGCTTCTGTTCAGGTCCTGACGGTAAGGGTAAAACTGTT 6598
Db	121	AAAACCTCCTTGGACGACATCTGCTTCTGTTCAGGTCCTGACGGTAAGGGTAAAACTGTT 180
Qy	6599	AAGCTTCCTTCGCGGTTGACCGGTACACACTGGTGTGGCGCATGCNACTTAATTTCGCGT 6658
Db	181	AAGCTTCCTTCGCGGTTGACCGGTACACACTGGTGTGGCGCATGCNACTTAATTTCGCGT 240
Qy	6659	GATGCATCTTGACACAATTCAGCTGTAATTCACAAAACAACTCCTAGTGTATGAAGCCGCA 6718
Db	241	GATGCATCTTGAGCAATTCAGCTGTAATTCATAAACAACACTCCTAGTGTATGAAGCCGCA 300
Qy	6719	GTGTCGCGCTCTTGTTCACACAGGAGTGTGGCGGTACAAACCNAATTGCTTGAGGCCAATT 6778
Db	301	GTGTCGCGCTCTTGTTCACACAGGAGTGTGGCGGTACAAACCNAATTGCTTGAGGCCAATT 360
Qy	6779	TCAGCTGGCGTTGACACACCAAACCTGCACGCCCTCC---ATCGAAGAGGTAGTGGA 6835
Db	361	TCAGCTGGCGTTGACACACCAAACCTGCACGCCCTCCCGAGATCGAAGAGGTAGTGGA 420
Qy	6836	AGAAAGCCGAGTTCCGGGCAGAACTGGTTCGCTTACCTTGCTCCCCCTCCGAGATC 6894
Db	421	AGAAAGCCGAGTTCCGGGCAGAACTGGTTCGCTTACCTTGCTCCCCCTCCGAGATC 479

```
RESULT 9
US-08-424-550B-29/c
; Sequence 29, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-424-550B-29

Query Match          3.4%; Score 319.6; DB 8; Length 337;
Best Local Similarity 98.5%; Pred. No. 7.2e-83;
Matches 333; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5855 GATCACTGGCCCAACAGACTCTTACTATGCTTGTAGGAGCAACACTGTATGTAATGAG 5914
DB 337 GATCACTGGCCCAACAGACTCTTACTATGCTTGTAGGAGCAACACTGTATGTAATGAG 278
QY 5915 TACTTTATTGGCCACTCGTGACATCCGCAAGGAAGATACCTGGGCATTTCTGGAGGCATCTACC 5974
DB 277 TACTTTATTGGCCACTCGTGACATCCGCA- GAAGATACCTGGGCATTTCTGGAGGCATCTACC 219
QY 5975 CCCTGGAGTGTCATATCAGCTTGCATCCGTTGGCTCCACACCCCGAGGAGATGATTCG 6034
DB 218 CCCTGGAGTGTCATATCAGCTTGCATCCGTTGGCTCCACACCCCGAGGAGATGATTCG 159
QY 6035 GGCCTCATTTGCTGGGGCTAGAGATTTGGCAGTAGTGTGCAATTTCTTTGTGATTTGC 6094
DB 158 GGCCTCATTTGCTGGGGCTAGAGATTTGGCAGTAGTGTGCAATTTCTTTGTGATTTGC 99
QY 6095 TTTAATGTCCTTAAAGCTGGAGTTGAGACATGGTTAAACATTCCTGGTTGTCCTTTCTAC 6154
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Db 98 TTTAATGTCCTTAAAGCTGGAGTTGAGCATGGTTAAACATTCCTGGTTGTCCTTTCTAC 39
QY 6155 AGCTGCCAGAGGGGTACAAGGGCCCTCGGATTCGATC 6192
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Db 38 AGCTGCCAGAGGGGTACGAGGGCCCTCGGATTCGATC 1
|||||

RESULT 10
US-08-424-550B-159/c
; Sequence 159, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-424-550B-159
```

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Query Match          3.4%; Score 319.6; DB 8; Length 337;
Best Local Similarity 98.5%; Pred. No. 7.2e-83;
Matches 333; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5855 GATCACTGGCCCAACAGACTCTTACTATGCTTGTAGGAGCAACACTGTATGTAATGAG 5914
DB 337 GATCACTGGCCCAACAGACTCTTACTATGCTTGTAGGAGCAACACTGTATGTAATGAG 278
QY 5915 TACTTTATTGGCCACTCGTGACATCCGCAAGGAAGATACCTGGGCATTTCTGGAGGCATCTACC 5974
DB 277 TACTTTATTGGCCACTCGTGACATCCGCA- GAAGATACCTGGGCATTTCTGGAGGCATCTACC 219
QY 5975 CCCTGGAGTGTCATATCAGCTTGCATCCGTTGGCTCCACACCCCGAGGAGATGATTCG 6034
DB 218 CCCTGGAGTGTCATATCAGCTTGCATCCGTTGGCTCCACACCCCGAGGAGATGATTCG 159
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Qy 6035 GGCCTCATTGCTTGGGGCTAGAGATTGGCAGTATGTGCAATTCTTTGTGATTGC 6094
Db 158 GGCCTCATTGCTTGGGGCTAGAGATTGGCAGTATGTGCAATTCTTTGTGATTGC 99
Qy 6095 TTTAATGTCCTTAAAGCTGGAGTTTCAGAGCATGGTTAAACATTCCTGTTGCTTCTTCTAC 6154
Db 98 TTTAATGTCCTTAAAGCTGGAGTTTCAGAGCATGGTTAAACATTCCTGTTGCTTCTTCTAC 39
Qy 6155 AGCTGCCAGAGGGGTACAAGGGCCCTCGGATTGGATC 6192
Db 38 AGCTGCCAGAGGGGTACGAGGGCCCTCGGATTGGATC 1

RESULT 11
US-08-424-550B-18
; Sequence 18, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-424-550B-18

Query Match 3.0%; Score 279.4; DB 8; Length 281;
Best Local Similarity 99.6%; Pred. No. 5e-71;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6637 GCGCATGCAACTTAATTGGCTGATGCACCTTGAGACAAATGACTGTAAATCCACAAACAA 6696
Db 1 GCGCATGCAACTTAATTGGCTGATGCACCTTGAGACAAATGACTGTAAATCCATACAA 60
Qy 6697 CACTCTAGTATGAAGCCGAGTGTCCGCTCTTTGTTTCAACAGGAGTTGCGCGGTAC 6756

Db 61 CACTCTAGTATGAAGCCGAGTGTCCGCTCTTTGTTTCAACAGGAGTTGCGCGGTAC 120
Qy 6757 AAACCAATTGCTTGAGCAATTTTCAGCTGGCGTTTGACACACCAACCACTGCCAGCCCCCTC 6816
Db 121 AAACCAATTGCTTGAGCAATTTTCAGCTGGCGTTTGACACACCAACCACTGCCAGCCCCCTC 180
Qy 6817 CATCGAAGAGTGTAGTAAAGAAAGCCAGTTCCGGGGCAAGAACTGGTTGCTTACCTT 6876
Db 181 CATCGAAGAGTGTAGTAAAGAAAGCCAGTTCCGGGGCAAGAACTGGTTGCTTACCTT 240
Qy 6877 GCCTCCCCCTCCGAGATCCGTCGCCAGGAGTGTATGTCCTG 6917
Db 241 GCCTCCCCCTCCGAGATCCGTCGCCAGGAGTGTATGTCCTG 281

RESULT 12
US-08-424-550B-20
; Sequence 20, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-424-550B-20

Query Match 3.0%; Score 279.4; DB 8; Length 281;
Best Local Similarity 99.6%; Pred. No. 5e-71;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6637 GCGCATGCAACTTAATTGGCTGATGCACCTTGAGACAAATGACTGTAAATCCACAAACAA 6696
Db 1 GCGCATGCAACTTAATTGGCTGATGCACCTTGAGACAAATGACTGTAAATCCATACAA 60

QY 6697 CACTCTAGTGATGAAGCGCAGTGTCCGCTCTTGTGTTTCAACAGGAGTTGCGCGGTAC 6756
D5 61 CACTCTAGTGATGAAGCGCAGTGTCCGCTCTTGTGTTTCAACAGGAGTTGCGCGGTAC 120
QY 6757 AAACCAATTTGTTGAGGCAATTTTCAAGTGTGGGTTGACACACCAAACTGCCAGCCCCCTC 6816
D5 121 AAACCAATTTGTTGAGGCAATTTTCAAGTGTGGGTTGACACACCAAACTGCCAGCCCCCTC 180
QY 6817 CATCGAAGAGGTAGTGGTTAAGAAAGCGCAGTTCCGGGCAAGAACTGGTTGCTTACCTT 6876
D5 191 CATCGAAGAGGTAGTGGTTAAGAAAGCGCAGTTCCGGGCAAGAACTGGTTGCTTACCTT 240
QY 6877 GCCTCCCTCCGAGATCCGTCCTCCAGGAGTGTGATGTCCTG 6917
D5 241 GCCTCCCTCCGAGATCCGTCCTCCAGGAGTGTGATGTCCTG 281

RESULT 13
US-10-328-127-1
; Sequence 1, Application US/10328127
; Publication No. US20030162168A1
; GENERAL INFORMATION:
; APPLICANT: Fellerin, C. and Lamarre, D.
; TITLE OF INVENTION: Surrogate cell-based system and method for assaying the
; FILE OF INVENTION: activity of Hepatitis C Virus NS3 protease
; FILE REFERENCE: 13/075-1-01
; CURRENT APPLICATION NUMBER: US/10/328,127
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/132,360
; PRIOR FILING DATE: 1999-05-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5211
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: partial cDNA
; OTHER INFORMATION: sequence of HCV (NS3-5B') fused to tTA
; OTHER INFORMATION: transactivator

US-10-328-127-1

Query Match 2.8%; Score 262.4; DB 17; Length 5211;
Best Local Similarity 49.6%; Pred. No. 2.8e-65;
Matches 733; Conservative 0; Mismatches 736; Indels 9; Gaps 2;

QY 3411 ACAAGCTGTTGATGCTGCTACCATGGCAGCAAGGGGCGCGGTGCTCATCCACAG 3470
D5 155 ACGGCGTGTGTTGGACTGTCTTCCATGCGCGCGCTCAAAGACCTTGGCGCGCCCAAG 214
QY 3471 GCTCTATACACCAATACCGTTGACGGGCTAATGACCGACATCTATCAACACCAT 3530
D5 215 GCCGATCACCAGATGTACATAATGTGACACGAGACCTCTCGGCTGGCAGGCGCCC 274
QY 3531 GTGAGCTGGGTCCCTTACTCGGTGCTCTTGGGGGAGACCAAGGGGTATCTGGTAAAC 3590
D5 275 CTGGGCGCGCTCCATGACACCATGCACTGCGGAGCTCGACCTCTATTGTTGTCAGA 334
QY 3591 GACTGGGTGCTATGGTTGAGGTCAACAAATCCGATGACCTTATTGTTGTTGTTGGGG 3650
D5 335 GACATGCCGACGTCTATTCGGTGCCTGGCGGGGCGACAGTAGGGGAGCCTGTCTGCC 394
QY 3651 CCCTTCCCATGGCTTGGCAGGGTCTTCAAGGTGCCCCGATTTGTTGCTCTCGGGC 3710
D5 395 CCAGGCGCTGTCTCTACTTTGAAGGGCTCTTGGGTGGGCCCATGTCTGTGCCCTTGGGG 454
QY 3711 ATGTTATTGGGATGTTACCGCTGCTAGAAATTTCTGGCGGTTTCAGTCAAGTATAGGG 3770
D5 455 ACGCTGTGGCATCTTCGGGCTGTGTGTGACCCGGGGGTTGAAAAGCGGTGGACT 514
QY 3771 TTAGGCGGTTGGTGTGTGATACCATCCCGAGTACACAGCATGCGCACTTTGATA 3830
D5 515 TCATACCTGTTGAGTCTATGGAAACTACTATGCGGTCTCCGGTCTTTCACAGCAACTCAT 574

QY 3831 CAAAACCTTACTGTGCTTAAACGAGTATTTCAGTGCAAAATTTTAAATTTGCCCCCTTGGCAGCG 3890
D5 575 CCCCCCAGCGGTATCCGAGACATTTCCAGTGGCCCTCTACACGCTCTTACTGCGCAGCG 634
QY 3891 GCAAGTCAACCAATATACCTTTTACATGAGGAGAAAGTATGAGTCTTTGGTCTCTAA 3950
D5 635 GCAAGAGCACATAAAGTGGCGCTGCTTATGACGAGCAAGGGTACAAAGTACTTGTCTTGA 694
QY 3951 ATCCAGTGTGGCTTACACAGCATCAATGCCAAAGTACATGACGCGAGCATGCGCGTGA 4010
D5 695 ACCCGTCCGTTTGGCGCCACCTTAGGTTTGGGGCGTATATGTCAAAGGACAGTGGCAGCG 754
QY 4011 ATCCAAATTTGCTATTTTAAATGGCAAAATGTACCAACACAGGGGCTTTCATCTTACGTACAGCA 4070
D5 755 ACCCTAACATCAGAACTGGGGTAAAGACCATCACACAGGCGCCCCCATCAGTACTCCA 814
QY 4071 CATATGGCATGTACTGACCGGAGATGTTTCCC-----GGAATATATGATGTAATCATTT 4124
D5 815 CCTATGGCAAGTTCTTGGCGACGCTGTTGCTCTGGGGGCGCTTATGACATCATAAATGT 874
QY 4125 GTGACGAATGCGATGCTACCGATGCAACACCGTGTGGGCAATGGAAAGTCTCTAAACG 4184
D5 875 GTGACGAATGCGATGCTACCGATGCAACACCGTGTGGGCAATGGAAAGTCTCTAAACG 934
QY 4185 AAGCTCCATCCAAAAATGTTAGGCTAGTGTGTTTGCACCGCTACCCCGCTCGGAGTAA 4244
D5 935 AAGCGGAGACGGCTGGAGCGCGCTTGTGCTGCTCGCACCGCTACGCTCGGAGTGG 994
QY 4245 TCCCTACACCATGCTCCAAATACTAGATTTCAATTAACCGATGAAGGCACTATCCCT 4304
D5 995 TCACGTCGCACACCCCAATATCAGGAGGTGGCGCTGTCCAACACATGAGAGATCCCT 1054
QY 4305 TTCTGGAAGAAATTAAGGAGGAAATCTGAGAGGAGGAGACCTTATCTTTGAGG 4364
D5 1055 TCTATGGCAAGGCAATCCCATCGAGGTCTCAAGGGGGGAGGCACTCTCTTTTCTGCC 1114
QY 4365 CTACCAAAAAACATGCTGATGAGCTTGTCTAACGAGTGTAGCTCGAAAGGAAATAACAGCTG 4424
D5 1115 ATTCCAAAAAGAGTGTGATGAGCTCGCGCAAGAGTCTCGGGCTCGGACTCAACGCG 1174
QY 4425 TCTCTTACTATAGGGGATGTGACATCTCAAAAAATCC---CTGAGGGCGACTGTGTAGTAG 4481
D5 1175 TAGCGTATTACCGGGCGCTTGTATGTCGCTCATACCGACGAGAGACGCTGTTGTTG 1234
QY 4482 TTGCCACTGATGCTTGTGTACAGGTACACTGTGTGACTTTGATTCCTGATGACTGCA 4541
D5 1235 TGGCAACAGACGCTTAAATACCGGCTTTACCGGCGACTTTGATTCAGTGTGACTGCA 1294
QY 4542 GCCTCATGTTAGAGGCAATGCTGATGTTGACCTTTGACCTTCTTCCACATGGGTGTTTC 4601
D5 1295 ATACGTGTTTACCGAGACAGTCTGATTTTCAAGTGGACCCCACTTCCACATTTAGAGCA 1354
QY 4602 GTGTGTGCGGGTTTTCAGCAATAGTTAAAGGCCAGCTGAGGGGCGCGACAGGCCCTGGGA 4661
D5 1355 CGACCGCTCCCTCAAGACGCGGTGTGCGCTCGACGCGGGGAGTGAAGTGAAGGAGGTA 1414
QY 4662 GAGCTGGCATATCTACTATGTAGCGGAGTTGTACCCCTTCGGGTATGGTTCCTGAAT 4721
D5 1415 GGAGAGGCAATCTACAGGTTTGTGACTCCAGGAGAACCGGCTTCGGGCAATGTTTCGATTCCT 1474
QY 4722 GCAACATTTGTTGAAGCCCTTCGACCGCAGCAAGGCAATGTTGTTGTTGTCATCAACAGAG 4781
D5 1475 CGGTCTATGTAGTGTCTATGACGGGGCTGTGCTTGTGTGTATGAGTCAAGCCGCTGAGA 1534
QY 4782 CTCAAACTATTTCTGACACCTTATCGACCCCACTGGGTATACCTCGGATAGGAGCAATTT 4841
D5 1535 CCACGCTCAGATTTGGGGCTTACCTTAAACACACAGGAGTGGCCGCTGTCTGTCAGGACCATC 1594
QY 4842 TGGACGAGTGGGCTGATCTCTTTTCTATGTTGTCACCCC 4879
D5 1595 TGGAGTCTGGGAGGGCGCTCTTTCAGGGCGCTCACCCAC 1632

Qy	4071	CATATGGCATGTACCTGACCGGAGCATGTTCC-----GGAACTATGATGTATCATTT	4121
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Qy	4125	GTGACCAATGGCCATGTACCGATGCAACACCAACCGTGTGGGCATTTGGAAAGGTCTTAACCG	4184
Db	875	GTGACGAGTGGCACTCAACTGACTCGACTACCATTTGGGCATCGGCACAGTCTCGGACC	934
Qy	4185	AAGCTCCATCCAAAAATGTTAGGCTAGTGGTCTTGGCCAGCGGTACCCCCCTCTGGAGTAA	4244
Db	935	AAGCGGAGACGGCTGGAGCGCGCTTGTGCTGCTCGCCACCGTACGCTCTCGGAGTCGG	994
Qy	4245	TCCCTACACACATGCCACATAAATGAGATTCAATTAAACCGATGAAGGCACATATCCCT	4304
Db	995	TCACCGTCCACACCCCAATATCGAGGAGTGGCCCTGTCCAACTCGAGAGATCCCT	1054
Qy	4305	TTCATTCGAAAAAGATTAAAGGAGGAAAAATCTGAAGAAAGGGAGACACCTTATCTTTGAGG	4364
Db	1055	TCATATGGCAAGCCATCCCATCGAGGTCAATCAAGGGGGGAGGCATCTCATTTCTGCC	1114
Qy	4365	CTACCAAAAAAACACTGTGTATGAGCTTGTCTAAACGATTTAGCTCGAAAGGGAATTAACAGCTG	4424
Db	1115	ATTCCAAAAAGAAAGTGTGATGAGCTCGCGCAAAAGCTGTGGGCGCTCGGACTCAACCGCG	1174
Qy	4425	TCTCTTACTATAGGGGATGTGACATCTCAAAAATCC--CTGAGGGCGACTGTGTACTAG	4481
Db	1175	TAGCGTATTACGGGGCCTTGATGTGCTCGTCAACGACCGGAGACGTGTTGTTG	1234
Qy	4482	TTGCCACTGATGCTTGTGTACAGGGTACACTCGGTGACTTTTGATTCGGTGTATGACTGCA	4541
Db	1235	TGSCAACAGACGGCTTAATGACCGGCTTTACCGGCACTTTTGATTCAGTGCATCGACTGCA	1294
Qy	4542	GCCTCATGTGTAGAGGCACATGCCATGTGTGACCTTACTTTACCATCGGTGTTTC	4601
Db	1295	ATACGTGTGTATCCACAGACAGTCGATTTACGCTTGGACCCCACTTCCACATTTGAGACGA	1354
Qy	4602	GTGTGTGCGGGTTCAGACAAATAGTTAAAGGCCAGCGTAGGGCCGCACAGGCCGTGGGA	4661
Db	1355	CGACCGTGCTCAAGACGCGGTGTCGGCTCGCAGCGGGGGTAGGACTGGCAGGGGTA	1414
Qy	4662	GAGCTGGCATATACTACTATGTAGACGGGAGTTGTACCCCTTCGGGTATGGTTCTCGAAT	4721
Db	1415	GGAGAGGCATCTACAGTTTGTACTCCAGGAGAACGGCCCTTCGGGCATGTTGATTCCT	1474
Qy	4722	GCAACATTTGTTGAAGCTTCGACGACGCCACAGGCATGTTATGTTGTCTCATCAACAGAA	4781
Db	1475	CGGTCTCTATGTGAGTGCTATGACGCGGGCTGTCTTGGTATGAGCTCACGCCCGCTGAGA	1534
Qy	4782	CTCAAACTATTCTGGACACCTATCTCGCACCAACCTCGGTTTACTTCGATAGGAGCAAAAT	4841
Db	1535	CCACGGTCAGATTGCGGGCTTACCTAAACACACAGGGTTGCCGCTCTGCAGGACCATC	1594
Qy	4842	TGGACGAGTGGGCTGATCTCTTTTCTATGCTCAACCCC	4879
Db	1595	TGGAGTTCTGGGAGGGGCTCTTCACGGGCGCTCACCCAC	1632

RESULT 15

US-11-140-379-1

; Sequence 1, Application US/11140379

; Publication No. US2005027226A1

; GENERAL INFORMATION:

; APPLICANT: Pellerin, C. and Lamarre, D.

; TITLE OF INVENTION: Surrogate cell-based system and method for assaying the

; TITLE OF INVENTION: activity of Hepatitis C Virus NS3 protease

; FILE REFERENCE: 13/075-1-D1

; CURRENT APPLICATION NUMBER: US/11/140,379

; CURRENT FILING DATE: 2005-05-27

; PRIOR APPLICATION NUMBER: US 60/132,360

; PRIOR FILING DATE: 1999-05-04

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 1
; LENGTH: 5211
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: partial cDNA
; OTHER INFORMATION: sequence of HCV (NS3-5B') fused to tTA
; OTHER INFORMATION: transactivator
US-11-140-379-1

Query Match      2.8%;   Score 262.4;   DB 26;   Length 5211;
Best Local Similarity 49.6%;   Pred. No. 2.8e-65;
Matches 733;   Conservative 0;   Mismatches 736;   Indels 9;   Gaps 2;

Qy 3411 ACAACGTTGTATACGTCTCACCATGGCAGCAAGGGCGCCGGTGGCTCATCCCNACAG 3470
Db 155 ACGGCGTGTGTGGAGCTGTCTTCATGCGCGCGGCTCAAAAGACCTTGGCGCGGCCAAAG 214
Qy 3471 GCTCTATACACCCAATAACCGTTGACCGGCTAATGACCAGGACATCTATCAACACCAT 3530
Db 215 GCCCGATCACCCAGATGTACACTAATGTGACACAGACCTCTGTCGGCTGCAGCGCGCCC 274
Qy 3531 GTGAGCTGGGTCCCTTACTCGGTGCTCTTCCGGGGAGACAAGGGGTATCTCGTAAACAC 3590
Db 275 CTGGGGCGGCTCCATGACACCATGCACTCGCGGAGCTCGGACCTCTATTTGGTCAAGA 334
Qy 3591 GACTGGGGTCATTTGGTGTAGGTCAACAAATCCGATGACCCCTTATTGGTGTGTGCGGG 3650
Db 335 GACATGCCGACGTCAATTCGGGTGCGCGGGGCGGACAGTAGGGGAGCCTGCTCTCCC 394
Qy 3651 CCCTTCCCATGGGTGTTGCCAAGGGTTCTTCAGGTGCCCGGATCTCTGTGCTCTCCGGGC 3710
Db 395 CCAGGCTGTCTCTACTTGAAGGGCTCTTCGGGTGSCCAGCTGCTGCCCCTCGGGGC 454
Qy 3711 ATGTTATTGGATGTTCAACGCTGCTAGAAATTTCTGGCGGTTTCAGTCAGTCAGATTAGG 3770
Db 455 ACGCTGTGGGCATCTTCCGGGCTCTGTGTGCAACCGGGGGGTTGCAAAAGCGGTGGACT 514
Qy 3771 TTAGGCGGTTGGTGTGTGCTGGATPACCATCCCAAGTACACAGCACATGCCACTCTTGATA 3830
Db 515 TCATACCTGTGTAGTCTATGGAAACTACTATGCGGTCTCGGTTCTCACAGACAATCAT 574
Qy 3831 CAATAACTATGTCCTTAACAGATTTTCAGTGCAAAATTTTAAATGCCCCCACTGGCAGCG 3890
Db 575 CCCCCCAGCGTACCCAGACATTCCAAGTGGGCCATCTACACGCTCTCTACTGGCAGCG 634
Qy 3891 GCAGTCAACCAATTAACCACTTCTTACATGCAGGAGAGATGAGGTCTTGGTCTCTAA 3950
Db 635 GCRAAGACATAAAGTCCGGCTCTTATGACGCCCAAGGGTCAAGGTACTTGTCTTTGA 694
Qy 3951 ATCCCAGTGTGGCTACACAGCATCAATGCCAAGTACATGCACGCGACGTAACGGCGTGA 4010
Db 695 ACCGTCGTTGCGCCACCTTAGTGTGGGGGTATATGTCAAAGGCAAGTGGCACCG 754
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Db 755 ACCCTTAAATCATCAGAACTGGGGTAAAGGACATCACACAGGCGCCCCCATCACGTACTCCA 814
Qy 4071 CATATGCACTGTACTCTGACCGGACATGTTCCC-----GSAACTATGATGTAATCATTT 4124
Db 815 CCTATGCAAGTTCCTTGGCGACGGTGTGCTCTGGGGGGCGCTTATGACATCATATGT 874
Qy 4125 GTGACGAATGCGATGTCACGATGCACACCAACCGTGTGGGCAATTTGGAAGGTCCTAACCG 4184
Db 875 GTGACGAGTGCATCAACTGACTCGACTACCATCTTGGGCATCGGCACAGTCTCTGGACC 934
Qy 4185 AAGCTCCATCCAAAATGTTAGGCTATGTTGCTTTCGCCAGGCTACCCCGCTGGAGTAA 4244
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Qy 4245 TCCTTACCAACATGCCCAACATTAAGTATCAATTTAAACCGATGAAGGCACTATCCCT 4304
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